

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 6.17442 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVPLFP 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4	44.4	11	2	I33098	173K exoantigen -
2	3	33.3	8	2	G33098	205K exoantigen -
3	3	33.3	9	2	PT0324	Ig heavy chain CRD
4	3	33.3	11	2	A57458	Gene Gax protein -
5	3	33.3	12	2	S21205	Ig heavy chain V r
6	3	33.3	12	2	S74196	3-hydroxy-3-methyl
7	3	33.3	13	2	S78766	ribosomal protein
8	3	33.3	13	2	PH0756	T-cell receptor be
9	3	33.3	13	2	I77387	AMP deaminase - ra
10	3	33.3	14	2	B36079	hypothetical prote
11	3	33.3	14	2	PL0152	metal-binding prot
12	3	33.3	14	2	A61308	hemocyanin chain 2
13	3	33.3	14	2	D61308	hemocyanin chain 5
14	3	33.3	14	2	PH1566	cerebrin 30 - huma
15	3	33.3	14	2	PH1614	Ig H chain V-D-J r
16	3	33.3	14	2	C59137	protein pf3 - gold
17	3	33.3	15	2	PA0059	protein QF200021 -
18	3	33.3	15	2	PA0080	translation elonga
19	3	33.3	15	2	S77988	cytochrome-c oxida
20	3	33.3	15	2	PH0772	T-cell receptor be
21	3	33.3	15	2	I67525	CD33 antigen homol
22	3	33.3	15	2	B59137	protein pf1 - gold
23	3	33.3	16	1	MTDFPS	melanotropin beta
24	3	33.3	16	2	T09741	photosystem I chai
25	3	33.3	16	2	PH0749	T-cell receptor be
26	3	33.3	16	2	B40291	cytochrome P450mtf
27	3	33.3	17	2	I55226	myosin heavy chain
28	3	33.3	17	2	S29165	quinaldine oxide
29	3	33.3	17	2	A61557	major merozoite su

30	33.3	17	2	S60171	sex-lethal protein
31	33.3	18	2	G02018	proteasome chain L
32	33.3	18	2	S09731	photosystem I prot
33	33.3	18	2	S36121	lectin - spurge (E
34	33.3	18	2	S40502	20-alpha-hydroxyst
35	33.3	18	2	B35910	neurofibromatosis-
36	33.3	18	2	S57518	T cell receptor be
37	33.3	19	2	PN0467	nitrogenase (EC 1.
38	33.3	19	2	B39845	pyrB leader peptid
39	33.3	19	2	S63153	Neb-collostatin -
40	33.3	19	2	A37968	neural surface pro
41	33.3	20	2	A39328	notechis II-5b non
42	33.3	20	2	C20554	hemocyanin subunit
43	33.3	4	2	A32039	tyrosine-melanocyt
44	33.3	4	2	A37832	phenol 2-monooxyge
45	33.3	4	2	S53508	starvation-induced
46	33.3	4	2	I54357	schwannomin - mous
47	33.3	5	2	A60521	glycogen phosphory
48	33.3	5	2	I40469	dnazx-like protein
49	33.3	5	2	B22565	R-phycocerythrin al
50	33.3	5	2	T14908	hypothetical prote
51	33.3	5	2	PT0308	Ig heavy chain CRD
52	33.3	5	2	JT0520	Ig kappa chain V-I
53	33.3	5	2	PT0610	T-cell receptor be
54	33.3	6	2	B34835	dnAA protein - Pse
55	33.3	6	2	A61049	halo-toxin - Pseud
56	33.3	6	2	A31263	dihydrofolate redu
57	33.3	6	2	B31263	dihydrofolate redu
58	33.3	6	2	I37263	Y protein - human
59	33.3	6	2	H48394	glycoprotein compo
60	33.3	6	2	I65546	MHC H2-L antigen -
61	33.3	7	1	XEYDGD	galactose oxidase
62	33.3	7	1	NYPG7	hypothalamic hepta
63	33.3	7	2	A60139	fatty-acid synthas
64	33.3	7	2	PH1408	Ig heavy chain V r
65	33.3	7	2	B34818	vicilin 57K chain
66	33.3	7	2	B61491	seed protein ws-5
67	33.3	7	2	I48105	dihydrofolate redu
68	33.3	7	2	I48086	DNA topoisomerase
69	33.3	7	2	A38081	amine oxidase (cop
70	33.3	7	4	I55382	hypothetical pepti
71	33.3	7	4	I56695	hypothetical L2 pr
72	33.3	8	2	PH1407	Ig heavy chain V r
73	33.3	8	2	B24749	neuropeptide B - b
74	33.3	8	2	PL0184	capsid protein vp-
75	33.3	8	2	PA0032	protein QA300040 -
76	33.3	8	2	S11078	glucose-6-phosphat
77	33.3	8	2	B33099	158K exoantigen -
78	33.3	8	2	A46306	spasmodic toxin
79	33.3	8	2	S66546	cardioacceleratory
80	33.3	8	2	B27867	homeotic protein U
81	33.3	8	2	A61328	trypsin (EC 3.4.21
82	33.3	8	2	S10783	enamelin f - bovin
83	33.3	8	2	A61597	cytochrome P450 AL
84	33.3	8	2	A42689	major postsynaptic
85	33.3	8	2	A35180	neutral proteinase
86	33.3	8	2	PC4373	telomeric and tetr
87	33.3	8	2	I57532	gene Tinslow prote
88	33.3	8	2	A25836	L-serine ammonia-1
89	33.3	8	4	I54017	granulocyte-colony
90	33.3	9	2	A91466	oxytocin - hippopo
91	33.3	9	2	A92774	oxytocin - spotted
92	33.3	9	2	A93147	oxytocin - finback
93	33.3	9	2	A93408	oxytocin - Austral
94	33.3	9	2	B90667	oxytocin - rabbit
95	33.3	9	2	A61230	calsequestrin, car
96	33.3	9	2	D28854	fibrinopeptide B -
97	33.3	9	2	E28854	fibrinopeptide B -
98	33.3	9	2	F28854	fibrinogen beta ch
99	33.3	9	2	C24180	fibrinogen beta ch
100	33.3	9	2	D24180	fibrinogen beta ch

ALIGNMENTS

RESULT 1

I33098
 C:Species: Plasmodium falciparum (fragments)
 C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C:Accession: I33098
 R:Nichols, J.H.; Hager, L.P.
 A:Title: Regulation of the Protein Sequence Database, May 1990
 A:Reference number: A33098
 A:Accession: I33098
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <NIC>

Query Match 44.4%; Score 4; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
 ||||
 Db 7 PLFP 10

RESULT 2

G33098
 C:Species: Plasmodium falciparum
 C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C:Accession: G33098
 R:Nichols, J.H.; Hager, L.P.
 A:Title: Regulation of the Protein Sequence Database, May 1990
 A:Reference number: A33098
 A:Accession: G33098
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <NIC>

Query Match 33.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
 ||||
 Db 2 VPL 4

RESULT 3

PT0324
 Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0324
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0324
 A:Molecule type: DNA
 A:Residues: 1-9 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4
 ||||
 Db 6 ESY 8

RESULT 4

A57458
 gene Gax protein - mouse (fragment)
 C:Species: Mus sp. (mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Oct-1999
 C:Accession: A57458
 R:Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.
 Mol. Cell. Biol. 15, 4272-4281, 1995
 A:Title: Regulation of Gax homeobox gene transcription by a combination of positive fact-
 A:Reference number: A57458; MUID:95349593; PMID:7623821
 A:Accession: A57458
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-11 <RES>
 A:Cross-references: GB:S79168; NID:G1050991
 C:Genetics:
 A:Gene: Gax
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 33.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
 ||||
 Db 4 PLF 6

RESULT 5

S1205
 Ig heavy chain V region - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 C:Accession: S1205
 R:Makiya, R.; Stigbrand, T.
 Eur. J. Biochem. 205, 341-345, 1992
 A:Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-
 A:Reference number: S1205; MUID:92209522; PMID:1555592
 A:Accession: S1205
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <MAK>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
 ||||
 Db 5 VES 7

RESULT 6

S74196
 3-hydroxy-3-methylglutaryl CoA synthase homolog - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 01-May-1998
 C:Accession: S74196
 R:Taketani, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Nishimura, K.; Ino
 Eur. J. Biochem. 230, 760-765, 1995
 A:Title: Induction of terminal enzymes for heme biosynthesis during differentiation of m
 A:Reference number: S65629; MUID:95331315; PMID:7607249
 A:Accession: S74196
 A:Molecule type: protein
 A:Residues: 1-12 <RAK>
 A:Experimental source: liver

Query Match 33.3%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 6 VPL 8

RESULT 7
S78766
ribosomal protein MRP-S28, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: S78766
R:Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A:Reference number: S78760
A:Accession: S78766
A:Molecule type: protein
A:Residues: 1-13 <GRA>
C:Keywords: mitochondrion
F,1-13/Product: ribosomal protein MRP-S28 (fragment) #status experimental <MAT>

Query Match 33.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 6 VES 8

RESULT 8
PH0756
T-cell receptor beta chain (I7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0756
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0756
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Cross-references: EMBL:X60850; NID:951482; PIDN:CAA43241.1; PID:951483
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 33.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
Db 10 PLF 12

RESULT 9
I77387
AMP deaminase - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I77387
R:Mineo, I.; Clarke, P.R.H.; Sabina, R.L.; Holmes, E.W.
Mol. Cell. Biol. 10, 5271-5278, 1990
A:Title: A novel pathway for alternative splicing: Identification of an RNA intermediate
A:Reference number: I57509; MUID:90377216; PMID:2398891
A:Accession: I77387
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-13 <RES>
A:Cross-references: GB:M58689; NID:9202877; PIDN:AAA40727.1; PID:9554414
C:Genetics:

A:Gene: AMPD1
A:Introns: 8/1

Query Match 33.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
Db 2 PLF 4

RESULT 10
B36079
hypothetical protein insulin-like growth factor I 5'-region - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Nov-1990 #sequence_revision 13-Sep-1991 #text_change 18-Aug-2000
C:Accession: B36079
R:Kajimoto, Y.; Rotwein, P.
Mol. Endocrinol. 4, 217-226, 1990
A:Title: Evolution of insulin-like growth factor I (IGF-I): structure and expression of
A:Reference number: A36079; MUID:90231335; PMID:2330002
A:Accession: B36079
A:Molecule type: mRNA
A:Residues: 1-14 <KAJ>
A:Cross-references: GB:M29857; NID:9214287; PIDN:AAA70329.1; PID:903887
A:Note: the authors translated the codon CAG for residue 4 as Gly
C:Superfamily: unassigned leader peptides

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
Db 5 LFP 7

RESULT 11
PL0152
metal-binding protein - reticulate massa (fragment)
C:Species: Nassarius reticulatus (reticulate massa)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 20-Jun-2000
C:Accession: PL0152
R:Andersen, R.A.; Eriksen, K.D.H.; Bakke, T.
Comp. Biochem. Physiol. B 94, 285-291, 1989
A:Title: Evidence of presence of a low molecular weight, non-metallothionein-like metal
A:Reference number: PL0152
A:Accession: PL0152
A:Molecule type: protein
A:Residues: 1-14 <AND>
C:Comment: This protein is induced in environments contaminated with heavy metal.

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
Db 11 PLF 13

RESULT 12
A61308
hemocyanin chain 2 - Sahara scorpion (fragment)
C:Species: Androctonus australis (Sahara scorpion)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C:Accession: A61308
R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
FEBS Lett. 106, 289-291, 1979
A:Title: Structural characterization of seven different subunits in Androctonus australis
A:Reference number: A61308; MUID:80047238; PMID:499512
A:Accession: A61308

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <JOL>

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8
|||
Db 11 PLF 13

RESULT 13

D61308
hemocyanin chain 5A - Sahara scorpion (fragment)
C:Species: Androctonus australis (Sahara scorpion)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C:Accession: D61308
R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
FEBS Lett. 106, 289-291, 1979
A:Title: Structural characterization of seven different subunits in Androctonus australis
A:Reference number: A61308; MUID:80047238; PMID:499512
A:Accession: D61308
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <JOL>

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8
|||
Db 11 PLF 13

RESULT 14

PH1566
cerebrin 30 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: PH1566
R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.
J. Neurochem. 61, 533-540, 1993
A:Title: Micropurification of two human cerebrospinal fluid proteins by high performance
A:Reference number: PH1566; MUID:93329419; PMID:8336140
A:Accession: PH1566
A:Molecule type: protein
A:Residues: 1-14 <LEO>

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8
|||
Db 10 PLF 12

RESULT 15

PH1614
Ig H chain V-D-J region (clone B-less 18) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1614
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1614
A:Molecule type: DNA
A:Residues: 1-14 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8
|||
Db 5 PLF 7

RESULT 16

C59137
protein Pf3 - golden needle mushroom (fragment)
C:Species: Flammulina velutipes (golden needle mushroom)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: C59137
R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
submitted to the Protein Sequence Database, November 1999
A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
A:Reference number: A59137
A:Accession: C59137
A:Molecule type: protein
A:Residues: 1-14 <SAK>

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6
|||
Db 8 YVP 10

RESULT 17

PA0059
protein QF200021 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0059
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0059
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match 33.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
|||
Db 11 VPL 13

RESULT 18

PA0080
translation elongation factor eEF-2 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0080
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0080
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: protein biosynthesis

Query Match 33.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
 |||
 Db 9 VPL 11

RESULT 19
 S77988
 cytochrome-c oxidase (EC 1.9.3.1) chain VIIa - bigeye tuna (fragment)
 C:Species: Thunnus obesus (bigeye tuna)
 C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Sep-1998
 C:Accession: S77988
 R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
 submitted to the Protein Sequence Database, June 1997
 A:Reference number: S77980
 A:Accession: S77988
 A:Molecule type: protein
 A:Residues: 1-15 <ARN>
 A:Experimental source: heart; liver
 C:Genetics:
 A:Genome: nuclear
 C:Function:
 A:Pathway: oxidative phosphorylation; respiratory chain
 C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 33.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6
 |||
 Db 3 YVP 5

RESULT 20
 PH0772
 T-cell receptor beta chain (J4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C:Accession: PH0772
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A:Reference number: PH0746; MUID:92078846; PMID:1836010
 A:Accession: PH0772
 A:Molecule type: mRNA
 A:Residues: 1-15 <CAS>
 A:Cross-references: EMBL:X60866; NID:g52749; PIDN:CAA43256.1; PID:g52750
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 33.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
 |||
 Db 12 PLF 14

RESULT 21
 I67525
 CD33 antigen homolog - mouse (fragment)
 C:Species: Mus sp. (mouse)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Jun-1998
 C:Accession: I67525
 R:Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
 Eur. J. Immunol. 24, 1657-1664, 1994
 A:Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is n

A:Reference number: I53392; MUID:94298870; PMID:8026526
 A:Accession: I67525
 A>Status: preliminary; translated from GB/EMBL/DBBJ
 A:Molecule type: mRNA
 A:Residues: 1-15 <RES>
 A:Cross-references: GB:S71349; NID:g550037
 C:Genetics:
 A:Gene: Ig VH7183

Query Match 33.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYV 5
 |||
 Db 11 SYV 13

RESULT 22
 B59137
 protein Pf1 - golden needle mushroom (fragment)
 C:Species: Flamulina velutipes (golden needle mushroom)
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: B59137
 R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
 submitted to the Protein Sequence Database, November 1999
 A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
 A:Reference number: A59137
 A:Accession: B59137
 A:Molecule type: protein
 A:Residues: 1-15 <SAK>
 A:Experimental source: strain FV-4

Query Match 33.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6
 |||
 Db 8 YVP 10

RESULT 23
 MDPFBS
 melanotropin beta - spiny dogfish
 C:Species: Squalus acanthias (spiny dogfish)
 C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
 C:Accession: A01471
 R:Bennett, H.P.J.; Lowry, P.J.; McMartin, C.; Scott, A.P.
 Biochem. J. 141, 439-444, 1974
 A:Title: Structural studies of alpha-melanocyte-stimulating hormone and a novel beta-me
 A:Reference number: A90277; MUID:75127390; PMID:4375978
 A:Accession: A01471
 A:Molecule type: protein
 A:Residues: 1-16 <BEN>
 C:Superfamily: corticotropin-lipotropin
 C:Keywords: hormone

Query Match 33.3%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
 |||
 Db 14 VPL 16

RESULT 24
 T09741
 photosystem I chain psaI - upland cotton chloroplast (fragment)
 C:Species: chloroplast Gossypium hirsutum (upland cotton)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T09741

R;Small, R.L.; Ryburn, J.A.; Cronn, R.C.; Seelanan, T.; Wendel, J.F.

Am. J. Bot. 85, 1301-1315, 1998

A;Title: The tortoise and the hare: choosing between noncoding plastome and nuclear Adh

A;Reference number: Z16323

A;Accession: T09741

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-16 <SMA>

A;Cross-references: EMBL:AF031581; NID:g2623684; PID:g3723945

C;Genetics:

A;Gene: psal

A;Genome: chloroplast

C;Keywords: chloroplast; photosynthesis; photosystem I

Query Match 33.3%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7

|||

12 VPL 14

Db

RESULT 25

PH0749

T-cell receptor beta chain (B83) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C;Accession: PH0749

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I

allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0749

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>

A;Cross-references: EMBL:X60840; NID:g501116; PIDN:CAA43233.1; PID:g50117

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 33.3%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8

|||

13 PLF 15

Db

RESULT 26

B40291

cytochrome P450mtf - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 30-Sep-1993

C;Accession: B40291

R;Addya, S.; Zheng, Y.M.; Shavik, R.M.; Fan, J.; Avadhani, N.G.

Biochemistry 30, 8323-8330, 1991

A;Title: Characterization of a female-specific hepatic mitochondrial cytochrome P-450 wh

A;Reference number: A40291; MUID:91355184; PMID:1883820

A;Accession: B40291

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <ADD>

Query Match 33.3%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9

|||

14 LFP 16

Db

RESULT 27

I55226

myosin heavy chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C;Accession: I55226

R;Meydert, A.; Daubas, P.; Catavatti, M.; Minty, A.; Bugalsky, G.; Cohen, A.; Robert, B.

J. Biol. Chem. 258, 13867-13874, 1983

A;Title: Sequential accumulation of mRNAs encoding different myosin heavy chain isoforms

in fast myosin heavy chain from mouse skeletal muscle.

A;Reference number: I55226; MUID:84061805; PMID:6196357

A;Accession: I55226

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-17 <RES>

A;Cross-references: GB:K00986; NID:g199975; PIDN:AAA39792.1; PID:g199979

C;Superfamily: myosin heavy chain; myosin motor domain homology

Query Match 33.3%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3

|||

7 VES 9

Db

RESULT 28

S29165

quinolindine oxidoreductase (BC 1.5.99.-) alpha chain - Arthrobacter sp. (isolate Rue 61a)

C;Species: Arthrobacter sp.

A;Variety: isolate Rue 61a

C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C;Accession: S29165

R;de Beyer, A.; Lingens, F.

Biol. Chem. Hoppe-Seyler 374, 101-110, 1993

A;Title: Microbial metabolism of quinoline and related compounds. XVI. Quinaldine oxidoreductase.

A;Reference number: S29165; MUID:93228843; PMID:8471177

A;Accession: S29165

A;Molecule type: protein

A;Residues: 1-17 <BEV>

A;Experimental source: isolate Rue 61a

C;Complex: heterohexamer; two alpha, two beta and two gamma chains

C;Function:

A;Description: catalyzes the oxidation of quinaldine to 1H-4-oxoquinaldine

A;Pathway: quinaldine degradation

C;Keywords: FAD; flavoprotein; heterohexamer; molybdopterin; oxidoreductase

Query Match 33.3%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3

|||

1 VES 3

Db

RESULT 29

A61557

major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (strain FCB-1

C;Species: Plasmodium falciparum

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000

C;Accession: A61557

R;Heidrich, H.G.

Biol. Cell 64, 205-214, 1988

A;Title: Isolation and functional characterization of Plasmodium falciparum merozoite an

A;Reference number: A61557; MUID:89150734; PMID:3067799

A;Accession: A61557

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <HEI>

C;Keywords: surface antigen

Query Match 33.3%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4
|||
Db 4 ESY 6

RESULT 30

S60171
sex-lethal protein - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 17-Mar-1999
C;Accession: S60171
R;Hoshijima, K.; Kohyama, A.; Watakabe, I.; Inoue, K.; Sakamoto, H.; Shimura, Y.
Nucleic Acids Res. 23, 3441-3448, 1995
A;Title: Transcriptional regulation of the Sex-lethal gene by helix-loop-helix proteins.
A;Reference number: S60171; MUID:96032836; PMID:7567454
A;Accession: S60171
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-17 <HOS>
A;Cross-references: EMBL:D50435
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C;Genetics:
A;Gene: FlyBase:Sxl
A;Cross-references: FlyBase:FBgn0003659

Query Match 33.3%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
|||
Db 5 VPL 7

RESULT 31

G02018
proteasome chain LMP7 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 22-Jun-1999
C;Accession: G02018
R;Kim, T.

submitted to the EMBL Data Library, July 1995
A;Reference number: G09054
A;Accession: G02018
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-18 <KIM>
A;Cross-references: EMBL:U32862; NID:g1045468; PIDN:AAA80234.1; PID:g1045469
C;Genetics:
A;Gene: LMP7
C;Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 33.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
|||
Db 11 VES 13

RESULT 32

S09731
photosystem I protein psal - spinach chloroplast (fragment)
C;Species: chloroplast Spinacia oleracea (spinach)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 19-Jan-1996
C;Accession: S09731

R;Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.
FEBS Lett. 263, 274-278, 1990

A;Title: Polypeptide composition of higher plant photosystem I complex. Identification of
A;Reference number: S09730; MUID:90242987; PMID:2185953

A;Accession: S09731
A;Molecule type: protein
A;Residues: 1-18 <IKE>
C;Genetics:
A;Gene: psal

A;Genome: chloroplast
C;Superfamily: photosystem I protein psal
C;Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I; thylakoid

Query Match 33.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
|||
Db 8 VPL 10

RESULT 33

S36121
lectin - spurge (Euphorbia characias)
C;Species: Euphorbia characias
C;Date: 09-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C;Accession: S36121
R;Stilpe, F.; Licastro, F.; Morini, M.C.; Parente, A.; Savino, G.; Abbondanza, A.; Boloc
Biochim. Biophys. Acta 1158, 33-39, 1993
A;Title: Purification and partial characterization of a mitogenic lectin from the latex
A;Reference number: S36120; MUID:93357266; PMID:8353129
A;Accession: S36121
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <SNI>

Query Match 33.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4
|||
Db 2 ESY 4

RESULT 34

S40502
20-alpha-hydroxysteroid dehydrogenase - Tetrahymena pyriformis
C;Species: Tetrahymena pyriformis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-Dec-1999
C;Accession: S40502
R;Inazu, A.; Sato, K.; Nakayama, T.; Deyashiki, Y.; Hara, A.; Nozawa, Y.
Biochem. J. 297, 195-200, 1994
A;Title: Purification and characterization of a novel dimeric 20-alpha-hydroxysteroid dehydrogenase from Tetrahymena pyriformis
A;Reference number: S40502; MUID:94107273; PMID:8280099
A;Accession: S40502
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <INA>
C;Genetics:
A;Genetic code: SGC5

Query Match 33.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
|||
Db 5 VPL 7

RESULT 35

B35910
neurofibromatosis-related protein NF1, long splice form - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 29-Aug-1997
C:Accession: B35910
R:Cawthon, R.M.; Weiss, R.; Xu, G.; Viskochil, D.; Culver, M.; Stevens, J.; Robertson, M.
Cell 62, 608b, 1990
A:Reference number: A35910
A:Accession: B35910
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-18 <CAW>
C:Genetics:
A:Gene: GDB:NFI
A:Cross-references: GDB:120231; OMIM:162200
A:Map position: 17q11.2-17q11.2
C:Keywords: alternative splicing; tumor suppressor

Query Match 33.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9
|||
Db 14 LFP 16

RESULT 36
S57518
T cell receptor beta chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57518
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argast, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A:Reference number: S57494
A:Accession: S57518
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-18 <BUR>
A:Cross-references: EMBL:Z49920; NID:g887490; PIDN:CAA90166.1; PID:g887491
C:Keywords: T-cell receptor

Query Match 33.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9
|||
Db 5 LFP 7

RESULT 37
PN0467
nitrogenase (EC 1.18.6.1) molybdenum-iron protein alpha chain - Azotobacter chroococcum
C:Species: Azotobacter chroococcum
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: PN0467
R:Jones, R.; Woodley, P.; Birkmann-Zinoni, A.; Robson, R.L.
Gene 123, 145-146, 1993
A:Title: The nifH gene encoding the Fe protein Component of the molybdenum nitrogenase f
A:Reference number: JN0516; MUID:93138425; PMID:8423000
A:Accession: PN0467
A:Molecule type: DNA
A:Residues: 1-19 <JON>
A:Cross-references: GB:M73020; NID:g142326; PIDN:AAA22141.1; PID:g289238
C:Genetics:
A:Gene: nifD
C:Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain
C:Keywords: ATP; nitrogen fixation; oxidoreductase

Query Match 33.3%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3
|||
Db 9 VES 11

RESULT 38
B39845
pyrB leader peptide - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 12-Dec-1997
R:Quinn, C.L.; Stephenson, B.T.; Switzer, R.L.
J. Biol. Chem. 266, 9113-9127, 1991
A:Title: Functional organization and nucleotide sequence of the Bacillus subtilis pyrimi
A:Reference number: A39845; MUID:91225016; PMID:1709162
A:Accession: B39845
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-19 <QUI>
A:Cross-references: GB:M59757
C:Superfamily: unassigned leader peptides

Query Match 33.3%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8
|||
Db 10 PLF 12

RESULT 39
S69153
Neb-colloostatin - flesh fly (Sarcophaga bullata)
C:Species: Sarcophaga bullata
C:Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 19-May-2000
R:Bylemans, D.; Proost, P.; Samijn, B.; Borovsky, D.; Grauwels, L.; Huybrechts, R.; van
Eur. J. Biochem. 228, 45-49, 1995
A:Title: Neb-colloostatin, a second folliculastain of the grey fleshfly, Neobellieria bu
A:Reference number: S69153; MUID:95188911; PMID:7883009
A:Accession: S69153
A:Molecule type: protein
A:Residues: 1-19 <BYL>

Query Match 33.3%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
|||
Db 3 VPL 5

RESULT 40
A37968
neural surface protein Bravo - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 15-Aug-1997
C:Accession: A37968; A36345
R:de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
J. Cell Biol. 112, 1049, 1991
A:Reference number: A37968; MUID:91154309; PMID:1999455
A:Contents: erratum
A:Accession: A37968
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19
R:de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
J. Cell Biol. 111, 3087-3096, 1990

A:Title: Topologically restricted appearance in the developing chick retinotectal system
 A:Reference number: A36345; MUID:91100421; PMID:2269667
 A:Accession: A36345
 A:Molecule type: protein
 A:Residues: 1-7,9-19 <DE2>

Query Match 33.3%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
 |||
 Db 3 VPL 5

RESULT 41

A39328

notechis II-5b nontoxic venom protein - common tiger snake (fragment)
 C:Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)
 C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 30-Sep-1993
 C:Accession: A39328
 R:fang, C.C.; Chang, L.S.; Wu, F.S.
 Toxicon 29, 1337-1344, 1991

A:Title: Venom constituents of Notechis scutatus scutatus (Australian tiger snake) from
 A:Reference number: A39328; MUID:92263371; PMID:1814009

A:Accession: A39328
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <YAN>
 C:Superfamily: phospholipase A2

Query Match 33.3%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
 |||
 Db 18 PLF 20

RESULT 42

C20554

hemocyanin subunit IIA - Atlantic horseshoe crab (fragment)
 C:Species: Limulus polyphemus (Atlantic horseshoe crab)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-May-1997
 C:Accession: C20554

R:Lamy, J.; Lamy, J.; Sizaret, P.Y.; Billiard, P.; Jolles, P.; Jolles, J.; Feldmann, R.J.
 Biochemistry 22, 5573-5583, 1983
 A:Title: Quaternary structure of Limulus polyphemus hemocyanin.
 A:Reference number: A90478

A:Accession: C20554
 A:Molecule type: protein
 A:Residues: 1-20 <LAM>
 C:Comment: Limulus polyphemus hemocyanin is an association of eight different subunits

Query Match 33.3%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
 |||
 Db 11 PLF 13

RESULT 43

A32039

tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000

C:Accession: A32039
 R:Horvath, A.; Kastin, A.J.
 J. Biol. Chem. 264, 2175-2179, 1989

A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor
 A:Reference number: A32039; MUID:89123285; PMID:2563371
 A:Accession: A32039
 A:Molecule type: protein
 A:Residues: 1-4 <HOR>

A:Experimental source: brain
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end
 F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 22.2%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
 |||
 Db 2 PL 3

RESULT 44

A37832

phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (fragment)
 C:Species: Pseudomonas sp.

C:Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993
 C:Accession: A37832

R:Powlowski, J.; Shingler, V.
 J. Bacteriol. 172, 6834-6840, 1990

A:Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydroxyl
 A:Reference number: A37832; MUID:91072231; PMID:2254259

A:Accession: A37832
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-4 <POW>
 C:Keywords: oxidoreductase

Query Match 22.2%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
 |||
 Db 1 SY 2

RESULT 45

S53508

starvation-induced ribonuclease - tomato
 C:Species: Lycopersicon esculentum (tomato)

C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
 C:Accession: S53508

R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
 Plant Mol. Biol. 27, 477-485, 1995

A:Title: cDNA structure and regulatory properties of a family of starvation-induced ribo
 A:Reference number: S53508; MUID:95201242; PMID:7894013

A:Accession: S53508
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-4 <ROE>

Query Match 22.2%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FP 9
 |||
 Db 1 FP 2

RESULT 46

I54357

schwannomin - mouse (fragment)
 C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

```

C;Accession: I54357
R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co
A;Reference number: I54357; MUID:95072570; PMID:7981675
A;Accession: I54357
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-4 <RES>
A;Cross-references: GB:L28838; NID:9454836; PIDN:AAA57150.1; PID:g601923
C;Genetics:
A;Gene: NF2

Query Match      22.2%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VP 6
      ||
Db      1 VP 2

RESULT 47
A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N;Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A;Reference number: A60521; MUID:90227907; PMID:2103669
A;Accession: A60521
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Superfamily: phosphorylase
A;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VP 6
      ||
Db      4 VP 5

RESULT 48
I40469
dnaX-like protein - Bacillus subtilis (fragment)
C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C;Accession: I40469
R;Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
Mol. Gen. Genet. 215, 478-482, 1989
A;Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
A;Reference number: I40469; MUID:89218958; PMID:2468993
A;Accession: I40469
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g4376204
C;Genetics:
A;Start codon: GTG

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SY 4
      ||

C;Accession: I54357
R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co
A;Reference number: I54357; MUID:95072570; PMID:7981675
A;Accession: I54357
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-4 <RES>
A;Cross-references: GB:L28838; NID:9454836; PIDN:AAA57150.1; PID:g601923
C;Genetics:
A;Gene: NF2

Query Match      22.2%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VP 6
      ||
Db      1 VP 2

RESULT 49
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastrocloonium coulteri) (fragment)
C;Species: Gastrocloonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: B22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: B22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VP 6
      ||
Db      3 VP 4

RESULT 50
TI4908
hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: TI4908
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weishaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Accession: TI4908
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-5 <KIR>
A;Cross-references: EMBL:Y10809; NID:g3336901; PIDN:CAA71767.1; PID:g3336902
A;Experimental source: Hamburger Schnitt

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VE 2
      ||
Db      4 VE 5

RESULT 51
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0308
R;Yanada, M.; Wasserman, R.; Reichard, B.A.; Shaue, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0308
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
A;Keywords: heterotetramer; immunoglobulin

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ES 3
      ||

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Db          3 ES 4
Query Match 22.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 52
JT0520
Ig kappa chain V-III region (SD1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 16-Aug-1996
C:Accession: JT0520
R:Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A:Reference number: JT0511; MUID:89279157; PMID:2786547
A:Accession: JT0520
A:Molecule type: mRNA
A:Residues: 1-5 <ANK>
A>Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
A:Title: a stop codon terminates the sequence in the V region
C:Keywords: heterotetramer; immunoglobulin
F:1-5/Domain: V kappa region <VRE>

Query Match 22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 ES 3
Db          2 ES 3

RESULT 53
PT0610
T-cell receptor beta chain V-D-J region (100-2E) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0610
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0610
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <VEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 ES 3
Db          4 ES 5

RESULT 54
B34835
dnaA protein - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C:Accession: B34835
R:Fee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
A:Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Escherichia coli
A:Reference number: A34835; MUID:90160310; PMID:2106132
A:Accession: B34835
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <VEE>
A:Cross-references: GB:M30125; NID:g151419; PIDN:AA25916.1; PID:g151421
C:Keywords: DNA binding

Query Match 22.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 ES 3
Db          4 ES 5

RESULT 57
B31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
C:Species: Plasmodium falciparum
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: B31263
R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886; PMID:2904149
A:Accession: B31263
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 22.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 ES 3
Db          4 ES 5

RESULT 55
A61049
halo-toxin - Pseudomonas syringae pv. mori
C:Species: Pseudomonas syringae pv. mori
A>Note: host mulberry tree
C:Accession: A61049
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;
Chem. Lett. 00, 679-680, 1989
A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syringae
A:Reference number: A61049
A:Accession: A61049
A:Molecule type: protein
A:Residues: 1-6 <KAJ>
A>Note: sequence confirmed by synthesis
C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry
C:Keywords: toxin

Query Match 22.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8 FP 9
Db          2 FP 3

RESULT 56
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
C:Species: Plasmodium falciparum
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886; PMID:2904149
A:Accession: A31263
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

```

A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-6 <PET>
 C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 22.2%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ES 3
 ||
 Db 4 ES 5

RESULT 58

I37263

Y protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999

C;Accession: I37263

R;Maeder, G.; Habener, J.F.

Endocrinology 131, 2010-2015, 1992

A;Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternative

A;Reference number: I37263; MUID:93010691; PMID:1396344

A;Accession: I37263

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-6 <RES>

A;Cross-references: EMBL:X68994; NID:G396171; PIDN:CAA48780.1; PID:G579816

C;Genetics:

A;Gene: CREB

Query Match 22.2%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LF 8
 ||
 Db 2 LF 3

RESULT 59

H48394

glycoprotein component 16/major fat-globule membrane protein/WFG-E8 homolog - bovine (fr

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997

C;Accession: H48394

R;Mather, I.H.; Banghart, L.R.; Lane, W.S.

Biochem. Mol. Biol. Int. 29, 545-554, 1993

A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig

II-like sequences.

A;Reference number: A48394; MUID:93250576; PMID:8485470

A;Accession: H48394

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-6 <MAT>

A;Experimental source: milk

A;Note: sequence extracted from NCBI backbone (NCBIP:131518)

C;Keywords: Glycoprotein

Query Match 22.2%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VE 2
 ||
 Db 1 VE 2

RESULT 60

I65546

MHC H2-L antigen - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C;Accession: I65546
 R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
 Cell 44, 261-272, 1986

A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their
 A;Reference number: I52778; MUID:86106202; PMID:3510743

A;Accession: I65546

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-6 <RES>

A;Cross-references: GB:M12483; NID:G199565; PIDN:AAA9663.1; PID:G554234

Query Match 22.2%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VP 6
 ||
 Db 2 VP 3

RESULT 61

XEYDGD

galactose oxidase inhibitor - fungus (Cladobotryum dendroides)

C;Species: Cladobotryum dendroides

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993

C;Accession: A01341

R;Avigad, G.; Markus, Z.

Fed. Proc. 31, 447, 1972

A;Reference number: A01341

A;Accession: A01341

A;Molecule type: protein

A;Residues: 1-7 <AVI>

C;Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase
 apoenzyme, may inactivate the enzyme by binding to its prosthetic copper group.

C;Superfamily: galactose oxidase inhibitor

C;Keywords: copper

Query Match 22.2%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ES 3
 ||
 Db 6 ES 7

RESULT 62

NYPG7

hypothalamic heptapeptide - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 23-Aug-1996

C;Accession: A01417

R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, I

Horm. Metab. Res. 13, 228-232, 1981

A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-release

A;Reference number: A01417; MUID:81213980; PMID:6263778

A;Accession: A01417

A;Molecule type: protein

A;Residues: 1-7 <CHA>

C;Superfamily: hypothalamic heptapeptide

C;Keywords: hypothalamus

Query Match 22.2%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SY 4
 ||
 Db 5 SY 6

RESULT 63

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A60139
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
C:Accession: A60139
R:Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
Biochim. Biophys. Acta 828, 380-382, 1985
A:Title: Amino acid sequence around the reactive serine residue of the thioesterase domain
A:Reference number: A60139; MUID:85175165; PMID:3921056
A:Accession: A60139
A:Molecule type: protein
A:Residues: 1-7 <HAR>
C:Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homodimer;
hydrolase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] S-
C:Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enz
F:5/Active site: Ser [of oleoyl-[acyl-carrier-protein] hydrolase] #status experimental
Query Match 22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 5 SY 6

RESULT 64
PH1408
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PH1408; PH1405
R:Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Taniguchi, M.
J. Exp. Med. 176, 1209-1214, 1992
A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
ia virus.
A:Reference number: PH1403; MUID:93018837; PMID:1402663
A:Accession: PH1408
A:Molecule type: DNA
A:Residues: 1-7 <SH1>
A:Experimental source: clone micro m+ 46-12-2
A:Accession: PH1405
A:Molecule type: DNA
A:Residues: 1-7 <SH12>
A:Experimental source: clone micro m+ 46-6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FP 9
DB 6 FP 7

RESULT 65
B34818
vicilin 57K chain - pigeon pea (fragment)
C:Species: Cajanus cajan (pigeon pea)
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C:Accession: B34818
R:Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A:Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A:Reference number: A34818; MUID:90165956; PMID:2306256
A:Accession: B34818
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAW>

Query Match 22.2%; Score 2; DB 2; Length 7;

A60139
seed protein ws-5 - winged bean (fragment)
C:Species: Psophocarpus tetragonolobus (winged bean)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C:Accession: E61491
R:Hiirano, H.
J. Protein Chem. 8, 115-130, 1989
A:Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional
A:Reference number: A61491; MUID:89351606; PMID:2765119
A:Accession: E61491
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <HIR>
C:Keywords: glycoprotein; seed

Query Match 22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 3 VP 4

RESULT 67
I48105
dihydrofolate reductase - Chinese hamster (fragment)
C:Species: Crictetus griseus (Chinese hamster)
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C:Accession: I48105
R:Azizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
Biochemistry 25, 6228-6236, 1986
A:Title: Nucleotide sequence and nuclease hypersensitivity of the Chinese hamster dihydrofolate reductase
A:Reference number: I48105; MUID:87076541; PMID:3024702
A:Accession: I48105
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <RES>
A:Cross-references: GB:M14771; NID:g191055; PIDN:AAA36975.1; PID:g191056

Query Match 22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
DB 4 PL 5

RESULT 68
I48086
DNA topoisomerase II alpha - Chinese hamster (fragment)
C:Species: Crictetus griseus (Chinese hamster)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I48086
R:Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.
J. Biol. Chem. 270, 25850-25858, 1995
A:Title: Molecular cloning and characterization of the promoter for the Chinese hamster
A:Reference number: I48086; MUID:96029684; PMID:7592770
A:Accession: I48086
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <RES>
A:Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232

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Query Match      22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PL 7
      ||
Db      5 PL 6

RESULT 69
A38081
A:Title: amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (Pichia angusta) (fragment)
C:Species: Pichia angusta
C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000
C:Accession: A38081
R;Mu, D.; Janes, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Klinman, J.P.
J. Biol. Chem. 267, 7979-7982, 1992
A:Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine o
A:Reference number: A38081; MUID:92235001; PMID:1569055
A:Accession: A38081
A:Molecule type: protein
A:Residues: 1-7 <DAW>
C:Keywords: copper; oxidoreductase; quinoprotein; topaquinone
F;4/Modified site: topaquinone (Tyr) #status experimental

Query Match      22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YV 5
      ||
Db      6 YV 7

RESULT 70
I55382
hypothetical peptide PALL promoter region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 20-Apr-2000
C:Accession: I55382
R;Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.
J. Biol. Chem. 268, 10739-10745, 1993
A:Title: The two allele sequences of a common polymorphism in the promoter of the plasmi
A:Reference number: I55382; MUID:93226509; PMID:8398372
A:Accession: I55382
A:Status: translation not shown; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-7 <DAW>
A:Cross-references: GB:M91557; NID:g190020; PIDN:AAA60110.1; PID:g190021
C:Comment: This is the hypothetical translation of a sequence from the PALL gene promote
C:Genetics:
A:Gene: GDB:PALL
A:Cross-references: GDB:I20297; OMIM:173360
A:Map position: 7q21.3-7q22

Query Match      22.2%; Score 2; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ES 3
      ||
Db      5 ES 6

RESULT 71
I56695
hypothetical L2 protein (mistranslated) - human papillomavirus type 16 (fragment)
C:Species: human papillomavirus type 16
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C:Accession: I56695
R;Schneider-Maunoury, S.; Croissant, O.; Orth, G.
J. Virol. 61, 3295-3298, 1987

A:Title: Integration of human papillomavirus type 16 DNA sequences: a possible early ever
A:Reference number: I56695; MUID:87311896; PMID:3041049
A:Accession: I56695
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-7 <SCH>
A:Cross-references: GB:M30709; NID:g190253; PIDN:AAA65995.1; PID:g553616
C:Comment: This is the hypothetical translation of a viral sequence integrated into the l
C:Comment: It is translated in an incorrect, -1, reading frame of the L2 protein.

Query Match      22.2%; Score 2; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SY 4
      ||
Db      2 SY 3

RESULT 72
PH1407
Ig heavy chain V region (clone micro m+ 46-6 PCR) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PH1407
R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Tan
J. Exp. Med. 176, 1209-1214, 1992
A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in t
ia virus.
A:Reference number: PH1403; MUID:93018837; PMID:1402663
A:Accession: PH1407
A:Molecule type: DNA
A:Residues: 1-8 <SHI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match      22.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 FP 9
      ||
Db      7 FP 8

RESULT 73
B24749
neuropeptide B - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
C:Accession: B24749
R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b;
A:Reference number: A94074; MUID:86067985; PMID:3865193
A:Accession: B24749
A:Molecule type: protein
A:Residues: 1-8 <IAM>
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide

Query Match      22.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LF 8
      ||
Db      2 LF 3

RESULT 74
PL0184
capsid protein VP-1 - murine poliovirus (fragment)

```

C;Species: murine poliovirus, Theiler's encephalomyelitis virus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C;Accession: PL0184
R;Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.
J. Exp. Med. 170, 2037-2049, 1989
A;Title: Alteration of amino acid 101 within capsid protein VP-1 changes the pathogenicity
A;Reference number: PL0184; MUID:90063468; PMID:2479706
A;Accession: PL0184
A;Molecule type: genomic RNA
A;Residues: 1-8 <ZUR>
C;Keywords: capsid protein

Query Match 22.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FP 9
Db 7 FP 8

RESULT 75

PA0032
protein QA300040 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0032
R;Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JFID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A;Reference number: PA0001
A;Accession: PA0032
A;Molecule type: protein
A;Residues: 1-8 <KAM>
A;Experimental source: stem

Query Match 22.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LP 8
Db 2 LP 3

Search completed: November 25, 2003, 19:36:13
Job time : 6.1742 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 3.19186 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVPLFP 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	44.4	9	UPA3_HUMAN	P30089 homo sapien
2	3	33.3	15	COXJ_THUOB	P80979 thunnus obe
3	3	33.3	15	PH2_PBRAM	P82695 periplaneta
4	3	33.3	16	MLB_SQUAC	P01207 squalus aca
5	3	33.3	17	PH3_PBRAM	P82896 periplaneta
6	3	33.3	18	AGI_EUPCH	P33888 euphorbia c
7	3	33.3	18	AND2_TETPY	P35430 tetrahymena
8	3	33.3	18	ALL2_CVDPO	P82153 cydia pomon
9	3	33.3	19	COOT_GARBU	Q09148 sarcophaga
10	3	33.3	19	LPGE_ECOLI	P33236 escherichia
11	2	22.2	5	PAR2_PARMA	P81864 pardachirus
12	2	22.2	6	EI01_LITRU	P82096 litoria rub
13	2	22.2	6	VP19_HSVIK	P01153 sus scrofa
14	2	22.2	7	HY7_PIG	P01153 sus scrofa
15	2	22.2	7	IGA0_DACDE	P06294 dactylium d
16	2	22.2	7	MNP1_LEPDE	P42984 leptinotars
17	2	22.2	7	PPH2_LYCES	P83379 lycopersico
18	2	22.2	7	TPFY_PACDA	P83455 pachymedusa
19	2	22.2	8	ALL6_CARMA	P81919 carcinus ma
20	2	22.2	8	ALL6_CVDPO	P82157 cydia pomon
21	2	22.2	8	CAD1_ENTPA	P13268 enterococcu
22	2	22.2	8	FUSS_FUSSO	P81010 fusarium so
23	2	22.2	8	NPB_BOVIN	P15507 bos taurus
24	2	22.2	8	PK3_PBRAM	P82618 periplaneta
25	2	22.2	8	UPA1_HUMAN	P30087 homo sapien
26	2	22.2	8	VGLG_HSV2B	P81780 herpes simp
27	2	22.2	9	COXE_THUOB	P80975 thunnus obe
28	2	22.2	9	FAR9_ASCSU	P43172 ascaris suu
29	2	22.2	9	FIBB_ERYPA	P19346 erythrocebu
30	2	22.2	9	FIBB_MACFU	P19345 macaca fusc
31	2	22.2	9	FIBB_PAPAN	P19344 papio anubi
32	2	22.2	9	FIBB_PAPHA	P19343 papio hamad
33	2	22.2	9	FIBB_THEGE	P19342 theropithec

34	2	22.2	9	1	FLA2_TREHY	P80159 treponema h
35	2	22.2	9	1	LMT3_LOCM1	P41489 locusta mig
36	2	22.2	9	1	NEUU_CAVPO	P34966 cavia porce
37	2	22.2	9	1	OXYA_SQUAC	P42999 squalus aca
38	2	22.2	9	1	OXYT_RABIT	P32878 oryctolagus
39	2	22.2	9	1	PGLR_DIAAB	P81179 diaprepes a
40	2	22.2	9	1	RT33_BOVIN	P82926 bos taurus
41	2	22.2	9	1	SAMP_MUSCA	P19095 mustelus ca
42	2	22.2	9	1	ULAE_HUMAN	P31931 homo sapien
43	2	22.2	9	1	UN19_CLOPA	P81355 clostridium
44	2	22.2	9	1	UPA7_HUMAN	P30093 homo sapien
45	2	22.2	10	1	ANG1_BOTJA	Q10581 bothrops ja
46	2	22.2	10	1	ANGT_BOVIN	P01017 bos taurus
47	2	22.2	10	1	ANGT_CHICK	P01018 gallus gall
48	2	22.2	10	1	APF_GAPGI	P80474 capnocytoph
49	2	22.2	10	1	BPP_VIPAS	P31351 vipera aspi
50	2	22.2	10	1	BRK_ONCMY	Q9PRZ1 oncorhynch
51	2	22.2	10	1	COXA_ONCMY	P80328 oncorhynch
52	2	22.2	10	1	COXH_ONCMY	P80331 oncorhynch
53	2	22.2	10	1	COXK_ONCMY	P80332 oncorhynch
54	2	22.2	10	1	GAJU_HUMAN	P01358 homo sapien
55	2	22.2	10	1	GON1_ALLMI	P37041 alligator m
56	2	22.2	10	1	GON3_ONCKE	P20367 oncorhynch
57	2	22.2	10	1	LPK2_LOCM1	P41488 locusta mig
58	2	22.2	10	1	NS1_MYCTU	P11135 mycobacteri
59	2	22.2	10	1	ODP2_BOVIN	P11180 bos taurus
60	2	22.2	10	1	PVK_LOCM1	P83382 locusta mig
61	2	22.2	10	1	QSOB_COMTE	P80465 comamonas t
62	2	22.2	10	1	SIAP_BACTG	P49325 bacillus th
63	2	22.2	10	1	TKL2_LOCM1	P16224 locusta mig
64	2	22.2	10	1	TRP7_LEUMA	P81739 leucophaea
65	2	22.2	10	1	UHA3_HUMAN	P40930 homo sapien
66	2	22.2	10	1	UPA4_HUMAN	P30090 homo sapien
67	2	22.2	10	1	UPA8_HUMAN	P30094 homo sapien
68	2	22.2	10	1	URE3_MORMO	P17339 morganella
69	2	22.2	11	1	ANGT_CRIGE	P09037 crinia geor
70	2	22.2	11	1	EPG_CLOPA	P81350 clostridium
71	2	22.2	11	1	HS70_PINPS	P81672 pinus pinas
72	2	22.2	11	1	MLG_THETS	P41989 theromyzon
73	2	22.2	11	1	MORN_HUMAN	P01163 homo sapien
74	2	22.2	11	1	NUHM_CANFA	P49820 canis fami
75	2	22.2	11	1	POQC_PSEFL	P55173 pseudomonas
76	2	22.2	11	1	TIN4_HOPTI	P82654 hoplobatr
77	2	22.2	12	1	LMT1_LOCM1	P22395 locusta mig
78	2	22.2	12	1	NUDM_CANFA	P54713 canis fami
79	2	22.2	12	1	PAZ1_MICFM	P25072 micrurus fu
80	2	22.2	12	1	PSF3_PHYPA	P80662 physcomitre
81	2	22.2	12	1	RF1_CONSP	P58805 conus spuri
82	2	22.2	12	1	TIN2_HOPTI	P82652 hoplobatr
83	2	22.2	12	1	TIN3_HOPTI	P82653 hoplobatr
84	2	22.2	12	1	TKN_KASSE	P08611 kassina sen
85	2	22.2	12	1	TM2A_METNA	P80652 methanosarc
86	2	22.2	12	1	YZFY_ECOLI	P17776 escherichia
87	2	22.2	13	1	ACT7_SOYEN	P15987 glycine max
88	2	22.2	13	1	ADFB_TENMO	P83109 tenebrio mo
89	2	22.2	13	1	AU11_LITRA	P82386 litoria ran
90	2	22.2	13	1	AU12_LITRA	P82387 litoria ran
91	2	22.2	13	1	BF37_LEUMA	P81754 leucophaea
92	2	22.2	13	1	CRBL_ICASP	P17237 icaria sp.
93	2	22.2	13	1	CRBL_VESCR	P01518 vespa crabr
94	2	22.2	13	1	CRTC_RANES	P31832 rana escul
95	2	22.2	13	1	E121_LITRU	P82097 litoria rub
96	2	22.2	13	1	E122_LITRU	P82098 litoria rub
97	2	22.2	13	1	FIBB_HYLLA	P14472 hylobates l
98	2	22.2	13	1	GER1_HORVU	P28525 hordium vul
99	2	22.2	13	1	GER2_HORVU	P28526 hordium vul
100	2	22.2	13	1	HPA1_PANES	P32415 rana escul

ALIGNMENTS

UPA3_HUMAN
ID UPA3_HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RC MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 44.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9
Db 2 PLFP 5

RESULT 2
COXJ_THUOB
ID COXJ_THUOB STANDARD; PRT; 15 AA.
AC P80979;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIa (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RC MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR PIR; S77988; S77988.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT MOD RES 1 1 BLOCKED.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1769 MW; C111B99419B69A1E CRC64;

Query Match 33.3%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6
Db 3 YVP 5

RESULT 3
PH2_PERAM
ID PH2_PERAM STANDARD; PRT; 15 AA.
AC P82695;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptide hormone 2 (Pea-VEAacid 2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Abdominal perisymphathetic organs;
RC Predel R.;
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: UNKNOWN.
KW Neuropeptide.
SQ SEQUENCE 15 AA; 1603 MW; F353DC8B1F92B8BD CRC64;

Query Match 33.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5
Db 11 SYV 13

RESULT 4
MLB_SQUAC
ID MLB_SQUAC STANDARD; PRT; 16 AA.
AC P01207;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin beta.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RC MEDLINE=75127390; PubMed=4375978;
RA Bennett H.P.J., Lowry P.J., McMartin C., Scott A.P.;
RT "Structural studies of alpha-melanocyte-stimulating hormone and a novel beta-melanocyte-stimulating hormone from the neurointermediate lobe of the pituitary of the dogfish Squalus acanthias.";
RL Biochem. J. 141:439-444(1974).
CC -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR PIR; A01471; MTDPBS.
KW Hormone.
SQ SEQUENCE 16 AA; 1939 MW; 993AF43C8A640A0E CRC64;

Query Match 33.3%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 14 VPL 16

RESULT 5

PH3 PERAM
ID PH3 PERAM STANDARD; PRT; 17 AA.
AC P82696;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptide hormone 3 (Pea-VEAacid 1)
OS Periplaneta americana (American cockroach)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattellidae; Periplaneta.
ON NCBI_TaxID=6978;
RX [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20140865; PubMed=10676456;
RA Predel R., Eckert M., Holman G.M.;
RT "The unique neuropeptide pattern in abdominal perisymphathetic organs
of insects.";
EL Ann. N.Y. Acad. Sci. 897:282-290 (1999).
CC -!- FUNCTION: UNKNOWN.
CC -!- MASS SPECTROMETRY: MW=1651.35; METHOD=MALDI.
KW Neuropeptide.
SQ SEQUENCE 17 AA; 1807 MW; 2374AC8B1F86E8EB CRC64;

Query Match 33.3%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYV 5
|||
DB 13 SYV 15

RESULT 6

AGI EUPCH
ID AGI EUPCH STANDARD; PRT; 18 AA.
AC P33888;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Lectin (Fragment).
OS Euphorbia characias (Spurge).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.
ON NCBI_TaxID=3991;
RX [1]
RP SEQUENCE.
RC TISSUE=Latex;
RX MEDLINE=93357266; PubMed=8353129;
RA Stirpe F., Licastro F., Morini M.C., Parente A., Savino G.,
RA Abbondanza A., Bolognesi A., Falasca A.I., Rossi C.A.;
RT "Purification and partial characterization of a mitogenic lectin from
the latex of Euphorbia marginata";
RL Biochim. Biophys. Acta 1158:33-39 (1993).
CC -!- FUNCTION: LECTIN THAT BINDS GALACTOSE, GALACTOSE-CONTAINING SUGARS
AND GENTIOTRIOSE. IT IS STRONGLY MITOGENIC FOR HUMAN T LYMPHOCYTES.
CC -!- SUBUNIT: Homodimer.
CC -!- PTM: N-GLYCOSYLATED.
CC -!- SIMILARITY: TO E.MARGINATA LECTIN.
DR PIR; S36121; S36121.
KW Lectin.
FT NON TER 18 18
SQ SEQUENCE 18 AA; 1923 MW; C6F6A1A7B2AB124F CRC64;

Query Match 33.3%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4
|||

Db 2 ESY 4

RESULT 7

AHD2 TETPY
ID AHD2 TETPY STANDARD; PRT; 18 AA.
AC P35430;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 20-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) (20-alpha-HSD)
(Fragment).
OS Tetrahymena pyriformis.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
ON NCBI_TaxID=5908;
RX [1]
RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=W;
RX MEDLINE=94107273; PubMed=8280099;
RA Inazu A., Sato K., Nakayama Y., Hara A., Nozawa Y.;
RT "Purification and characterization of a novel dimeric 20 alpha-
hydroxysteroid dehydrogenase from Tetrahymena pyriformis.";
RL Biochem. J. 297:195-200 (1994).
CC -!- FUNCTION: SPECIFIC FOR THE OXIDATION OF THE 20-ALPHA-HYDROXY
GROUP OF 17-ALPHA-HYDROXYPROGESTERONE AND 17-ALPHA-
HYDROXYPROGESTENOLONE.
CC -!- CATALYTIC ACTIVITY: 17-alpha, 20-alpha-dihydroxypregn-4-en-3-one +
NAD(P)(+) = 17-alpha-hydroxyprogesterone + NAD(P)H.
CC -!- SUBUNIT: Homodimer.
DR PIR; S40502; S40502.
KW Oxidoreductase; NADP.
FT NON TER 18 18
SQ SEQUENCE 18 AA; 1861 MW; 16DF6B287E3B0A0D CRC64;

Query Match 33.3%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
|||
DB 5 VPL 7

RESULT 8

ALL2 CYDPO
ID ALL2 CYDPO STANDARD; PRT; 18 AA.
AC P82153;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 2.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricodea; Tortricidae; Olethreutinae; Cydia.
ON NCBI_TaxID=82600;
RX [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309 (1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 18 18
SQ SEQUENCE 18 AA; 2169 MW; 8E66679C0CDF175C CRC64;

Query Match 33.3%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY      3 SYV 5
Db      3 SYV 5

RESULT 9
COOT_SARBU
ID_COOT_SARBU STANDARD; PRT; 19 AA.
AC Q09148;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NEB-colloostatatin (Folliculostatatin).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota, Metazoa; Arthropoda, Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OC NCBI_TaxID=7385;
RN [1]
RP SEQUENCE
RX MEDLINE=95188911; PubMed=7883009;
RA Bylemans D., Proost P., Samijn B., Borovsky D., Grauwels L.,
RA Huybrechts R., van Damme J., van Beeumen J., de Loof A.;
RT "Neb-colloostatatin, a second folliculostatatin of the grey fleshfly,
RT Neobellieria bullata."
RL Eur. J. Biochem. 228:45-49 (1995).
CC -!- FUNCTION: HAS AN OSTATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO
CC -!- INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC
CC FOLLICLES.
CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.
CC -!- CAUTION: NEB-COLLOOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM
CC COLLAGEN IV.
DR PIR: S69153; S69153.
SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CBB8251 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VPL 7
Db      7 VPL 9

RESULT 11
PAP2_PARMA
ID_PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleioidae; Soleidae; Pardachirus.
OC NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RX TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarevici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713 (1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
PT NON TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FP 9
Db      4 FP 5

RESULT 12
E101_LITRU
ID_E101_LITRU STANDARD; PRT; 6 AA.
AC P82056;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Electrin 1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OC NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella."
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD RES 6
 FT SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
 SQ
 Query Match 22.2%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 VP 6
 DB 2 VP 3
 RESULT 13
 VP19 HSV1K
 ID ID_P19 HSV1K STANDARD; PRT; 6 AA.
 AC P23210;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Capsid assembly and DNA maturation protein (Virion protein UL38)
 DE (Capsid protein VP19C) (Fragment).
 GN UL38.
 OS Herpes simplex virus (type 1 / strain KOS).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphan herpesvirinae; Simplexvirus.
 OC NCBI_TaxID=10306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91101287; PubMed=1846198;
 RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
 RA Silverstein S., Wagner E.K.;
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the
 RT expression of UL38, a true late gene involved in capsid assembly.";
 RL J. Virol. 65:769-786(1991).
 CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
 CC EMBEDDED. BINDS DNA.
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
 CC
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 CC
 DR EMBL; M57646; AAA45830.1; -;
 KW Capsid assembly; Coat protein; DNA-binding.
 FT NON TER 6
 FT SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;
 SQ
 Query Match 22.2%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 VP 6
 DB 2 VP 3

QY 6 PL 7
 DB 5 PL 6
 RESULT 14
 HY7_PIG
 ID HY7_PIG STANDARD; PRT; 7 AA.
 AC P01153;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Hypothalamic heptapeptide.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=81213980; PubMed=6263778;
 RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
 RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
 RT "Isolation, structure and synthesis of a heptapeptide with in vitro
 RT ACTH-releasing activity from porcine hypothalamus.";
 RL Horm. Metab. Res. 13:228-232(1981).
 DR PIR; A01417; NYPG7.
 SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SY 4
 DB 5 SY 6
 RESULT 15
 IGAA_DACDE
 ID IGAA_DACDE STANDARD; PRT; 7 AA.
 AC P06294;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Galactose oxidase inhibitor.
 OS Dactylium dendroides (Cladobotryum dendroides).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
 OC NCBI_TaxID=5132;
 RN [1]
 RP SEQUENCE.
 RA Avigad G., Markus Z.;
 RT "Identification of a peptide inhibitor of galactose oxidase from
 RT Dactylium dendroides.";
 RL Fed. Proc. 31:447-447(1972).
 CC -!- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE
 CC GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY
 CC BINDING TO ITS PROSTHETIC COPPER GROUP.
 KW PIR; A01341; KEYDGD.
 DR Copper; Metalloenzyme inhibitor.
 SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ES 3
 DB 6 ES 7
 RESULT 16
 MNPI_LEPDE

ID MNF1_LEPDE STANDARD; PRT; 7 AA.
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Myotropic neuroreptide 1 (Ied-MNP-I).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=95380343; PubMed=7651886;
 RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of
 RT a novel myotropic neuroreptide in the Colorado potato beetle,
 RT Leptinotarsa decemlineata.";
 RL Peptides 16:365-374 (1995).
 CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 KW Neuroreptide; Amidation.
 FT MOD RES 7 7
 SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 PL 7
 Db 5 PL 6
 RESULT 17
 ID _P2H2_LYCES STANDARD; PRT; 7 AA.
 AC P83379;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
 RP GLYCOSYLATION.
 RC STRAIN=cv. Moneymaker; TISSUE=Seed;
 RX MEDLINE=22361242; PubMed=12473124;
 RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
 RT "Purification and characterization of two secreted purple acid
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
 RT esculentum) cell cultures.";
 RL Eur. J. Biochem. 259:6278-6286 (2002).
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: Glycosylated.
 CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of
 CC purple acid phosphatase.
 KW Hydrolase; Glycoprotein.
 FT NON TER 1 1
 FT NON TER 7 7
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LF 8
 Db 2 LF 3
 RESULT 18
 ID TPFY_PACDA STANDARD; PRT; 7 AA.
 AC P83455;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tryptophyllin-1 (PdT-1).
 OS Pachymedusa dactylophora (Giant mexican leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Phyllomedusinae; Pachymedusa.
 OX NCBI_TaxID=75988;
 RN [1]
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
 RP PRO-7.
 RC TISSUE=Skin secretion;
 RA Chen T.B., Orr D.F., Shaw C.;
 RT "Pachymedusa dactylophora tryptophyllin-1 (PdT-1): structural
 RT characterization, pharmacological activity and cloning of precursor
 RT cDNA.";
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.
 CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
 CC smooth muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
 KW Amphibian defense peptide; Amidation; Hydroxylation.
 FT MOD RES 3 3
 FT MOD RES 7 7
 SQ SEQUENCE 7 AA; 794 MW; 777D37DC7776350 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 VP 6
 Db 6 VP 7
 RESULT 19
 ID AL16_CARMA STANDARD; PRT; 8 AA.
 AC P81819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 16.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Jommsen A.H., Maestrio J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734 (1997).

CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476978 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SY 4
 Db 5 SY 6

RESULT 20
 ALL6_CYPDO STANDARD; PRT; 8 AA.
 ID ALL6_CYPDO
 AC P82157;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 6;
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricoidea; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily."
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PL 7
 Db 2 PL 3

RESULT 21
 CAD1_ENTFA STANDARD; PRT; 8 AA.
 ID CAD1_ENTFA
 AC P13268;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CAD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=13351;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=85051889; PubMed=6437872;
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B., Suzuki A.;
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that induces plasmid transfer in Streptococcus faecalis."
 RL FEBS Lett. 178:97-100(1984).
 CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC PHEROMONE.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LF 8
 Db 1 LF 2

RESULT 22
 FUSO_FUSO STANDARD; PRT; 8 AA.
 ID FUSO_FUSO
 AC P81010;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Allergen Fus s I3596* (Fragment).
 OS Fusarium solani (subsp. pisi) (Nectria haematococca).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
 OX NCBI_TaxID=70791;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=IARI 3596; TISSUE=Mycelium;
 RA Verma J., Gangal S.V.;
 RL Submitted (JUL-1997) to the SWISS-PROT data bank.
 KW Allergen.
 FT NON TER
 SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VP 6
 Db 7 VP 8

RESULT 23
 NPB_BOVIN STANDARD; PRT; 8 AA.
 ID NPB_BOVIN
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
 RT "Isolation, sequencing, synthesis, and pharmacological characterization of two brain neuropeptides that modulate the action of morphine."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
 DR PIR; B24749; B24749.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LF 8

Db ||
2 LF 3

RESULT 24

PPK3 PERAM STANDARD; PRT; 8 AA.
AC P82618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
OC Blattellidae; Periplaneta.
OC NCBI_TaxID=6978;
RN [1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Retrocerebral complex;
RC MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach.";
RN Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RN TISSUE SPECIFICITY.
RP MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RN J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
Db ||
2 VP 3

RESULT 25

UPAL HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RP TISSUE=Plasma;
RC MEDLINE=93092937; PubMed=1450907;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RN Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.

DR SWISS-2DPAGE; P30087; HUMAN.
FT NON TER 1
FT UNSURE 8
FT NON TER 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
Db ||
3 ES 4

RESULT 26

VGLG HSV2B STANDARD; PRT; 8 AA.
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OC NCBI_TaxID=103921;
RN [1]
RN SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RT Submitted (APR-1999) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GG, GD, GI, AND GE.
CC -!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
FT NON TER 8
SQ SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
Db ||
4 VP 5

RESULT 27

COXE THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OC NCBI_TaxID=8241;
RN [1]
RN SEQUENCE.
RP TISSUE=Heart;
RC MEDLINE=97454291; PubMed=93103366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottespeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RN Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN

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CC      MITOCHONDRIAL ELECTRON TRANSPORT.
CC      -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC      c + 2 H(2)O.
CC      -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC      -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR      PIR; S77984; S77984.
DR      InterPro; IPR001349; COX6A.
DR      PROSITE; PS01329; COX6A; PARTIAL.
KW      Oxidoreductase; Inner membrane; Mitochondrion.
FT      NON_TER      1
FT      PEPTIDE      1
FT      NON_TER      9
SQ      SEQUENCE      9 AA; 1136 MW; 628072C9CB0776DB CRC64;

Query Match      22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      5 VP 6
DB      ||
      7 VP 8

RESULT 28
FAR9_ASCSU      STANDARD;      PRT;      9 AA.
AC      P43172;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      01-FEB-1996 (Rel. 33, Last annotation update)
DE      FMRFamide-like neuropeptide Af9.
OS      Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC      Ascarididae; Ascaris.
OX      NCBI_TaxID=6253;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=95380362; PubMed=7651904;
RA      Cowden C., Stretton A.O.W.;
RT      "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT      Ascaris suum.";
RL      Peptides 16:491-500(1995).
CC      -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC      FAMILY.
KW      Neuropeptide; Amidation.
FT      MOD_RES      9
FT      SEQUENCE      9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match      22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      6 PL 7
DB      ||
      6 PL 7

RESULT 29
FIBB_ERYPA      STANDARD;      PRT;      9 AA.
AC      P19346;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN      FGB.
OS      Erythrocybus patas (Red guenon) (Hussar).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Erythrocybus.
OX      NCBI_TaxID=9538;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=85289140; PubMed=3928610;

Query Match      22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      6 PL 7
DB      ||
      6 PL 7

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RA      Nakamura S., Takenaka O., Takahashi K.;
RT      "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT      patas monkey (Erythrocybus patas): their amino acid sequences,
RT      restricted mutations, and a molecular phylogeny for macaques,
RT      guenons, and baboons.";
RL      J. Biochem. 97:1487-1492(1985).
CC      -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC      POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC      AGGREGATION.
CC      -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC      (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC      -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC      THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC      CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC      RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR      PIR; D24180; D24180.
DR      InterPro; IPR002181; Fibrinogen C.
DR      PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW      Blood coagulation; Plasma.
FT      PEPTIDE      1
FT      NON_TER      9
FT      NON_TER      9
SQ      SEQUENCE      9 AA; 1020 MW; 69FE7979C732CB1B CRC64;

Query Match      22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      7 LP 8
DB      ||
      5 LP 6

RESULT 30
FIBB_MACFU      STANDARD;      PRT;      9 AA.
AC      P19345;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN      FGB.
OS      Macaca fuscata fuscata (Japanese macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9543;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=85289140; PubMed=3928610;
RA      Nakamura S., Takenaka O., Takahashi K.;
RT      "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT      patas monkey (Erythrocybus patas): their amino acid sequences,
RT      restricted mutations, and a molecular phylogeny for macaques,
RT      guenons, and baboons.";
RL      J. Biochem. 97:1487-1492(1985).
CC      -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC      POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC      AGGREGATION.
CC      -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC      (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC      -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC      THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC      CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC      RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR      PIR; C24180; C24180.
DR      InterPro; IPR002181; Fibrinogen C.
DR      PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW      Blood coagulation; Plasma.
FT      PEPTIDE      1
FT      NON_TER      9
FT      NON_TER      9
SQ      SEQUENCE      9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;

Query Match      22.2%; Score 2; DB 1; Length 9;

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
Db 3 ES 4

RESULT 31

FIBB_PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RQ MEDLINE=84161822; PubMed=6423621;
RX Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DDFE409C7287B06 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8
Db 5 LF 6

RESULT 32

FIBB_PAPHA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE.
RQ MEDLINE=84161822; PubMed=6423621;
RX Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DDFE409C7287B06 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1057 MW; DDFE71E9C7287B06 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8
Db 5 LF 6

RESULT 33

FIBB_THEGE STANDARD; PRT; 9 AA.
AC P19342;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Theropithecus.
OX NCBI_TaxID=9565;
RN [1]
RP SEQUENCE.
RQ MEDLINE=84161822; PubMed=6423621;
RX Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8
Db 5 LF 6

QY 7 LF 8
DB 5 LF 6

RESULT 34
FLA2 TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (Fragment).
GN FLA22.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RC STRAIN=C5;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,
RA van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are
RT composed of two sheath proteins and three core proteins.";
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -!- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
CC SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE
CC THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND
CC FLAB3 (32 kDa)
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagella; Periplasmic.
FT UNSURE 2
FT UNSURE 2
FT NON TER 8 9
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 3 VP 4

RESULT 35
LMT3 LOCM1 STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).

CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 6 VP 7

RESULT 36
NEUU CAVPO STANDARD; PRT; 9 AA.
AC P34966;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuromedin U-9 (Nmu-9).
GN NMU.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=90341105; PubMed=2381877;
RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
RT "Isolation and microsequence analysis of a novel form of neuromedin U
RT from guinea pig small intestine.";
RL Peptides 11:613-617(1990).
CC -!- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES
CC SELECTIVE VASOCONSTRICTION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE NMU FAMILY.
DR InterPro; IPR001942; NMU.
DR Pfam; PF02070; NMU; 1.
DR PROSITE; PS00967; NMU; 1.
KW Amidation; Hormone.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1169 MW; 1ECF177409C729DB CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8
DB 4 LF 5

RESULT 37
OXYA SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspargtocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;

RA Acher R., Chauvet J., Chauvet M.-T.;
 RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
 RL isolated from a cartilaginous fish, *Squalus acanthias*.";
 RN Eur. J. Biochem. 29:12-19(1972).
 RP SEQUENCE.
 RC MEDLINE=72128038; PubMed=4622083;
 RX Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
 RA "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
 RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
 RL spiny dog-fish (*Squalus acanthias*).";
 CC C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
 CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro: IPR000981; Neurohyp_horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT MOD RES 1 6
 FT DISULFID 1 6
 FT MOD RES 9 9
 SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
 DB 7 PL 8

RESULT 38
 ID OXYT_RABIT STANDARD; PRT; 9 AA.
 AC P32878; F01188;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Oxytocin (Oxytocin).
 OS Oryctolagus cuniculus (Rabbit).
 OS Hippopotamus amphibius (Hippopotamus),
 OS Balaenoptera physalus (Finback whale),
 OS Tachyglossus aculeatus aculeatus (Australian echidna), and
 OS Hydroglossus collii (Spotted ratfish) (Pacific ratfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
 [1]
 RN SEQUENCE.
 RC SPECIES=Rabbit;
 RC MEDLINE=72215060; PubMed=5150741;
 RX Chauvet J., Chauvet M.-T., Acher R.;
 RA "Evolution of neurohypophysial hormones: isolation of active
 RT principles from rabbits and rats.";
 RL Biochimie 53:1099-1104(1971).
 [2]
 RN SEQUENCE.
 RC SPECIES=H.amphibius;
 RC MEDLINE=71232719; PubMed=5406007;
 RX Ferguson D.R., Pickering B.T.;
 RA "Arginine and lysine vasopressins in the hippopotamus
 RT neurohypophysis.";
 RL Gen. Comp. Endocrinol. 13:425-429(1969).
 [3]
 RN SEQUENCE.
 RC SPECIES=B.physalus;
 RC Acher R., Chauvet J., Chauvet M.-T.;
 RA "Isolation of finback whale oxytocin and vasopressin.";
 RL Nature 201:191-192(1964).
 [4]
 RN SEQUENCE.
 RC SPECIES=A.aculeatus;
 RC RX MEDLINE=73223515; PubMed=4515919;
 RA Acher R., Chauvet J., Chauvet M.-T.;

RT "Neurohypophysial hormones and evolution of tetrapods.";
 RL Nature New Biol. 244:124-126(1973).
 RN [5]
 RP SEQUENCE.
 RC SPECIES=H.collii;
 RX MEDLINE=70088110; PubMed=5366118;
 RA Pickering B.T., Heller H.;
 RT "Oxytocin as a neurohypophysial hormone in the holoccephalian
 RL elasmobranch fish, *Hydrolagus collei*.";
 CC J. Endocrinol. 45:597-606(1969).
 CC -|- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
 CC UTERUS AND OF THE MAMMARY GLAND.
 CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; A91466; A91466.
 DR PIR; A92774; A92774.
 DR PIR; A93147; A93147.
 DR PIR; A93408; A93408.
 DR PIR; B90667; B90667.
 DR PDB; 1XV1; 15-OCT-90.
 DR PDB; 1XV2; 15-OCT-90.
 DR InterPro: IPR000981; Neurohyp_horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Hypothalamus; Amidation; 3D-structure.
 FT DISULFID 1 6
 FT MOD RES 9 9
 FT SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
 DB 7 PL 8

RESULT 39
 ID PGLR_DIAAB STANDARD; PRT; 9 AA.
 AC P81179;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-polygalacturonase (PG) (EC 3.2.1.15) (Fragment).
 OS Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Curculionidae; Entiminae; Entimini; Diaprepes.
 OX NCBI_TaxID=13040;
 [1]
 RN SEQUENCE.
 RC TISSUE=Larval gut;
 RC Doostdar H., McCollum T.G., Mayer R.T.;
 RA "Purification and characterization of an endo-polygalacturonase from
 RT the gut of West Indies sugarcane rootstalk borer weevil (Diaprepes
 RT abbreviatus L.) larvae.";
 RL Comp. Biochem. Physiol. 118B:861-867(1997).
 CC -|- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
 CC galactosiduronic linkages in pectate and other galacturonans.
 CC -|- INDUCTION: INHIBITED BY CITRUS PGIP.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 CC 9.4, ITS MW IS: 44.5 kDa.
 CC -|- SIMILARITY: WEAK, TO OTHER POLYGALACTURONASES.
 KW Hydrolase; Glycosidase; Cell wall.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1041 MW; 1F49087042DB41BB CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YV 5

SQ SEQUENCE 9 AA; 1128 MW; E33E9B0AF5BB19DA CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ES 3
 ||
 Db 4 ES 5

RESULT 44
 UPA7 HUMAN
 ID UPA7 HUMAN STANDARD; PRT; 9 AA.
 AC P30093;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RC TISSUE=Plasma;
 RP Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing."
 RL Electrophoresis 13:707-714(1992).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.
 CC SWISS-2DPAGE; P30093; HUMAN.
 DR NON_TER 1 1
 FT UNSURE 5 5
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 VP 6
 ||
 Db 3 VP 4

RESULT 45
 ANGI BOTJA
 ID ANGI BOTJA STANDARD; PRT; 10 AA.
 AC Q10581;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide I (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OC NCBI_TaxID=8724;
 RN [1]
 RN SEQUENCE.
 RC TISSUE=Plasma;
 RP Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RA "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca".
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR InterPro; IPR000215; Serpin.

KW Vasoconstrictor; Plasma; Serpin.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YV 5
 ||
 Db 4 YV 5

RESULT 46
 ANGT BOVIN
 ID ANGT BOVIN STANDARD; PRT; 10 AA.
 AC P01017;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
 OC Mammalia; Eutheria; Bovidae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE.
 RP Elliott D.F., Peart W.S.;
 RA "The amino acid sequence in a hypertensin.";
 RL Biochem. J. 65:246-254(1957).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC plasma.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR; A90345; A90345.
 DR PDB; 3ER5; 15-JUL-92.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1282 MW; CEF5BDD761F2DB42 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YV 5
 ||
 Db 4 YV 5

RESULT 47
 ANGT CHICK
 ID ANGT CHICK STANDARD; PRT; 10 AA.
 AC P01018;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]

(Fragment).
 GN AGT OR SERPINA8.
 OS Gallus gallus (Chicken), and
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OK NCBI_TaxID=9031, 93934;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Chicken;
 RX MEDLINE=74127845; PubMed=4361802;
 RA Nakayama T., Nakajima T., Sokabe H.;
 RT "Comparative studies on angiotensins. 3. Structure of fowl
 RT angiotensin and its identification by DNS-method.";
 RL Chem. Pharm. Bull. 21:2085-2087(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.C.japonica;
 RX MEDLINE=90284684; PubMed=2191893;
 RA Takei Y., Hasegawa Y.;
 RT "Vasopressor and depressor effects of native angiotensins and
 RT inhibition of these effects in the Japanese quail.";
 RL Gen. Comp. Endocrinol. 79:12-22(1990).
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOGENSIN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR; A60624; A60624.
 DR PIR; A90917; A90917.
 DR InterPro; IPR002115; Serpin.
 DR PROSITE; PS00284; SERPIN, PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 2 8 ANGIOTENSIN II.
 FT NON_TER 10 10 ANGIOTENSIN III.
 SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No.1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YV 5
 DB ||
 4 YV 5

RESULT 48
 APE CAPGI STANDARD; PRT; 10 AA.
 ID APE CAPGI
 AC P80474;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Aminopeptidase (EC 3.4.11.-) (Fragment).
 OS Capnocytophaga gingivalis.
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
 OC Flavobacteriaceae; Capnocytophaga.
 OK NCBI_TaxID=1017;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 33624;
 RX MEDLINE=96118234; PubMed=8574402;
 RA Spratt D.A., Greenman J., Schaffer A.G.;
 RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
 RT factor";
 RL Microbiology 141:3087-3093 (1995).

-!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
 CC TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.
 CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5.. MAY BE IMPORTANT IN THE
 CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
 CC CAVITY.
 CC -!- COFACTOR: REQUIRES MAGNESIUM OR CALCIUM.
 KW Hydrolase; Aminopeptidase; Magnesium; Calcium.
 FT NON_TER 1 10
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No.1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YV 5
 DB ||
 7 YV 8

RESULT 49
 BPP VIPAS STANDARD; PRT; 10 AA.
 ID BPP VIPAS
 AC P31351;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 DE enzyme inhibitor).
 OS Vipera aspis (Aspic viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 OK NCBI_TaxID=8706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90382616; PubMed=2169439;
 RA Komori Y., Sugihara H.;
 RT "Characterization of a new inhibitor for angiotensin converting
 RT enzyme from the venom of Vipera aspis aspis.";
 RL Int. J. Biochem. 22:767-771(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A60377; XASNPC.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;
 Query Match 22.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No.1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 YP 6
 DB ||
 8 YP 9

RESULT 50
 BRK ONCMY STANDARD; PRT; 10 AA.
 ID BRK ONCMY
 AC Q9PRZ1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lysyl-bradykinin-like.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OK NCBI_TaxID=8022;

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RN [1]
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RL trout plasma.";
RL FEBS Lett. 334:75-78(1993).
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
DB 8 PL 9

RESULT 51
COXA_ONCMY
ID COXA_ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIa
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
DR PIR; S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C33D CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2
DB 5 VE 6

RESULT 52
COXH_ONCMY
ID COXH_ONCMY STANDARD; PRT; 10 AA.
AC P80331;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)

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DE Cytochrome c oxidase polypeptide VIc (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIa
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
DR PIR; S43630; S43630.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 977 MW; E11B40769DC772DA CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 4 VP 5

RESULT 53
COXK_ONCMY
ID COXK_ONCMY STANDARD; PRT; 10 AA.
AC P80332;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIa-heart (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIa
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR PIR; S43631; S43631.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1174 MW; 4C8D81CAFAF772C3 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 4 VP 5

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Db          4 VP 5
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 54
GAJU HUMAN
ID_GAJU_HUMAN STANDARD; PRT; 10 AA.
AC P01356;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Gastric juice peptide.
OS Homo sapiens (Human).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=75150968; PubMed=5538385;
RA Heathcote J.G., Washington R.J.;
RT "Peptides of normal human gastric juice.";
RL Int. J. Protein Res. 2:117-126(1970).
DR PIR; A01628; GXHUL.
DR MIM; 137220;
DR GO; GO:0007586; P:digestion; NAS.
FT PEPTIDE 1 10 GASTRIC JUICE PEPTIDE 1.
FT PEPTIDE 2 10 GASTRIC JUICE PEPTIDE 2.
SQ SEQUENCE 10 AA; 1004 MW; CFEEC6AB02C3387D CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2
DB 6 VE 7

RESULT 55
GONI ALLMI
ID_GONI_ALLMI STANDARD; PRT; 10 AA.
AC P37041; P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)
DE (Luliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatoridae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE
RX TISSUE=Brain;
RC MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A60066; RHAQ1.
DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 10 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 284B32D7286B45A3 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 4 SY 5

RESULT 56
GON3 ONCKE
ID_GON3_ONCKE STANDARD; PRT; 10 AA.
AC P20367; P81751;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III) (LH-
DE RH III) (Luliberin III).
GN GNRH3.
OS Oncorhynchus keta (Chum salmon), and
OS Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018; 30724;
RN [1]
RP SEQUENCE
RC SPECIES=O.keta;
RX MEDLINE=83195140; PubMed=6341999;
RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
RT "Characterization of a teleost gonadotropin-releasing hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
RN [2]
RP SEQUENCE AND FUNCTION
RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10850929;
RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A21114; A21114.
DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 10 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 4 SY 5

RESULT 57
LPK2 LOCM1
ID_LPK2_LOCM1 STANDARD; PRT; 10 AA.
AC P41488;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

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OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94094539; PubMed=7903606;
RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
de Loof A.; identification and synthesis of locustapyrokinin II from
RT Locusta migratoria, another member of the FXPR-amide peptide
RT family.";
RL Comp. Biochem. Physiol. 106C:103-109(1993).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC
CC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
KW Neuropeptide; Amidation; Pyrokinin; Pyroliidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
Db 3 VP 4

RESULT 58
NS1_MYCTU
ID NS1_MYCTU STANDARD; PRT; 10 AA.
AC P81135;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 1 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RC STRAIN=H37Rv;
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
Db 4 PL 5

RESULT 59
ODP2_BOVIN
ID ODP2_BOVIN STANDARD; PRT; 10 AA.
AC P11180;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2) (Fragment).
GN DLAT.

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OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=88024154; PubMed=3117054;
RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;
RT "Primary structure around the lipote-attachment site on the E2
RT component of bovine heart pyruvate dehydrogenase complex.";
RL Biochem. J. 245:919-922(1987).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL
CC COFACTOR.
CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
CC SYMMETRY.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
DR InterPro; IPR003016; Lipoyl.
DR PROSITE; PS00189; LIPOYL; PARTIAL.
KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
KW Lipoyl.
FT NON_TER 1 1
FT BINDING 5 5 LIPOYL.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1066 MW; 889BECD1ADD33AB1 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2
Db 1 VE 2

RESULT 60
PVK_LOCOMI
ID PVK_LOCOMI STANDARD; PRT; 10 AA.
AC P83382;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Periviscerokinin (Lom-PVK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=21896327; PubMed=11897380;
RA Predel R., Gaede G.;
RT "Identification of the abundant neuropeptide from abdominal
RT perisymphathetic organs of locusts.";
RL Peptides 23:621-627(2002).
CC -!- FUNCTION: Myotropic peptide; increases the frequency of
CC contraction of the heart and stimulates amplitude and tonus of the
CC foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
DR GO; GO:0007218; F:neuropeptide signaling pathway; IDA.

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KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LF 8
Db 4 LF 5

RESULT 61
Q2OB COMTE STANDARD; PRT; 10 AA.
AC P80455;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni)
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OKO-
CC 1,2-DIHYDROQUINOLINE.
CC -1- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -1- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -1- PATHWAY: Degradation of quinoline and (3-methyl)-quinoline; first
CC step.
CC -1- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC TWO GAMMA CHAINS (PROBABLE).
CC Oxidoreductase; Flavoprotein; FAD; Molybdenum.
KW NON TER 10
FT SEQUENCE 10 AA; 1241 MW; C2E2C25DD9DCD769 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FP 9
Db 3 FP 4

RESULT 62
SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckeivich M.D.; Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
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RL J. Bacteriol. 171:6656-6667(1989).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.
DR PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON TER 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FP 9
Db 5 FP 6

RESULT 63
TKL2 LOCM1 STANDARD; PRT; 10 AA.
ID -TKL2 LOCM1
AC P16224;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin II (TK-II).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
RT homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PL 7
Db 2 PL 3

RESULT 64
TRP7 LEUMA STANDARD; PRT; 10 AA.
ID -TRP7 LEUMA
AC P81739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 7 (LemTRP 7).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE. AND MASS SPECTROMETRY.
RC TISSUE=Brain;
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RX MEDLINE=97269266; PubMed=9114447;
RA Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT madeira cockroach; evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- MASS SPECTROMETRY: MW=1069.7; METHOD=MALDI.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1068 MW; C4541679C9C865BD CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
Db 1 VP 2

RESULT 65
UPA3_HUMAN
ID UHA3_HUMAN STANDARD; PRT; 10 AA.
AC P40930;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 47.3 kDa.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1049 MW; 6BBCDE41A041B76B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2
Db 2 VE 3

RESULT 66
UPA4_HUMAN
ID UPA4_HUMAN STANDARD; PRT; 10 AA.
AC F30090;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Fruiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8, ITS MW IS: 40.5 kDa.
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30090; HUMAN.
FT NON_TER 1 1
FT UNSURE 4 4
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
Db 2 VP 3

RESULT 67
UPA8_HUMAN
ID UPA8_HUMAN STANDARD; PRT; 10 AA.
AC P30094;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 34) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Fruiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.2, ITS MW IS: 16 kDa.
DR SWISS-2DPAGE; P30094; HUMAN.
FT NON_TER 1 1
FT VARIANT 4 4
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 977 MW; 2EA6E0C77AE325B8 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
Db 9 VP 10

RESULT 68
URE3_MORMO
ID URE3_MORMO STANDARD; PRT; 10 AA.
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
 DB amidohydrolase) (Fragment).
 GN UREA.
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90264298; PubMed=2345135;
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
 RT "Morganella morganii urease: purification, characterization, and
 RT isolation of gene sequences."
 RL J. Bacteriol. 172:3073-3080(1990).
 CC -|- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -|- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
 DR PIR; C35389; C35389.
 KW Hydrolase.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2
 ||
 DB 8 VE 9

RESULT 69
 ANGT CRIGE STANDARD; PRT; 11 AA.
 ID _ANGT CRIGE STANDARD; PRT; 11 AA.
 AC P09037;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Crinia-angiotensin II.
 OS Crinia georgiana (Quacking frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Crinia.
 OX NCBI_TaxID=8374;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80024575; PubMed=488254;
 RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
 RT "Amino acid composition and sequence of crinia-angiotensin, an
 RT angiotensin II-like endecapeptide from the skin of the Australian
 RT frog Crinia georgiana.";
 RL Experientia 35:1132-1133(1979).
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Skin.
 DR PIR; S07207; S07207.
 KW Vasoconstrictor.
 SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 22.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YV 5
 ||
 DB 7 YV 8

RESULT 70
 EFG_CLOPA STANDARD; PRT; 11 AA.
 ID _EFG_CLOPA STANDARD; PRT; 11 AA.
 AC P81350;
 DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor G (EF-G) (CP 5) (Fragment).
 GN FUSA.
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RX STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9623918;
 RA Fiengerud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -|- FUNCTION: This protein promotes the GTP-dependent translocation of
 CC the nascent protein chain from the A-site to the P-site of the
 CC ribosome.
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -|- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 CC EF-G/EF-2 SUBFAMILY.
 DR InterPro; IPR000795; EF_GTPbind.
 DR PROSITE; PS00301; EFACOR GTP; PARTIAL.
 KW Elongation factor; Protein biosynthesis; GTP-binding.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
 ||
 DB 3 PL 4

RESULT 71
 HS70_PINPS STANDARD; PRT; 11 AA.
 ID HS70_PINPS STANDARD; PRT; 11 AA.
 AC P81672;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Heat shock 70 kDa protein (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
 CC (SPOT N164) IS: 5.4, ITS MW IS: 73 kDa.
 CC -|- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 KW ATP-binding; Heat shock; Multigene family.
 FT NON TER 1 1
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2
 ||
 DB 1 VE 2

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RESULT 72
MLG-THETS
ID MLG-THETS STANDARD; PRT; 11 AA.
AC P41989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1] SEQUENCE.
RP TISSUE=Brain;
RC MEDLINE=94298944; PubMed=8026574;
RA Salzet M., Watzet C., Bulet P., Malecha J.;
RT "Isolation and structural characterization of a novel peptide related
to gamma-melanocyte stimulating hormone from the brain of the leech
Theromyzon tessulatum."
RT FEBS Lett. 348:102-106(1994).
RL -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR PIR; S45698; S45698.
KW Hormone; Amidation.
FT MOD RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E9 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YV 5
DB 1 YV 2

RESULT 73
MORN_HUMAN
ID MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1] SEQUENCE.
RP SPECIES=Human, Rat, and Bovine;
RC MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
from coelenterates to humans."
RL Nature 293:579-580(1981).
RN [2] SEQUENCE.
RP SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
hydra."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3] SYNTHESIS.
RP MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;

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RT "Synthesis of a new neuropeptide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4] FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
in the G2/mitosis transition."
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
IN THE G2/MITOSIS TRANSITION.
CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHAE.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJFHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8
DB 10 LF 11

RESULT 74
NUHM_CANEA
ID NUHM_CANEA STANDARD; PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1] SEQUENCE.
RP TISSUE=Heart;
RC MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
FRAGMENT OF THE ENZYME.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
CC THIS IS A COMPONENT OF THE FLAVOPROTEIN FRACTION.
CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 24 kDa SUBUNIT FAMILY.
DR HSC-2DPAGE; P49820; DOG.
DR InterPro; IPR002023; Cmplx1_24kDa.
DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
Iron-sulfur; Iron; 2Fe-2S.

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FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match      22.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LF 8
      ||
Db      6 LF 7

RESULT 75
PQQC_PSEFL
ID PQQC_PSEFL STANDARD; PRT; 11 AA.
AC P55173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Coenzyme PQQ synthesis protein C (Fragment).
GN PQQC.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHAO;
RX MEDLINE=96064397; PubMed=8526497;
RA Schnider U., Keel C., Defago G., Haas D.;
RT "Tns-directed cloning of pqq genes from Pseudomonas fluorescens CHAO:
RT mutational inactivation of the genes results in overproduction of the
RT antibiotic pyoluteorin.";
RL Appl. Environ. Microbiol. 61:3856-3864(1995).
CC -!- FUNCTION: REQUIRED FOR COENZYME PYROLO-QUINOLINE-QUINONE (PQQ)
CC -!- BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER BACTERIAL PQQC.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; X87299; CAA60734.1; -.
DR PIR; S58244; S58244.
KW PQQ.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1182 MW; 89DF4654C5B73771 CRC64;

Query Match      22.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PL 7
      ||
Db      5 PL 6

Search completed: November 25, 2003, 19:28:26
Job time : 3.26329 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 16.9012 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESVPLFP 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL_23:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp rvirus:*
16: sp bacteriap:*
17: sp archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	44.4	16	10	O82407 fragaria vi
2	4	44.4	16	10	O82404 fragaria ni
3	4	44.4	16	10	O82406 fragaria mo
4	4	44.4	16	10	O82402 fragaria nu
5	4	44.4	16	10	O82403 fragaria ve
6	4	44.4	16	10	O82781 fragaria ve
7	4	44.4	16	10	O82405 fragaria ii
8	3	33.3	7	13	O42564 fugu rubrip
9	3	33.3	8	4	Q15898 homo sapien
10	3	33.3	9	11	O35953 mus musculu
11	3	33.3	10	11	O8VHM9 mus musculu
12	3	33.3	10	12	O39957 hepatitis g
13	3	33.3	11	4	Q9NY38 homo sapien
14	3	33.3	11	7	O77876 oreochromis
15	3	33.3	12	6	Q9TRY4 sus sp. ins
16	3	33.3	13	8	Q9T2U1 bos taurus

17	3	33.3	13	11	O63047	O63047 rattus norv
18	3	33.3	13	13	P82881	P82881 rana clamit
19	3	33.3	13	15	O66746	O66746 equine infe
20	3	33.3	14	4	P78359	P78359 homo sapien
21	3	33.3	14	4	Q9P2A2	Q9P2A2 homo sapien
22	3	33.3	14	5	P82219	P82219 bombyx mori
23	3	33.3	14	10	Q9FYT0	Q9FYT0 allium cepa
24	3	33.3	14	13	Q91777	Q91777 xenopus lae
25	3	33.3	14	13	P82824	P82824 rana catesb
26	3	33.3	15	2	Q9R4U7	Q9R4U7 acinetobact
27	3	33.3	15	4	O81ZQ0	O81ZQ0 homo sapien
28	3	33.3	15	8	Q35795	Q35795 saccharomyc
29	3	33.3	15	10	Q9S929	Q9S929 glycine max
30	3	33.3	15	10	P82431	P82431 nicotiana t
31	3	33.3	15	11	Q9QV16	Q9QV16 rattus sp.
32	3	33.3	15	11	O88175	O88175 mus musculu
33	3	33.3	15	12	Q86869	Q86869 lymphocytic
34	3	33.3	15	12	Q91PD8	Q91PD8 rabies viru
35	3	33.3	15	12	Q91PE5	Q91PE5 rabies viru
36	3	33.3	15	12	Q91PE4	Q91PE4 rabies viru
37	3	33.3	16	2	Q9S566	Q9S566 micrococcc
38	3	33.3	16	2	Q53399	Q53399 bacillus th
39	3	33.3	16	2	P83155	P83155 anabaena sp
40	3	33.3	16	4	Q9UC53	Q9UC53 homo sapien
41	3	33.3	16	6	Q9BGG8	Q9BGG8 sorex arane
42	3	33.3	16	8	O19977	O19977 gossypium m
43	3	33.3	16	8	O19975	O19975 gossypium t
44	3	33.3	16	8	O19973	O19973 gossypium b
45	3	33.3	16	8	O19971	O19971 gossypium h
46	3	33.3	16	8	Q9T2P6	Q9T2P6 rattus sp.
47	3	33.3	16	11	Q9CW70	Q9CW70 mus musculu
48	3	33.3	17	2	Q9RSB1	Q9RSB1 arthrobacte
49	3	33.3	17	3	Q9URC6	Q9URC6 saccharomyc
50	3	33.3	17	4	Q9NY39	Q9NY39 homo sapien
51	3	33.3	17	11	O61932	O61932 mus musculu
52	3	33.3	17	15	Q78374	Q78374 human immun
53	3	33.3	17	15	Q85463	Q85463 avian sarco
54	3	33.3	18	2	Q9FAC6	Q9FAC6 streptomyce
55	3	33.3	18	5	Q9TWL5	Q9TWL5 lucilia cup
56	3	33.3	18	8	Q9GB22	Q9GB22 calyptomena
57	3	33.3	18	8	O19979	O19979 gossypium d
58	3	33.3	18	8	O19969	O19969 gossypium a
59	3	33.3	18	8	Q9ZY79	Q9ZY79 idaris sp. c
60	3	33.3	18	15	Q78376	Q78376 human immun
61	3	33.3	18	17	Q825Z9	Q825Z9 pyrobaculum
62	3	33.3	19	2	Q43964	Q43964 azotobacter
63	3	33.3	19	4	Q9UCL1	Q9UCL1 homo sapien
64	3	33.3	19	4	Q9UCE4	Q9UCE4 homo sapien
65	3	33.3	19	10	Q947M7	Q947M7 vitis vinif
66	3	33.3	19	10	Q41567	Q41567 triticum ae
67	3	33.3	19	11	Q8KON2	Q8KON2 mus musculu
68	3	33.3	19	13	Q9PS17	Q9PS17 gallus gall
69	3	33.3	19	13	Q9PS14	Q9PS14 gallus gall
70	3	33.3	19	13	Q9PRT0	Q9PRT0 gallus gall
71	3	33.3	19	15	Q78351	Q78351 human immun
72	3	33.3	20	2	Q9R4N0	Q9R4N0 rhodococcus
73	3	33.3	20	4	Q96FU6	Q96FU6 homo sapien
74	3	33.3	20	4	O8WX06	O8WX06 homo sapien
75	3	33.3	20	4	O8T841	O8T841 homo sapien
76	3	33.3	20	6	O62720	O62720 cryctolagus
77	3	33.3	20	6	Q9TQX5	Q9TQX5 bos taurus
78	3	33.3	20	10	Q9S8J6	Q9S8J6 triticum ae
79	3	33.3	20	10	Q9S900	Q9S900 vigna sinen
80	2	22.2	5	13	P83308	P83308 gallus gall
81	2	22.2	7	4	O8NHU7	O8NHU7 homo sapien
82	2	22.2	7	10	P93233	P93233 lycopersico
83	2	22.2	8	2	Q45615	Q45615 bacillus su
84	2	22.2	8	2	Q8KFX4	Q8KFX4 microcystis
85	2	22.2	8	2	Q9R3X0	Q9R3X0 planktothri
86	2	22.2	8	2	Q49534	Q49534 mycoplasma
87	2	22.2	8	2	Q9X3K1	Q9X3K1 prochloroco
88	2	22.2	8	2	Q56140	Q56140 streptococc
89	2	22.2	8	2	Q938F2	Q938F2 pseudomonas

Q45899 clostridium
Q96433 pseudomonas
Q8gmms acinetobact
O13591 saccharomyc
Q9byy5 homo sapien
O15893 homo sapien
O16468 homo sapien
O60773 homo sapien
Q9twh6 perinereis
O15899 babesia ovi
Q94623 manduca sex

ALIGNMENTS

RESULT 1

O82407 PRELIMINARY; PRT; 16 AA.
AC O82407;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria viridis (Wild strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64942;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRA 341;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000220; AAC36547.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

6 PLFP 9
4 PLFP 7

Db

RESULT 2

O82404 PRELIMINARY; PRT; 16 AA.
AC O82404;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria nilgerrensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berlin 1;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000217; AAC36544.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16

SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;
Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
4 PLFP 7

Db

RESULT 3

O82406 PRELIMINARY; PRT; 16 AA.
AC O82406;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria moschata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRA 157;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000219; AAC36546.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
4 PLFP 7

Db

RESULT 4

O82402 PRELIMINARY; PRT; 16 AA.
AC O82402;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria nubicola.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=60188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRAS20;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000213; AAC36540.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
4 PLFP 7

Db

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QY      6 PLFP 9
Db      4 PLFP 7

RESULT 5
ID O82403 PRELIMINARY; PRT; 16 AA.
AC O82403;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria vesca (Woodland strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=57918;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pawtuckaway;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000215; AAC36542.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1666 MW; CEF73B5B28A4CA87 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLFP 9
Db      4 PLFP 7

RESULT 6
ID O82781 PRELIMINARY; PRT; 16 AA.
AC O82781;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Aldehyde reductase) (Fragment).
GN ADH.
OS Fragaria vesca (Woodland strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=57918;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YELLOW WONDER, and BARON SOLEWACHER;
RA Yu H., Davis T.M.;
RL "Genetic relationships among Fragaria species based on RAPDs and an
RT alcohol dehydrogenase (ADH) gene.";
RL Genome 0:0-0(1997).
CC -!- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) = AN ALDEHYDE OR KETONE +
CC NADH.
CC -!- COFACTOR: ZINC OR IRON.
DR EMBL; AF000216; AAC36543.1; -.
DR EMBL; AF000214; AAC36541.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLFP 9
Db      4 PLFP 7

RESULT 7
ID O82405 PRELIMINARY; PRT; 16 AA.
AC O82405;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria inumae.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64939;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRA 377;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000218; AAC36545.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLFP 9
Db      4 PLFP 7

RESULT 8
ID O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97442476; PubMed=9295353;
RX Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
KW Ionic channel.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 33.3%; Score 3; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VPL 7

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Db 1 VPL 3

RESULT 9

Q15898 PRELIMINARY; PRT; 8 AA.
AC Q15898;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XPeAllIB) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32078; AAA73888.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;

Query Match 33.3%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4

Db 1 ESY 3

RESULT 10

O35953 PRELIMINARY; PRT; 9 AA.
AC O35953;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R111;
RA MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells."
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97672; AAB80914.1; -.
DR MGD; MGI:103169; Scn8a.
KW Ionic channel.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 898 MW; 22D92865B735B737 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7

Db 1 VPL 3

RESULT 11

Q8VHM9 PRELIMINARY; PRT; 10 AA.
AC Q8VHM9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interferon receptor 2a' (Fragment).
GN IFNAR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The genomic structure and expression patterns of the gene encoding
RT the second chain of the murine interleukin 10 receptor, IL-10R2."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The organization, transcriptional regulation and chromosomal
RT localization of the locus encoding the gene for the murine type I
RT interferon receptor, Ifnar2."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440786; AAL40944.1; -.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1139 MW; 322A36A72449C737 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8

Db 3 PLF 5

RESULT 12

O39957 PRELIMINARY; PRT; 10 AA.
AC O39957;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
OS Hepatitis GB virus C.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=39839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Edinburgh haemophilic;
RC MEDLINE=97368412; PubMed=9225026;
RA Smith D.B., Cuconu N., Davidson F., Jarvis L.M., Mokili J.L.,
RA Hamid S., Ludlam C.A., Simmonds P.;
RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
RT analysis of the 5' non-coding region."
RL J. Gen. Virol. 78:1533-1542(1997).
DR EMBL; AF003175; AAC57986.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1067 MW; CC88FE27273772 CRC64;

Query Match 33.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
|
|
|
Db 3 VPL 5

RESULT 13

Q9NY38 PRELIMINARY; PRT; 11 AA.
ID Q9NY38
AC Q9NY38
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Heavy metal-responsive transcription factor (Fragment).
GN MTF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,
RA Georgiev O., Schaffner W.;
RT "Characterization of the mouse gene for the heavy metal-responsive
transcription factor MTF-1."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251891; CAB71327.1; -
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1099 MW; A8653693773772C6 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
|
|
|
Db 5 VPL 7

RESULT 14

O77876 PRELIMINARY; PRT; 11 AA.
ID O77876
AC O77876
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 1 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
class II B loci."
RL Genetics 149:1527-1537(1998).
DR EMBL; AF049985; AAC41324.1; -
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1178 MW; 9AC131FAB2D2DB45 CRC64;

Query Match 33.3%; Score 3; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5
|
|
|
Db 4 SYV 6

RESULT 15

Q9TRY4 PRELIMINARY; PRT; 12 AA.
ID Q9TRY4
AC Q9TRY4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE
RX MEDLINE=92049376; PubMed=1719383;
RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
protein-6."
RL Mol. Endocrinol. 5:938-948(1991).
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1317 MW; 4DAAABE6CC72DB57 CRC64;

Query Match 33.3%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6
|
|
|
Db 6 YVP 8

RESULT 16

Q9T2U1 PRELIMINARY; PRT; 13 AA.
ID Q9T2U1
AC Q9T2U1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADH:ubiquinone oxidoreductase (complex I) iron-sulfur protein
fraction 20 kDa polypeptide T-9 (Fragment).
OS Bos taurus (Bovine).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RX MEDLINE=92138662; PubMed=1778979;
RA Masui R., Wakabayashi S., Matsubara H., Hatafi Y.;
RT "The amino acid sequence of the 9 kDa polypeptide and partial amino
acid sequence of the 20 kDa polypeptide of mitochondrial
NADH:ubiquinone oxidoreductase."
RL J. Biochem. 110:575-582(1991).
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1369 MW; 0E61A5EAB35FDB50 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6
|
|
|
Db 7 YVP 9

RESULT 17

Q63047 PRELIMINARY; PRT; 13 AA.
ID Q63047

AC Q63047;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE AMP deaminase (Fragment).
 GN AMPD1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Soleus muscle;
 RX MEDLINE=90377216; PubMed=2398891;
 RA Mineo I., Clarke P.R.H., Sabina R.L., Holmes E.W.;
 RT "A novel pathway for alternative splicing: Identification of an RNA
 RT intermediate that generates an alternative 5' splice donor site not
 RT present in the primary transcript of AMPD1.";
 RL Mol. Cell. Biol. 10:5271-5278 (1990).
 DR EMBL; MS8689; AAA40727.1; -.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1524 MW; 526CSA93EF6201A7 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
 ||||
 Db 2 PLF 4

RESULT 18

P82881
 ID P82881 PRELIMINARY; PRT; 13 AA.
 AC P82881;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Temporin-1CB.
 OS Rana clamitans (green frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=145282;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=20283865; PubMed=10822101;
 RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
 RT "Purification and characterization of antimicrobial peptides from the
 RT skin of the North American green frog Rana clamitans.";
 RL Peptides 21:469-476 (2000).
 CC -|- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
 CC S.AUREUS.
 CC -|- SUBCELLULAR LOCATION: SECRETED.
 CC -|- MASS SPECTROMETRY: MW=1430.0; MW ERR=0.02; METHOD=ELECTROSPRAY.
 CC -|- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 CC Antibiotic; Amidation.
 KW MOD RES 13 13 AMIDATION
 FT MOD RES 13 13
 SQ SEQUENCE 13 AA; 1432 MW; C4A71A76SA8935BD CRC64;

Query Match 33.3%; Score 3; DB 13; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
 ||||
 Db 3 PLF 5

RESULT 19

Q66746
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Polymerase (Fragment).
 OS Equine infectious anemia virus.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90204701; PubMed=2157066;
 RX Noiman S., Yaniv A., Sherman L., Tronick S.R., Gazit A.;
 RT "Pattern of transcription of the genome of equine infectious anemia
 RT virus.";
 RL J. Virol. 64:1839-1843 (1990).
 DR EMBL; M33845; AAA66411.1; -.
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1493 MW; 978D390905A92321 CRC64;

Query Match 33.3%; Score 3; DB 15; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
 ||||
 Db 1 VPL 3

RESULT 20

P78359
 ID P78359 PRELIMINARY; PRT; 14 AA.
 AC P78359;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NF-kappa-B transcription factor p65 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein;
 RA Remacle J.E., Brys R., Pyde S., Nelles L., Huylebroeck D.;
 RT "5' cDNA sequence Re1a isolated from Human umbilical vein endothelial
 RT cells.";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88316; AAB48487.1; -.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
 ||||
 Db 4 LFP 6

RESULT 21

Q9P2A2
 ID Q9P2A2 PRELIMINARY; PRT; 14 AA.
 AC Q9P2A2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Truncated aldo-keto reductase (Fragment).
 GN TRUNCATED AKR.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20138537; PubMed=10672042;
RA Nishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,
RA Watanabe K., Ito S.;
RT "Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with
RL three aldo-keto reductase genes.";
RL Genes Cells 5:111-125(2000).
DR EMBL; AB037903; BAA92888.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 5 VPL 7

RESULT 22
P82219 ID P82219 PRELIMINARY; PRT; 14 AA.
AC P82219;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Unknown protein from 2D-page (fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCB1_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
RT silkworm";
RL I Chuan Hsueh Pao 28:217-224(2001).
FT NON TER 14
SQ SEQUENCE 14 AA; 1535 MW; 4E659A7257BAA3C7 CRC64;

Query Match 33.3%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8
Db 6 PLF 8

RESULT 23
Q9FYT0 ID Q9FYT0 PRELIMINARY; PRT; 14 AA.
AC Q9FYT0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Alliinase (EC 4.4.1.4) (Fragment).
OS Allium cepa (Onion).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC Allium.
OX NCB1_TaxID=4679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wase Showman Red;
RA Kaminishi A., Nomura K., Ohya T., Kita N.;

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RT "Cloning of Novel Promoter of Alliinase gene from Onion by Inverse
RT PCR.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF291183; AAG00599.1; -.
KW Lyase.
FT NON TER 14
SQ SEQUENCE 14 AA; 1573 MW; C3547CA8BE1B8162 CRC64;

Query Match 33.3%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
Db 2 ESY 4

RESULT 24
Q91777 ID Q91777 PRELIMINARY; PRT; 14 AA.
AC Q91777;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
DE Hypothetical 1.6 kDa protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCB1_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90231335; PubMed=2330002;
RA Kajimoto Y., Kotwein P.;
RT "Evolution of insulin-like growth factor I (IGF-I): structure and
RT expression of an IGF-I precursor from Xenopus laevis.";
RL Mol. Endocrinol. 4:217-226(1990).
DR EMBL; M29857; AAA70329.1; -.
KW Hypothetical protein.
SQ SEQUENCE 14 AA; 1627 MW; 3002F6B29B887BD7 CRC64;

Query Match 33.3%; Score 3; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9
Db 5 LFP 7

RESULT 25
P82824 ID P82824 PRELIMINARY; PRT; 14 AA.
AC P82824;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RANATUERIN 9.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCB1_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Gorava J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC -|- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
CC S.AUREUS.

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CC -!- SUBCELLULAR LOCATION: SECRETED.

KW Antibiotic. 14 AA; 1625 MW; 8941FA6337030BA1 CRC64;

SQ SEQUENCE 14 AA; 1625 MW; 8941FA6337030BA1 CRC64;
 Query Match 33.3%; Score 3; DB 13; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9
 Db 2 LFP 4

RESULT 26

Q9R4U7 ID Q9R4U7 PRELIMINARY; PRT; 15 AA.
 AC Q9R4U7;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE Malonate decarboxylase gamma subunit (Fragment).
 OS Acinetobacter calcoaceticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=471;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95050812; PubMed=7961952;
 RA Kim Y.S., Byun H.S.;
 RT "Purification and Properties of a novel type of malonate decarboxylase
 from Acinetobacter calcoaceticus";
 RL J. Biol. Chem. 269:29636-29641(1994).
 SQ SEQUENCE 15 AA; 1816 MW; 4E14F10E389F9FEA CRC64;

Query Match 33.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9
 Db 10 LFP 12

RESULT 27

Q81ZQ0 ID Q81ZQ0 PRELIMINARY; PRT; 15 AA.
 AC Q81ZQ0;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Protein kinase A catalytic subunit beta (Fragment).
 GN PKACB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu K.-J., Mattioli M., Morse H.C., Dalla-Favera R.;
 RT "c-MYC activates protein kinase A (PKA) by direct transcriptional
 activation of the PKA catalytic subunit beta (PKA-CB) gene.";
 RL Oncogene 0:0-0(2002).
 DR ENBL; AF538872; AAN16454.1; -.
 KW Kinase.
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1480 MW; 52FE569E5C19B70A CRC64;

Query Match 33.3%; Score 3; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3
 Db 1

Db 13 VES 15

RESULT 28

Q35795 ID Q35795 PRELIMINARY; PRT; 15 AA.
 AC Q35795;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE OX13 locus in yeast MITOCHONDRION (Strain D273-10B) (CODES for
 cytochrome oxidase subunit 1).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OG Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81069885; PubMed=6254986;
 RA Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;
 RT "Assembly of the mitochondrial membrane system. Structure and
 nucleotide sequence of the gene coding for subunit 1 of yeast
 cytochrome oxidase.";
 RL J. Biol. Chem. 255:11927-11941(1980).
 DR ENBL; V00694; CAA24069.1; -.
 KW Mitochondrion.
 SQ SEQUENCE 15 AA; 1741 MW; 0E7A612E14FCC394 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3
 Db 3 VES 5

RESULT 29

Q9S929 ID Q9S929 PRELIMINARY; PRT; 15 AA.
 AC Q9S929;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Pyroline-5-carboxylate reductase, P5CR (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91378472; PubMed=1898034;
 RA Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;
 RT "Pyroline-5-carboxylate reductase in soybean nodules:
 isolation/partial primary structure/evidence for isozymes.";
 RL Arch. Biochem. Biophys. 288:350-357(1991).
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1715 MW; D9821F773F3DF524 CRC64;

Query Match 33.3%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
 Db 9 ESY 11

RESULT 30

P82431 ID P82431 PRELIMINARY; PRT; 15 AA.

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AC P82431;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 100 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; famids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -|- SUBCELLULAR LOCATION: CELL WALL.
CC -|- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1694 MW; 5F3B8D2E48187626 CRC64;

Query Match 33.3%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 13 VPL 15

RESULT 31
Q9QV16
ID O9QV16 PRELIMINARY; PRT; 15 AA.
AC O9QV16;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Prolactin-binding protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RA Cohen H., Cohen O., Gagnon J.;
RA MEDLINE=95094032; PubMed=8000909;
RT "Serum prolactin-binding protein (PRL-BP) of human and rat are
RT identified as IgG.";
RL C. R. Acad. Sci., III, Sci. Vie 317:293-298(1994).
SQ SEQUENCE 15 AA; 1469 MW; 35ED2512PF3FA369 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 5 VES 7

RESULT 32
O88175
ID O88175 PRELIMINARY; PRT; 15 AA.
AC O88175;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neutral cell adhesion molecule (Fragment).
GN NCAM1 OR NCM.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-c; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RT of a muscle-specific exon in the mouse NCM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31274.1; -.
DR MGD; MGI:97281; Ncam1.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1481 MW; 41868EF6117732C2 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 9 VPL 11

RESULT 33
O86869
ID O86869 PRELIMINARY; PRT; 15 AA.
AC O86869;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE S-RNA product protein (Fragment).
GN S-RNA PRODUCT.
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX NCBI_TaxID=11623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskophidis D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
RT choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).
DR EMBL; S75753; AAB33673.1; -.
DR InterPro; IPR001535; Arena_glycoprot.
DR Pfam; PF00798; Arena_glycoprot; 1.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1571 MW; 2D25ABF4F776C1A7 CRC64;

Query Match 33.3%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 4 VES 6

RESULT 34
O91PD8
ID O91PD8 PRELIMINARY; PRT; 15 AA.
AC O91PD8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=j598;
RA Sabeta C.T., Bingham J., Nel L.H.;
RT "Molecular epidemiology of rabies associated with canine species in
RL Zimbabwe and South Africa."; EMBL/GenBank/DBJ databases.
DR EMBL; AF171117; AAK84649.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1700 MW; 5E0F9BF995E1E09E CRC64;

Query Match 33.3%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
Db 5 ESY 7

RESULT 35
Q91PE5
ID Q91PE5 PRELIMINARY; PRT; 15 AA.
AC Q91PE5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=j544;
RA Sabeta C.T., Bingham J., Nel L.H.;
RT "Molecular epidemiology of rabies associated with canine species in
RL Zimbabwe and South Africa.";
DR EMBL; AF171109; AAK84642.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1700 MW; 5E0F9BF995E1E09E CRC64;

Query Match 33.3%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
Db 5 ESY 7

RESULT 36
Q91PF4
ID Q91PF4 PRELIMINARY; PRT; 15 AA.
AC Q91PF4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=d352;
RA Sabeta C.T., Bingham J., Nel L.H.;
RT "Molecular epidemiology of rabies associated with canine species in
RL Zimbabwe and South Africa.";
DR EMBL; AF171100; AAK84633.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1700 MW; 5E0F9BF995E1E09E CRC64;

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Query Match 33.3%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
Db 5 ESY 7

RESULT 37
Q9R596
ID Q9R596 PRELIMINARY; PRT; 16 AA.
AC Q9R596;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE DNA topoisomerase I (Fragment).
OS Micrococcus luteus (Micrococcus lysodeikticus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococcaceae; Micrococcus.
OX NCBI_TaxID=1270;
RN [1]
RP SEQUENCE.
RX MEDLINE=93249439; PubMed=8387285;
RA Anderluzzi D., Pedrini A.M.;
RT "Structural similarities between M. luteus and E. coli DNA
RT topoisomerase I.";
RL Biochem. Biophys. Res. Commun. 192:657-664(1993).
SQ SEQUENCE 16 AA; 1672 MW; 0B5A23304332200F CRC64;

Query Match 33.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 10 VPL 12

RESULT 38
Q53399
ID Q53399 PRELIMINARY; PRT; 16 AA.
AC Q53399;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CryII protein (Fragment).
GN CRYIIB.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94123945; PubMed=8293956;
RA Hodgman T.C., Ziniu Y., Shen J., Ellar D.J.;
RT "Identification of a cryptic gene associated with an insertion
RT sequence not previously identified in Bacillus thuringiensis.";
DR FEMS Microbiol. Lett. 114:23-29(1993).
RL EMBL; S68408; AAC60457.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1944 MW; 132368F185FD4F90 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVV 5
Db 14 SVV 16

RESULT 39

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P83155
ID P83155 PRELIMINARY; PRT; 16 AA.
AC P83155;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fructose-bisphosphate aldolase (EC 4.1.2.13) (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apke S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE
CC PHOSPHATE + D-GLYCERALDEHYDE 3-PHOSPHATE.
CC -!- COFACTOR: ZINC (BY SIMILARITY).
CC -!- PATHWAY: SIXTH STEP IN GLYCOLYSIS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS II FRUCTOSE-BISPHOSPHATE ALDOLASE
CC FAMILY.
DR InterPro; IPR000771; K_bp aldolase.
DR PROSITE; PS00602; ALDOLASE CLASS II_1; PARTIAL.
DR PROSITE; PS00806; ALDOLASE CLASS II_2; PARTIAL.
KW Lyase; Glycolysis; Zinc; Metal-binding.
FT NON TER 16
SQ SEQUENCE 16 AA; 1702 MW; 5D2670D9E4833A8B CRC64;

Query Match 33.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 3 VPL 5

RESULT 40

Q9UC53
ID Q9UC53 PRELIMINARY; PRT; 16 AA.
AC Q9UC53;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 77 kDa SPONTANEOUS RECURRENT ABORTION-associated human embryonic
DE antigen/IGVHII homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=96033130; PubMed=8582963;
RA Shiraishi Y., Shiraishi Y., Yamamoto D., Hasegawa T., Kitamura W.,
RA Miki S., Tanaka T., Suzuki T., Soma H.;
RT "Diagnostic relevance of abortion-associated human embryonic antigen
RT expressed on the cell surface of tumour promoter-treated Bloom syndrome
RT cells."
RL Hum. Reprod. 10:1694-1701(1995).
SQ SEQUENCE 16 AA; 1626 MW; C9C5ED2512FF3FB9 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3
Db 5 VES 7

RESULT 41

Q9BGG8
ID Q9BGG8 PRELIMINARY; PRT; 16 AA.

Q9BGG8;
AC 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Thyroid hormone receptor alpha (Fragment).
GN THRA1.
OS Sorex araneus (Eurasian common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
OX NCBI_TaxID=42254;
RN [1]
RP SEQUENCE FROM N.A.
RA Latkin D., Serov O., Zhdanova N.;
RT "Mapping of five genes from human chromosome 17 to chromosome 17 of
RT the common shrew (Sorex araneus).";
RL Acta Theriol. (Warsz) 45:143-146(2000).
DR EMBL; AF314827; AAK13419.1; -.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 16 AA; 1951 MW; 775186E3FE5F52E2 CRC64;

Query Match 33.3%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9
Db 2 LFP 4

RESULT 42

O19977
ID O19977 PRELIMINARY; PRT; 16 AA.
AC O19977;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSI.
OS Gossypium mustelinum.
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34275;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronm R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031584; AAC63566.2; -.
KW Chloroplast.
FT NON TER 16
SQ SEQUENCE 16 AA; 1730 MW; A3145FAEFB57841E CRC64;

Query Match 33.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 12 VPL 14

RESULT 43

O19975
ID O19975 PRELIMINARY; PRT; 16 AA.

AC O19975;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE Photosystem I subunit (Fragment).
GN PSAL.
OS Gossypium tomentosum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34277;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group."
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031583; AAC63564.2; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1730 MW; A3145FAEFB57841E CRC64;
Query Match 33.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 VPL 7
DB 12 VPL 14
RESULT 44
O19973 PRELIMINARY; PRT; 16 AA.
AC O19973;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAL.
OS Gossypium barbadense (Sea-island cotton) (Egyptian cotton).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3634;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group."
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031582; AAC63562.2; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1730 MW; A3145FAEFB57841E CRC64;
Query Match 33.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 VPL 7
DB 12 VPL 14
RESULT 45
O19971 PRELIMINARY; PRT; 16 AA.
AC O19971;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAL.
OS Gossypium tomentosum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3634;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group."
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031582; AAC63562.2; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1730 MW; A3145FAEFB57841E CRC64;
Query Match 33.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 VPL 7
DB 12 VPL 14

GN PSAL.
OS Gossypium hirsutum (Upland cotton).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group."
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031581; AAC63560.2; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1730 MW; A3145FAEFB57841E CRC64;
Query Match 33.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 VPL 7
DB 12 VPL 14
RESULT 46
O9T2P6 PRELIMINARY; PRT; 16 AA.
AC O9T2P6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome P-450-FEMALE-specific isoform (Fragment).
GN Rattus sp.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91355184; PubMed=1883820;
RA Addya S., Zheng Y.M., Shayiq R.M., Fan J.Y., Avadhani N.G.;
RT "Characterization of a female-specific hepatic mitochondrial
RT cytochrome P-450 whose steady-state level is modulated by
RT testosterone.";
RL Biochemistry 30:8323-8330(1991).
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1837 MW; 7889F9F622765DAC CRC64;
Query Match 33.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 LFP 9
DB 14 LFP 16
RESULT 47
O9CW70 PRELIMINARY; PRT; 16 AA.
AC O9CW70;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adult male brain cDNA, RIKEN full-length enriched library,
DE clone:071008B15, full insert sequence (fragment).
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gofjohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003029; BAB22519.1; -.
DR MGD; MGI:96912; Mag.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1867 MW; 65BB8C02CB69FDB5 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
DB 8 PLF 10

RESULT 48
QPR5B1
ID QPR5B1 PRELIMINARY; PRT; 17 AA.
AC QPR5B1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE QUINALDINE oxidoreductase alpha-subunit (Fragment).
OS Arthrobacter.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Micrococcaceae.
OX NCBI_TaxID=1663;
RN [1]
RP SEQUENCE
RX MEDLINE=93228843; PubMed=8471177;
RA de Beyer A., Lings F.;
RT "Microbial metabolism of quinoline and related compounds. XVI.
RT Quinaldine oxidoreductase from Arthrobacter spec. Ru 61a: a molybdenum-
RT containing enzyme catalysing the hydroxylation at C-4 of the
RT heterocycle.";
RL Biol. Chem. Hoppe-Seyler 374:101-109(1993).
SQ SEQUENCE 17 AA; 1768 MW; A2EB35201E43B3E8 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
DB 1 VES 3

RESULT 49

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Q9URC6
ID Q9URC6 PRELIMINARY; PRT; 17 AA.
AC Q9URC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Lipid-binding protein (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91353077; PubMed=18825448;
RA Creutz C.E., Snyder S.L., Kambouris N.G.;
RT "Calcium-dependent secretory vesicle-binding and lipid-binding
RT proteins of Saccharomyces cerevisiae.";
RL Yeast 7:229-244(1991).
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1959 MW; C2EB6543287744D2 CRC64;

Query Match 33.3%; Score 3; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4
DB 15 ESY 17

RESULT 50
Q9NY39
ID Q9NY39 PRELIMINARY; PRT; 17 AA.
AC Q9NY39;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHI3L1 protein (Fragment).
GN CHI3L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ammon C., Rehli M., Andreessen R., Krause S.W.;
RT "Alternative splicing of the human cartilage gp-39 gene generates
RT multiple mRNA transcripts encoding for at least four putative protein
RT isoforms with distinct carboxyl termini.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251847; CAB76474.1; -.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 2099 MW; 086B9AA863393785 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
DB 15 PLF 17

RESULT 51
Q61932
ID Q61932 PRELIMINARY; PRT; 17 AA.
AC Q61932;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adult skeletal muscle myosin heavy chain mRNA carboxyl-end, segment 1
DE (Fragment).

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GN MYH4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=84061805; PubMed=6196357;
 RA Weydert A., Daubas P., Caravatti M., Minty A., Bugaisky G., Cohen A.,
 RA Robert B., Buckingham M.B.;
 RT "Sequential accumulation of mRNAs encoding different myosin heavy
 RT chain isoforms during skeletal muscle development in vivo detected
 RT with a recombinant plasmid identified as coding for an adult fast
 RT myosin heavy chain from mouse skeletal muscle.";
 RL J. Biol. Chem. 258:13867-13874(1983).
 DR EMBL: K00986; AAA39792.1; --
 DR MGD; MGI:1339713; Wny4.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1985 MW; 40EA696BF87181E2 CRC64;
 Query Match 33.3%; Score 3; DB 11; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VES 3
 Db 7 VES 9
 RESULT 52
 ID Q78374 PRELIMINARY; PRT; 17 AA.
 AC Q78374;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Viral sample FLPBR4E (Florida patient B), partial env cds, V4 region
 DE (Fragment).
 DE Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang L.Q., Leigh-Brown A.J.;
 RA Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92271245; PubMed=1589796;
 RA Ou C.-Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
 RA Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
 RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
 RA Jaffe H.W.;
 RT "Molecular Epidemiology of HIV Transmission in a Dental Practice.";
 RL Science 256:1165-1171(1992).
 DR EMBL: M92121; AAA44491.1; --
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1877 MW; 9925A5E497E51505 CRC64;
 Query Match 33.3%; Score 3; DB 15; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LFP 9
 Db 1 LFP 3
 RESULT 53
 Q85463
 ID Q85463 PRELIMINARY; PRT; 17 AA.
 AC Q85463, .

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Pol gene (Fragment).
 OS Avian sarcoma virus.
 OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=11876;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=88275035; PubMed=2839694;
 RA Katz R.A., Kotler M., Skalka A.M.;
 RT "cis-acting intron mutations that affect the efficiency of avian
 RT retroviral RNA splicing: Implication for mechanisms of control.";
 RL J. Virol. 62:2686-2695(1988).
 DR EMBL: M21395; AAA42414.1; --
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1835 MW; F43A1834E07A2C3A CRC64;
 Query Match 33.3%; Score 3; DB 15; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 PLF 8
 Db 4 PLF 6
 RESULT 54
 ID Q9FAC6 PRELIMINARY; PRT; 18 AA.
 AC Q9FAC6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Transposase (Fragment).
 OS Streptomyces coelicolor A3(2).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=100226;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21080545; PubMed=11212918;
 RA Yamasaki M., Redenbach M., Kinashi H.;
 RT "Integrated structures of the linear plasmid SCP1 in two bidirectional
 RT donor strains of Streptomyces coelicolor A3(2).";
 RL Mol. Gen. Genet. 264:634-642(2001).
 DR EMBL: AB042600; BAB17790.1; --
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1855 MW; 7B38501811F74BFE CRC64;
 Query Match 33.3%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VES 3
 Db 3 VES 5
 RESULT 55
 ID Q9TWL5 PRELIMINARY; PRT; 18 AA.
 AC Q9TWL5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE 24 kDa chymotrypsin-like enzyme (Fragment).
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Lucilia.
 OX NCBI_TaxID=7375;

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RN SEQUENCE.
RX MEDLINE=95219141; PubMed=7704304;
RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Riding G.A.,
RA Tellam R.L.;
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,
RT enzymatic specificity and amino acid sequence deduced from mRNA.";
RL Insect Mol. Biol. 3:201-211(1994).
SQ SEQUENCE 18 AA; 2002 MW; AC29200B9B184300 CRC64;

Query Match 33.3%; Score 3; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
Db 11 LFP 13

RESULT 56
Q9GB22 PRELIMINARY; PRT; 18 AA.
AC Q9GB22;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Cytochrome c oxidase subunit II (Fragment).
GN CoII.
OS Calyptomena viridis (Lesser green broadbill).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Eurylaimidae;
OC Calyptomena.
OX NCBI_TaxID=135972;
RN [1]
RP SEQUENCE FROM N.A.
RA Slikas B., Jones I.B., Derricks S.R., Fleischer R.C.;
RT "Phylogenetic relationships of Micronesian white-eyes (Zosteropidae)
RT based on mitochondrial sequence data.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF168455; AAG12310.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 18 AA; 1993 MW; 59773229B49CF327 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 1 VES 3

RESULT 57
O19979 PRELIMINARY; PRT; 18 AA.
AC O19979;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 13, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAl.
OS Gossypium darwinii (Darwin's cotton).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsida II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34276;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and

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RT nuclear Adh sequences" for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031585; AAC63568.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 18 AA; 1942 MW; AC14C3145FAEPB57 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 12 VPL 14

RESULT 58
O19969 PRELIMINARY; PRT; 18 AA.
AC O19969;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAl.
OS Gossypium arboreum (Tree cotton).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsida II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=29729;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031580; AAC63558.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 18 AA; 1942 MW; AC14C3145FAEPB57 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 12 VPL 14

RESULT 59
Q9ZY79 PRELIMINARY; PRT; 18 AA.
AC Q9ZY79;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Idris sp.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Platygastroidae;
OC Scelionidae; Idris.
OX NCBI_TaxID=81086;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Dowton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera.";

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RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL; AF082922; AAD1782.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 18 AA; 2131 MW; BBB4F286AEA31D08 CRC64;
Query Match 33.3%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PLF 8
DB 9 PLF 11

RESULT 60
Q78376 PRELIMINARY; PRT; 18 AA.
AC Q78376;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Viral sample FLPR41 (Florida patient B), partial env cds, V4 region (Fragment).
DE (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.-Y., Gieselski C.A., Myers G., Bandea C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
RA Jaffe H.W.;
RT "Molecular Epidemiology of HIV Transmission in a Dental Practice.";
RL Science 256:1165-1171(1992).
DR EMBL; M92122; AAA44492.1; -.
FT NON TER 1
FT NON TER 18
SQ SEQUENCE 18 AA; 2000 MW; DB1E4794679B050A CRC64;
Query Match 33.3%; Score 3; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 LFP 9
DB 1 LFP 3

RESULT 61
Q82S29 PRELIMINARY; PRT; 18 AA.
AC Q82S29;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAE3501a.
GN PAE3501a.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;

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RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AR00934; AAL64964.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 18 AA; 2362 MW; BCF4D6923A98943 CRC64;
Query Match 33.3%; Score 3; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ESY 4
DB 3 ESY 5

RESULT 62
Q43964 PRELIMINARY; PRT; 19 AA.
ID Q43964;
AC Q43964;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nitrogenase molybdenum-iron protein (Fragment).
DE Nitrogenase molybdenum-iron protein (Fragment).
GN NIFD.
OS Azotobacter chroococcum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=353;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93138425; PubMed=8423000;
RA Jones R.L., Woodley P., Zinoni A.B., Robson R.L.;
RT "The nif gene encoding the Fe protein of the molybdenum nitrogenase
RT from Azotobacter chroococcum.";
RL Gene 123:145-146(1993).
DR EMBL; M73020; AAA22141.1; -.
FT NON TER 19
FT NON TER 19
SQ SEQUENCE 19 AA; 2165 MW; OAC46CC8BF500CD7 CRC64;
Query Match 33.3%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VES 3
DB 9 VES 11

RESULT 63
Q9UCU1 PRELIMINARY; PRT; 19 AA.
ID Q9UCU1;
AC Q9UCU1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Gelatinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93099930; PubMed=1464361;
RA Kjeldsen L., Bjerrum O.W., Hovgaard D., Johnsen A.H., Sehested M.,
RA Borregaard N.;
RT "Human neutrophil gelatinase: a marker for circulating blood
RT neutrophils. Purification and quantitation by enzyme linked
RT immunosorbent assay.";
RL Eur. J. Haematol. 49:180-191(1992).
SQ SEQUENCE 19 AA; 2200 MW; 968209EF26B87375 CRC64;
Query Match 33.3%; Score 3; DB 4; Length 19;

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Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
Db 10 LFP 12

RESULT 64
Q9UCB4 PRELIMINARY; PRT; 19 AA.
ID Q9UCB4;
AC Q9UCB4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE PROCATHEPSIN E (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93349047; PubMed=8346912;
RA Takeda-Ezaki M., Yamamoto K.;
RT "Isolation and biochemical characterization of procathepsin E from
RT human erythrocyte membranes.";
RL Arch. Biochem. Biophys. 304:352-358(1993)
SQ SEQUENCE 19 AA; 2293 MW; 3217AB8670A65FC CRC64;

Query Match 33.3%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 5 VPL 7

RESULT 65
Q947M7 PRELIMINARY; PRT; 19 AA.
ID Q947M7;
AC Q947M7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Leucoanthocyanidin dioxygenase (Fragment).
GN LDOX.
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OC Vitis.
OX NCBI_TaxID=29760;
RN [1]
RP SEQUENCE FROM N.A.
RA Gollop R., Farhi S., Perl A.;
RT "Regulation of the leucoanthocyanidin dioxygenase gene expression in
RT Vitis vinifera.";
RL Plant Sci. 161:579-588(2001).
DR EMBL; AF290432; AAK96258.1; -.
KW Dioxygenase.
FT NON_TER
SQ SEQUENCE 19 AA; 1935 MW; 95D58D008AE5E27F CRC64;

Query Match 33.3%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 9 VES 11

RESULT 66
Q9PS17 PRELIMINARY; PRT; 19 AA.
ID Q9PS17;
AC Q9PS17;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Puromycin-sensitive aminopeptidase isozyme II (Fragment).

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Q41567 PRELIMINARY; PRT; 19 AA.
ID Q41567;
AC Q41567;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Heat shock protein 16.9 (Fragment).
GN HSP16.9-3LC2.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Mustang;
RX MEDLINE=96382426; PubMed=8790290;
RA Joshi C.P., Nguyen H.T.;
RT "Differential display-mediated rapid identification of different
RT members of a multigene family, HSP 16.9 in wheat.";
RL Plant Mol. Biol. 31:575-584(1996).
DR EMBL; L37074; AAA51394.1; -.
FT NON_TER
SQ SEQUENCE 19 AA; 1769 MW; 7A77E05EFD609CEFC CRC64;

Query Match 33.3%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 4 VPL 6

RESULT 67
Q8KON2 PRELIMINARY; PRT; 19 AA.
ID Q8KON2;
AC Q8KON2;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030921; AAH30921.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 19 AA; 2255 MW; 66C5F38861B749AE CRC64;

Query Match 33.3%; Score 3; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
Db 6 LFP 8

RESULT 68
Q9PS17 PRELIMINARY; PRT; 19 AA.
ID Q9PS17;
AC Q9PS17;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Puromycin-sensitive aminopeptidase isozyme II (Fragment).

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OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN NCBI_TaxID=9031;
 RP SEQUENCE.
 RX MEDLINE=93250542; PubMed=8485450;
 RA Hui K.S., Saito M., Hui M., Saito M., Lajtha A., Yamamoto K.,
 RA Osawa T.;
 RL Neurochem. Int. 22:445-453(1993).
 DR HSP; P29312; 1QJA.
 SQ SEQUENCE 19 AA; 2159 MW; 8091278C84691774 CRC64;

Query Match 33.3%; Score 3; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
 Db 16 ESY 18

RESULT 69
 Q9PS14
 ID Q9PS14 PRELIMINARY; PRT; 19 AA.
 AC Q9PS14;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Puromycin-sensitive aminopeptidase isozyme I (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN SEQUENCE.
 RP MEDLINE=93250542; PubMed=8485450;
 RX Hui K.S., Saito M., Hui M., Saito M., Lajtha A., Yamamoto K.,
 RA Osawa T.;
 RL Neurochem. Int. 22:445-453(1993).
 DR HSP; P29312; 1QJA.
 SQ SEQUENCE 19 AA; 2132 MW; 8091278C8478E774 CRC64;

Query Match 33.3%; Score 3; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
 Db 16 ESY 18

RESULT 70
 Q9PR70
 ID Q9PR70 PRELIMINARY; PRT; 19 AA.
 AC Q9PR70;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE 23A7 antigen (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN SEQUENCE.
 RP MEDLINE=95332492; PubMed=7608337;
 RX Denburg J.L., Caldwell R.T., Marner J.M.;
 RA "Developmental changes in epitope accessibility as an indicator of
 RT multiple states of an immunoglobulin-like neural cell adhesion

RT molecule.";
 RL J. Comp. Neurol. 354:533-550(1995).
 SQ SEQUENCE 19 AA; 2051 MW; 83E67BEE484EED03 CRC64;
 Query Match 33.3%; Score 3; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
 Db 3 VPL 5

RESULT 71
 Q78351
 ID Q78351 PRELIMINARY; PRT; 19 AA.
 AC Q78351;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Viral sample FLPR4A (Florida patient B), partial env cds, V4 region (Fragment).
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA Zhang L.Q., Leigh-Brown A.J.;
 RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92271245; PubMed=1589796;
 RA Ou C.-Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
 RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
 RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
 RA Jaffe H.W.;
 RA "Molecular Epidemiology of HIV Transmission in a Dental Practice.";
 RL Science 256:1165-1171(1992).
 DR EMBL; M92118; AAA44488.1; -.
 FT NON_TER 1
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 1985 MW; 5FFC8787D98CEA1C CRC64;

Query Match 33.3%; Score 3; DB 15; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9
 Db 1 LFP 3

RESULT 72
 Q9R4N0
 ID Q9R4N0 PRELIMINARY; PRT; 20 AA.
 AC Q9R4N0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Muconate cycloisomerase (EC 5.5.1.1) (Fragment).
 OS Rhodococcus erythropolis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Nocardiaceae; Rhodococcus.
 OC NCBI_TaxID=1833;
 RN SEQUENCE.
 RP MEDLINE=95270600; PubMed=7751292;
 RX Solyanikova I.P., Maltseva O.V., Vollmer M.D., Golovleva L.A.,
 RA Schliemann M.;
 RA "Characterization of muconate and chloromuconate cycloisomerase from
 RT Rhodococcus erythropolis 1CP; indications for functionally convergent
 evolution among bacterial cycloisomerases.";
 RL J. Bacteriol. 177:2821-2826(1995).

SQ SEQUENCE 20 AA; 2167 MW; 1490DD0BA27A5773 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 15 VPL 17

RESULT 73

Q96FJ6 PRELIMINARY; PRT; 20 AA.
AC Q96FJ6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010734; AAH10734.1; -.
KW Hypothetical protein.
SQ SEQUENCE 20 AA; 2406 MW; CC51FC8C824E6D52 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
Db 18 PLF 20

RESULT 74

Q8WX06 PRELIMINARY; PRT; 20 AA.
AC Q8WX06;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE B212B22.1 (Diaphanous (Drosophila, homolog 2) (Fragment).
GN DIAPH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL391821; CAD13462.1; -.
FT NON_TER
SQ SEQUENCE 20 AA; 2321 MW; 8821A82DF9B73B78 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 4 VPL 6

RESULT 75

Q8TE41

ID Q8TE41 PRELIMINARY; PRT; 20 AA.
AC Q8TE41;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Truncated steroid 11beta-hydroxylase (Fragment).
GN CYP11B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Penachioni J.Y.; de Castro M., Bachega T.A., Mendonca B.B.,
RA de Mello M.P.;
RT "CYP11B1 new mutations R404+C and G267S leading to 11beta-hydroxylase
deficiency in Brazilian patients."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Penachioni J.Y.;
RT "Mutations and polymorphisms in CYP11B1 human gene in individuals with
11-beta-Hydroxylase deficiency."
RL Thesis (2001), Department of College of Medical Sciences,
RL Campinas State University, Campinas, SP, Brazil.
DR EMBL; AJ431375; CAD24087.1; -.
FT NON_TER
SQ SEQUENCE 20 AA; 2130 MW; 78B715D5A3CD45BF CRC64;

Query Match 33.3%; Score 3; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 6 VPL 8

Search completed: November 25, 2003, 19:34:13
Job time : 17.9012 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 22.9709 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVLPFP 9

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

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Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	AAW42101	Colostrinin derive
2	9	100.0	9	AAW72276	Colostrinin derive
3	9	100.0	9	AAW72529	Colostrinin peptid
4	9	100.0	9	AAW72561	Colostrinin peptid
5	9	100.0	9	AAW20258	Colostrinin consti
6	9	100.0	9	AAW51067	Colostrinin consti
7	9	100.0	9	AAW14607	Neural cell regula
8	8	88.9	8	AAW07189	Colostrinin peptid
9	8	88.9	9	AAW07199	Modified colostrin

10	5	55.6	15	22	AB98131	Interferon-gamma s
11	5	55.6	15	22	AB98132	Interferon-gamma s
12	5	55.6	15	22	AB98133	Interferon-gamma s
13	5	55.6	15	22	AB97741	gp100 derived IPN-
14	5	55.6	15	22	AB97742	gp100 derived IPN-
15	5	55.6	15	22	AB97743	gp100 derived IPN-
16	5	55.6	15	23	AB946299	Human Blys binding
17	5	55.6	16	23	AB946252	Human Blys binding
18	4	44.4	7	12	AA12158	Cyclo-octa peptide
19	4	44.4	7	19	AAW46013	Peptide #45 based
20	4	44.4	7	20	AAV17016	Heat shock protein
21	4	44.4	7	22	AAU72158	Melanoma antigen,
22	4	44.4	7	23	AAU80708	Javelin peptide #1
23	4	44.4	8	15	AA58322	Hypotensive polype
24	4	44.4	8	20	AAV16845	Heat shock protein
25	4	44.4	8	22	AB804380	Carrot partial ant
26	4	44.4	8	22	ABG20475	Mouse contactin pr
27	4	44.4	8	23	ABG78590	Multiple sclerosis
28	4	44.4	8	24	ABJ20030	MHC binding peptid
29	4	44.4	9	14	AA946514	Plasmodium yoelii
30	4	44.4	9	19	AAW68359	MHC binding peptid
31	4	44.4	9	21	AA523654	Cytotoxic T lympho
32	4	44.4	9	21	AAV96361	HLA-A24 binding pe
33	4	44.4	9	21	AAV86776	Telomerase peptide
34	4	44.4	9	21	AAV68305	Altered MHC determ
35	4	44.4	9	21	AAV52959	Altered MHC determ
36	4	44.4	9	22	AAW98253	Human peptide #152
37	4	44.4	9	22	AAW63512	Amino acid sequenc
38	4	44.4	9	22	AAW63517	Amino acid sequenc
39	4	44.4	9	22	AAW66424	Circumsporozoite p
40	4	44.4	9	23	AAW79591	Malarial epitope #
41	4	44.4	9	24	ABR06327	Human cancer-relat
42	4	44.4	9	24	ABR07074	Human cancer-relat
43	4	44.4	9	24	ABR07293	Human cancer-relat
44	4	44.4	9	24	ABP72311	Plasmodium yoelii
45	4	44.4	9	24	ABP58362	CSP peptide. Mus
46	4	44.4	10	16	AAW79143	Fructosyltransfera
47	4	44.4	10	22	AAW85227	Saccharomyces cere
48	4	44.4	10	23	AB883032	Transferrin recept
49	4	44.4	10	24	ABR06228	Human cancer-relat
50	4	44.4	10	24	ABR06458	Human cancer-relat
51	4	44.4	10	24	ABR06590	Human cancer-relat
52	4	44.4	10	24	ABR07254	Human cancer-relat
53	4	44.4	10	24	ABR07442	Human cancer-relat
54	4	44.4	11	16	ABR72659	Cladosporium herba
55	4	44.4	11	22	AAE11116	Tryptic peptide #1
56	4	44.4	11	22	AAW99185	Vaccine related MH
57	4	44.4	11	22	AAW63527	An epitope which m
58	4	44.4	11	24	ABP99426	Beta-amyloid bindi
59	4	44.4	12	21	AAV67307	Malarial epitope o
60	4	44.4	12	22	AAW99153	Vaccine related MH
61	4	44.4	12	22	AAW63518	Amino acid sequenc
62	4	44.4	13	13	AAW21802	Epitope, from alle
63	4	44.4	13	22	AAW17675	Novel signal trans
64	4	44.4	13	22	AAW68132	Peptide derived fr
65	4	44.4	13	24	ABP53814	Human CNTF potenti
66	4	44.4	13	24	ABP53834	Human CNTF potenti
67	4	44.4	13	24	ABP53835	Human CNTF potenti
68	4	44.4	13	24	ABP53854	Human CNTF potenti
69	4	44.4	13	24	ABP53874	Human CNTF potenti
70	4	44.4	14	16	AAW83142	Human CNTF potenti
71	4	44.4	14	22	ABW56665	[4-Leu, 12-D-Arg,
72	4	44.4	14	22	AAW97755	Human peptide #103
73	4	44.4	14	22	AAW99155	Vaccine related MH
74	4	44.4	14	22	ABW70401	Rabies matrix prot
75	4	44.4	14	23	ABP46338	Human Blys binding
76	4	44.4	14	23	ABP46377	Human Blys binding
77	4	44.4	14	23	ABP46412	Human Blys binding
78	4	44.4	14	23	ABP46436	Human Blys binding
79	4	44.4	14	23	ABP46456	Human Blys binding
80	4	44.4	14	23	ABP46522	Human Blys binding
81	4	44.4	14	23	ABP46629	Human Blys binding
82	4	44.4	14	23	ABP46646	Human Blys binding

83 Human BlyS binding
 84 Purified cis-9,10-
 85 Purified cis-9,10-
 86 Beta (1 -> 4)-N-ac
 87 Fatty acid amide h
 88 Fatty acid amide h
 89 Transforming growth
 90 Transforming growth
 91 Transforming growth
 92 Human cytomagalovi
 93 Human cytomagalovi
 94 Human cytomagalovi
 95 Human myosin heavy
 96 Human BlyS binding
 97 Human BlyS binding
 98 Human BlyS binding
 99 Human BlyS binding
 100 Human BlyS binding

ALIGNMENTS

RESULT 1

AAW42101
 ID AAW42101 standard; peptide; 9 AA.

XX AAW42101;
 DT 09-SEP-1998 (first entry)
 XX Colostrinin derived nanopptide.
 DE Colostrinin; nanopptide; NP; central nervous system; CNS;
 KW neurological disorder; mental disorder; dementia; Alzheimer's disease;
 KW motor neurone disease; Parkinson's disease; psychosis; neurosis;
 KW immunological deficiency; cancer therapy; stimulation; modulator;
 KW dietary supplement; cachexia; inhibition.
 XX Homo sapiens.
 XX WO9814473-A1.
 XX 09-APR-1998.
 XX 03-OCT-1997; 97WO-GB02721.
 XX 03-OCT-1996; 96PL-0316416.
 XX (GEOR-) GEORGIADES BIOTECH LTD.
 XX (HRS-) HIRSZPFLD INST IMMUNOLOGY & EXPERIMENTAL.

XX Dubowska-Inglot A, Janusz M, Lisowski J;
 XX WPI; 1998-250967/22.

XX Use of colostrinin, or derived nanopptide for treating chronic
 XX diseases of the central nervous system - and immune system, also as
 XX dietary supplement and for inhibiting development of Alzheimer's
 XX disease
 XX Claim 51; Page 27; 34pp; English.
 XX This is the amino acid sequence of the colostrinin derived nanopptide
 XX (NP). In the method of the invention colostrinin, and its NP are used
 XX to treat chronic disorders of the central nervous system (CNS),
 XX particularly neurological and mental disorders such as dementia
 XX (Alzheimer's disease); motor neurone disease (e.g. Parkinson's disease);
 XX psychosis and neurosis (including assisting withdrawal from addictive
 XX drugs) and the immune system, particularly bacterial or viral infections
 XX or acquired immunological deficiency (e.g. where caused by cancer
 XX therapy). Colostrinin is a stimulant/modulator of the immune system and
 XX may also be used as a dietary supplement, e.g. in babies who have not

CC received colostrum, young children or adults being given chemotherapy or
 CC suffering from cachexia due to chronic disease, and to inhibit
 CC development of Alzheimer's disease.

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9

Db 1 VESYVPLFP 9

RESULT 2

AAW72276
 ID AAW72276 standard; peptide; 9 AA.

XX AAW72276;

XX 14-MAY-2001 (first entry)

DE Colostrinin derived cytokine inducing peptide SEQ ID 31.

XX Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.

XX Synthetic.
 XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA) UNIV TEXAS SYSTEM.
 XX (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for
 XX treating central nervous system diseases and bacterial and viral
 XX infections, comprises administering colostrinin as an immunological
 XX regulator -
 XX Claim 1; Page 34; 50pp; English.

XX Sequences AAW72246 - AAW72275 represent peptides derived from colostrinin,
 XX a proline rich polypeptide aggregate contained in colostrum. The
 XX peptides have immune response modulatory activity, and are capable of
 XX inducing cytokines. Colostrinin and its derived peptides are useful for
 XX inducing cytokine production, for modulating an immunological response
 XX and for inducing blood cell proliferation. The peptides are useful in the
 XX treatment of disorders of the central nervous system, neurological
 XX disorders, mental disorders, dementia, neurodegenerative diseases,
 XX Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 XX disorders of the immune system, bacterial and viral infections and
 XX acquired immunological deficiencies.

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9

Db 1 VESYVPLFP 9
|||||

RESULT 3

AAE72529
ID AAE72529 standard; Peptide; 9 AA.

XX AC AAE72529;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #30.

XX NW Dermatological; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX PN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22665.

XX PR 17-AUG-1999; 99US-0149310.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations -

XX PS Claim 6; Page 26; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidizing species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9
|||||

Db 1 VESYVPLFP 9

RESULT 4

AAE72561
ID AAE72561 standard; Peptide; 9 AA.

XX AC AAE72561;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #30.

XX NW Neuroprotective; neural cell differentiation regulator; colostrinin; colostrum.

XX OS Unidentified.

XX PN WO200112651-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22774.

XX PR 17-AUG-1999; 99US-0149633.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Boldogh I;

XX DR WPI; 2001-226545/23.

XX PT Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient -

XX PS Claim 6; Page 22; 35pp; English.

XX CC The present invention relates to a method for promoting neural cell differentiation and treating damaged neural cells, using colostrinin and colostrinin constituent peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9
|||||

Db 1 VESYVPLFP 9

RESULT 5

AAE20258

ID AAE20258 standard; peptide; 9 AA.

XX AC AAE20258;

XX DT 18-JUN-2002 (first entry)

XX DE Colostrinin constituent peptide #30.

XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue; organ; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnery.

XX OS Unidentified.

XX PH Key Location/Qualifiers

XX FT Modified-site 9

XX FT /note= "Optionally C-terminal amide"

XX PN WO200213850-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22776.

XX PR 17-AUG-2000; 2000WO-US22776.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2002-269151/31.

XX PT Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog -

XX Claim 6; Page 26; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/
 CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrin constituent peptide.

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9
 |||||
 Db 1 VESYVPLFP 9

RESULT 6

AA051067
 ID AA051067 standard; Peptide; 9 AA.

AC AA051067;

XX 30-MAY-2002 (first entry)

XX Colostrin constituent peptide.

XX Colostrin; colostrum; beta-casein; human.

XX Homo sapiens.

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrin, its constituent peptide
 PT and/or analogue -

XX Example 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrin constituent peptide
 CC that has been classified as having a beta-casein homologue precursor.
 CC The peptide has previously been identified as being useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,

CC Alzheimer's disease, motor neurone disease, psychosis, neurosis,
 CC chronic disorders of the immune system, diseases with a bacterial
 CC or viral aetiology, and acquired immunological deficiencies. The
 CC present invention provides claimed colostrin constituted peptides
 CC (see AM51036-66) that are useful as immunological regulators and
 CC as blood cell regulators. These are used in claimed methods of the
 CC invention to modulate specific or nonspecific immune responses in
 CC patients, and to modulate cellular proliferation or differentiation
 CC of blood cells, such as leucocytes. These methods specifically do
 CC not use the present colostrin peptide.

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9
 |||||
 Db 1 VESYVPLFP 9

RESULT 7

AA014607
 ID AA014607 standard; peptide; 9 AA.

XX AC AA014607;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrin peptide 30.

XX Neural cell differentiation; neural cell regulator; colostrin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 9 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 22; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrin peptide used in
 CC the method of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9
 |||||
 Db 1 VESYVPLFP 9

RESULT 8

AAE07189
 ID AAE07189 standard; peptide; 8 AA.

AC
 XX
 DT 06-NOV-2001 (first entry)
 DE
 DE Colostrinin peptide 5.

Colostrinin; neurotropic; neuroprotective; immunomodulatory; antibacterial;
 Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 central nervous system disorder; neurodegenerative disorder; weight loss;
 beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 acquired immunological deficiency; neurological disorder; dementia;
 antiviral.

XX Unidentified.

OS
 XX WO200155199-A1.

FN
 XX 02-AUG-2001.

PD 26-JAN-2001; 2001WO-GB00329.

PF 26-JAN-2000; 2000GB-0001825.

PR (REGE-) REGEN THERAPEUTICS PLC.

PA Georgiades JA;

PI WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -

XX Claim 1; Page 15; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is colostrinin peptide 5 related to the invention.

XX Sequence 8 AA;

Query Match 88.9%; Score 8; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYVPLFP 9
 |||||
 Db 1 ESYVPLFP 8

RESULT 9

AAE07199
 ID AAE07199 standard; peptide; 9 AA.

XX
 AC AAE07199;

XX 06-NOV-2001 (first entry)
 DT
 DE Modified colostrinin cyclic peptide #5.

Colostrinin; neurotropic; neuroprotective; immunomodulatory; antibacterial;
 Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 central nervous system disorder; neurodegenerative disorder; weight loss;
 beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 acquired immunological deficiency; neurological disorder; dementia;
 antiviral; cyclic.

XX Synthetic.

OS
 XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl; this residue forms a cyclic

FT linkage with Pro found at the C-terminal end"

XX WO200155199-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-GB00329.

XX 26-JAN-2000; 2000GB-0001825.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -

XX Example 2; Page 9; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is modified colostrinin cyclic peptide #5 related to
 CC the invention.

```

XX SQ Sequence 9 AA;
Query Match 88.9%; Score 8; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9
Db 2 ESYVPLFP 9
|||||

RESULT 10
AAB98131
ID AAB98131 standard; Peptide; 15 AA.
XX AC AAB98131;
XX DT 17-AUG-2001 (first entry)
XX DE Interferon-gamma stimulation gp100 derived peptide 1365.
XX DX Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
XX KW modified gp100; vaccine; gene therapy; cancer.
XX OS Homo sapiens.
XX PN WO200130847-A1.
XX PD 03-MAY-2001.
XX PF 20-OCT-2000; 2000WO-CA01254.
XX PR 22-OCT-1999; 99US-0160879.
XX PR 07-AUG-2000; 2000US-0223325.
XX PA (AVET ) AVENTIS PASTEUR LTD.
XX PI Berinsein N, Tartaglia J, Moingeon P, Barber B, Tine JA;
XX DR WPI; 2001-316326/33.
XX PT New isolated and purified gp100 useful for the prophylactic treatment
XX PS of cancer -
XX PS Example 4; Page 61; 89pp; English.
XX CC The present invention describes an isolated and purified modified gp100
XX CC molecule (gp100M) capable of modulating an immune response in an animal.
XX CC gp100M has cytostatic activity and can be used in vaccine production and
XX CC gene therapy. Nucleic acids and proteins of the invention are useful as
XX CC vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and
XX CC AAB98098 to AAB98206 represent sequence used in the exemplification of
XX CC the present invention. More specifically AAB98098 to AAB98205 represent
XX CC peptides derived from gp100; AAH22084 to AAH22097 and AAH22100 to
XX CC AAH22106 represent primers used in the present invention; AAH22099
XX CC represents the plasmid nucleotide sequence comprising the Vaccinia virus
XX CC H6 promoter and the human gp100 gene; and AAH22098 encodes the human
XX CC gp100M protein given in AAB22106.
XX SQ Sequence 15 AA;
Query Match 55.6%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVPL 7
Db 6 SYVPL 10
|||||

RESULT 12
AAB98133
ID AAB98133 standard; Peptide; 15 AA.
XX AC AAB98133;
XX DX 17-AUG-2001 (first entry)
XX DE Interferon-gamma stimulation gp100 derived peptide 1366.
XX DX Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
XX KW modified gp100; vaccine; gene therapy; cancer.
XX OS Homo sapiens.
XX PN WO200130847-A1.

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XX PD 03-MAY-2001.
 XX PF 20-OCT-2000; 2000WO-CA01254.
 XX PR 22-OCT-1999; 99US-0160879.
 XX PR 07-AUG-2000; 2000US-0223325.
 XX PA (AVET) AVENTIS PASTEUR LTD.
 XX PI BerinSTEIN N, Tartaglia J, Moingeon P, Barber B, Tine JA;
 XX PI WPI; 2001-316326/33.
 XX DR New isolated and purified gp100 useful for the prophylactic treatment
 XX PT of cancer -
 XX PS Example 4; Page 61; 89pp; English.
 XX CC The present invention describes an isolated and purified modified gp100
 XX CC molecule (gp100M) capable of modulating an immune response in an animal.
 XX CC gp100M has cytostatic activity and can be used in vaccine production and
 XX CC gene therapy. Nucleic acids and proteins of the invention are useful as
 XX CC vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and
 XX CC AAB98098 to AAB98206 represent sequence used in the exemplification of
 XX CC the present invention. More specifically AAB98098 to AAB98205 represent
 XX CC peptides derived from gp100; AAH22084 to AAH22097 and AAH22100 to
 XX CC AAH22106 represent primers used in the present invention; AAH22099
 XX CC represents the plasmid nucleotide sequence comprising the Vaccinia virus
 XX CC H6 promoter and the human gp100 gene; and AAH22098 encodes the human
 XX CC gp100M protein given in AAB22106.
 XX SQ Sequence 15 AA;
 Query Match 55.6%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SYVPL 7
 DB 1 SYVPL 5
 RESULT 13
 AAB97741
 ID AAB97741 standard; Peptide; 15 AA.
 XX AC AAB97741;
 XX DT 08-AUG-2001 (first entry)
 XX DE gp100 derived IFN-gamma production stimulation peptide SEQ ID NO:34.
 XX KW Virus; adenovirus; poxvirus; alphavirus; immune response; gp100;
 XX KW tumour antigen; CEA; carcinoembryonic antigen; immunostimulant;
 XX KW cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer.
 XX OS Virus.
 XX OS Synthetic.
 XX PN WO200130382-A1.
 XX PD 03-MAY-2001.
 XX PF 20-OCT-2000; 2000WO-CA01253.
 XX PR 22-OCT-1999; 99US-0160879.
 XX PR 07-AUG-2000; 2000US-0223325.
 XX PA (AVET) AVENTIS PASTEUR LTD.
 XX PI BerinSTEIN N, Tartaglia J, Moingeon P, Barber B;
 XX PI WPI; 2001-308587/32.
 XX PT Inducing immune response to tumor antigen, useful in immunotherapy of
 XX PT cancer, by administering the antigen to a lymphatic site -

DR WPI; 2001-308587/32.
 XX Inducing immune response to tumor antigen, useful in immunotherapy of
 XX PT cancer, by administering the antigen to a lymphatic site -
 XX PS Example 1; Page 39; 60pp; English.
 XX CC The present invention describes a method for inducing an immune response,
 XX CC in an animal, to a tumour antigen (Ag) comprising administering Ag, or
 XX CC nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys
 XX CC (Macaca fascicularis) were injected with a modified form of gp100 antigen
 XX CC (a) into the left inguinal lymph node or (b) subcutaneously. Both animals
 XX CC of (a) developed a cell-mediated response (indicated by production of
 XX CC interferon-gamma from T lymphocytes when exposed to gp100 peptides), but
 XX CC only 2 of 4 animals of (b) did so. Also animals in (a) produced a far
 XX CC greater antibody response to gp100. The method is used in immunotherapy
 XX CC of a wide range of cancers through induction of a specific immune
 XX CC response (humoral and cellular) against the tumour antigens. When
 XX CC administered to a lymphatic site, Ag (or (I)) induces a stronger immune
 XX CC response than administration by other routes and may also break tolerance
 XX CC to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to
 XX CC AAB97815 represent peptides derived from gp100 which stimulate interferon
 XX CC (IFN)-gamma production; AAH20120 encodes the modified gp100 protein given
 XX CC in AAB97816; AAH20121 encodes the modified carcinoembryonic antigen (CEA)
 XX CC protein given in AAB97817; and AAB97818 represents a CEA modified antigen
 XX CC peptide, all of which are used in the exemplification of the present
 XX CC invention.
 XX SQ Sequence 15 AA;
 Query Match 55.6%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SYVPL 7
 DB 11 SYVPL 15
 RESULT 14
 AAB97742
 ID AAB97742 standard; Peptide; 15 AA.
 XX AC AAB97742;
 XX DT 08-AUG-2001 (first entry)
 XX DE gp100 derived IFN-gamma production stimulation peptide SEQ ID NO:35.
 XX KW Virus; adenovirus; poxvirus; alphavirus; immune response; gp100;
 XX KW tumour antigen; CEA; carcinoembryonic antigen; immunostimulant;
 XX KW cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer.
 XX OS Virus.
 XX OS Synthetic.
 XX PN WO200130382-A1.
 XX PD 03-MAY-2001.
 XX PF 20-OCT-2000; 2000WO-CA01253.
 XX PR 22-OCT-1999; 99US-0160879.
 XX PR 07-AUG-2000; 2000US-0223325.
 XX PA (AVET) AVENTIS PASTEUR LTD.
 XX PI BerinSTEIN N, Tartaglia J, Moingeon P, Barber B;
 XX PI WPI; 2001-308587/32.
 XX PT Inducing immune response to tumor antigen, useful in immunotherapy of
 XX PT cancer, by administering the antigen to a lymphatic site -

XX Example 1; Page 39; 60pp; English.

PS CC The present invention describes a method for inducing an immune response, in an animal, to a tumour antigen (Ag) comprising administering Ag, or nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys (Macaca fascicularis) were injected with a modified form of gp100 antigen (a) into the left inguinal lymph node or (b) subcutaneously. Both animals of (a) developed a cell-mediated response (indicated by production of interferon-gamma from T lymphocytes when exposed to gp100 peptides), but only 2 of 4 animals of (b) did so. Also animals in (a) produced a far greater antibody response to gp100. The method is used in immunotherapy of a wide range of cancers through induction of a specific immune response (humoral and cellular) against the tumour antigens. When administered to a lymphatic site, Ag (or (I)) induces a stronger immune response than administration by other routes and may also break tolerance to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to AAB97815 represent peptides derived from gp100 which stimulate interferon (IFN)-gamma production; AAB97816; AAB97817; and AAB97818 represents a CEA modified antigen protein given in AAB97817; and AAB97818 represents a CEA modified antigen peptide, all of which are used in the exemplification of the present invention.

XX Sequence 15 AA;

SQ Query Match 55.6%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVPL 7
Db |||||
6 SYVPL 10

RESULT 15
AAB97743
ID AAB97743 standard; Peptide; 15 AA.

XX AC AAB97743;

XX DT 08-AUG-2001 (first entry)

DE gp100 derived IFN-gamma production stimulation peptide SEQ ID NO:36.

XX Virus; adenovirus; poxvirus; alphavirus; immune response; gp100;
tumour antigen; CEA; carcinoembryonic antigen; immunostimulant;
cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer.

XX OS Virus.

OS Synthetic.

XX WO200130382-A1.

XX PD 03-MAY-2001.

XX PF 20-OCT-2000; 2000WO-CA01253.

XX PR 22-OCT-1999; 99US-0160879.

XX PR 07-AUG-2000; 2000US-0223325.

XX (AVET) AVENTIS PASTEUR LTD.

XX Berinstein N, Tartaglia J, Moingeon P, Barber B;

XX WPI; 2001-308587/32.

XX Inducing immune response to tumor antigen, useful in immunotherapy of cancer, by administering the antigen to a lymphatic site -

XX Example 1; Page 39; 60pp; English.

XX The present invention describes a method for inducing an immune response,

CC in an animal, to a tumour antigen (Ag) comprising administering Ag, or nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys (Macaca fascicularis) were injected with a modified form of gp100 antigen (a) into the left inguinal lymph node or (b) subcutaneously. Both animals of (a) developed a cell-mediated response (indicated by production of interferon-gamma from T lymphocytes when exposed to gp100 peptides), but only 2 of 4 animals of (b) did so. Also animals in (a) produced a far greater antibody response to gp100. The method is used in immunotherapy of a wide range of cancers through induction of a specific immune response (humoral and cellular) against the tumour antigens. When administered to a lymphatic site, Ag (or (I)) induces a stronger immune response than administration by other routes and may also break tolerance to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to AAB97815 represent peptides derived from gp100 which stimulate interferon (IFN)-gamma production; AAB97816; AAB97817; and AAB97818 represents a CEA modified antigen protein given in AAB97817; and AAB97818 represents a CEA modified antigen peptide, all of which are used in the exemplification of the present invention.

XX Sequence 15 AA;

SQ Query Match 55.6%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVPL 7
Db |||||
1 SYVPL 5

RESULT 16
ABP46299
ID ABP46299 standard; peptide; 15 AA.

XX AC ABP46299;

XX DT 19-AUG-2002 (first entry)

DE Human BlyS binding scFv VH CDR3 SEQ ID 2310.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
tumour necrosis factor; B cell proliferation; B cell differentiation;
immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US19110.

XX PR 16-JUN-2000; 2000US-212210P.

XX PR 17-OCT-2000; 2000US-240816P.

XX PR 16-MAR-2001; 2001US-276248P.

XX PR 21-MAR-2001; 2001US-277379P.

XX PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -

XX Claim 2; Page 2968; 3149pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
 CC and so may be used to detect and quantitate the presence of BLYS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLYS. They may also be
 CC administered to treat diseases associated with aberrant BLYS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 55.6%; Score 5; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVPL 7
 Db 8 SYVPL 12

RESULT 17
 ABP46252
 ID ABP46252 standard; peptide; 16 AA.
 XX
 AC ABP46252;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BLYS binding scFv VH CDR3 SEQ ID 2263.

BLYS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 DR

XX Antibodies against B lymphocyte stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 PT
 XX Claim 2; Page 2960; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
 CC and so may be used to detect and quantitate the presence of BLYS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLYS. They may also be
 CC administered to treat diseases associated with aberrant BLYS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 16 AA;

Query Match 55.6%; Score 5; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVPL 7
 Db 8 SYVPL 12

RESULT 18
 AAR12158
 ID AAR12158 standard; peptide; 7 AA.
 XX
 AC AAR12158;
 XX
 DT 25-MAR-2003 (updated)
 DT 05-AUG-1991 (first entry)
 XX
 DE Cyclo-octa peptide, hymenistatin.

KW Tumour growth inhibitor; cyclic.
 XX
 OS Hymeniadon sp.
 XX
 PN EP430538-A.
 XX
 PD 05-JUN-1991.

XX 20-NOV-1990; 90EP-0312606.
 XX
 PR 30-NOV-1989; 89US-0443882.
 XX
 PA (UYAR-) UNIV ARIZONA STATE.
 PA (YUAR-) ARIZONA BOARD REGEN.
 XX
 PI Pettitt GR;

XX WPI; 1991-166026/23.

XX New cyclo-octa peptide, hymenistatin - having inhibiting tumour
 PT growth activity e.g. against national cancer institute P-388
 PT leukaemia cell line.

XX Claim 1; Page 8; 10pp; English.

XX The cpd., isolated from South Pacific sponge, is active as a
 CC tumour growth inhibitor against P388 murine leukaemia cell line
 CC (ED50 = 3.5ug/ml). The peptide sequence was determined by -NOE
 CC expts. and FAB ms/ms.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 7 AA;

Query Match 44.4%; Score 4; DB 12; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
 ||||
 Db 2 YVPL 5

RESULT 19
 AAW46013
 ID AAW46013 standard; peptide; 7 AA.
 AC AAW46013;
 XX
 DT 03-JUL-1998 (first entry)
 XX
 DE Peptide #45 based on human SSTR 5 (residues 1-7).
 XX Hormone; receptor; antibody; vaccine; immunogen; somatostatin; IGF;
 KW insulin-like growth factor binding protein; ILGFBP; SSTR; diabetes;
 KW somatostatin receptor; insulin-like growth factor.
 XX Synthetic.
 OS Homo sapiens.
 OS
 PN WO9744352-A1.
 XX
 PD 27-NOV-1997.
 XX
 PF 22-MAY-1997; 97WO-AU00312.
 XX
 PR 22-MAY-1996; 96AU-0009990.
 XX
 PA (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.
 XX
 PI Gerraty NL, Kingston DJ, Westbrook SL;
 XX WPI; 1998-018427/02.
 XX
 PT New non-naturally occurring peptide(s) - which are based on portions
 of somatostatin, somatostatin receptors and insulin-like growth
 factor binding protein
 XX
 PS Disclosure; Page 9; 136pp; English.
 XX
 CC Peptides AAW45983-W456025 are based on portions of somatostatin,
 somatostatin receptors (SSTR) and insulin-like growth factor binding
 proteins (IGFBP). They are capable of increasing weight gain, birth
 weight, growth rates, milk production, levels of circulating insulin,
 IGF-I and IGF-III, fibre production and muscle weight. They may be used
 to modulate carbohydrate metabolism and in treatment of diabetes. The
 oil carrier may be used for delivery of the peptides.
 XX
 SQ Sequence 7 AA;

Query Match 44.4%; Score 4; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
 ||||
 Db 3 PLFP 6

RESULT 20
 AAY17016
 ID AAY17016 standard; peptide; 7 AA.
 XX AAY17016;
 XX
 DT 20-JUL-1999 (first entry)
 XX

DE Heat shock protein (hsp) binding peptide.
 XX Conjugate peptide; heat shock protein; hsp; phage display library; virus;
 KW surface protein; tethering peptide; chaperone process; cytokine; cancer;
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
 KW acquired immune deficiency; autoimmune disease.
 XX Synthetic.
 OS
 PN WO922761-A1.
 XX
 PD 14-MAY-1999.
 XX
 PF 22-OCT-1998; 98WO-US22335.
 XX
 PR 31-OCT-1997; 97US-0961707.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;
 PI Querfelli O, Rothman JE;
 XX WPI; 1999-313177/26.
 DR Identifying peptides which bind heat shock proteins
 XX Examples; Page 24; 155pp; English.
 XX
 CC The invention relates to conjugate peptides engineered to noncovalently
 bind to heat shock proteins (hsp). A method of identifying a hsp binding
 peptide comprises (a) contacting a phage display library having
 bacteriophage expressing, in a surface protein, inserted peptides with a
 hsp target, and bound to a benzoquinone ansamycin antibiotic (BAA), in a
 physiologic binding buffer; (b) isolating a phage binding to the hsp
 target; and (c) identifying the inserted peptide expressed. The peptides
 which bind to a hsp can be used as tethering peptides for a hsp which may
 serve as an accessory in a chaperone process and/or may comprise a
 cytokine. They can also be coupled to antigens to induce an immune
 response. Such compositions can be used for treating neoplastic disease,
 e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
 virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
 disease of the immune system, e.g. acquired immune deficiencies or
 autoimmune diseases.
 XX
 SQ Sequence 7 AA;

Query Match 44.4%; Score 4; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
 ||||
 Db 2 YVPL 5

RESULT 21
 AAU72158
 ID AAU72158 standard; Peptide; 7 AA.
 XX
 AC AAU72158;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE Melanoma antigen, javelin peptide #144.
 XX Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;
 KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYEs01; GM2;
 KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;
 KW javelin molecule; melanoma antigen recognised by T cells-1; human.
 XX Bacteriophage M13.
 OS
 XX WO200178655-A2.
 PN

XX PD 25-OCT-2001.
 XX PF 17-APR-2001; 2001WO-US12449.
 XX PR 17-APR-2000; 2000US-197462P.
 XX PA (HOUG/) HOUGHTON A.
 XX PA (LIVI/) LIVINGSTON P.
 XX PA (ALAW/) AL-AWOATI Q.
 XX PA (MAYH/) MAYHEW M.
 XX PA (HOEM/) HOE M.
 XX PI Houghton A, Livingston P, Al-awqati Q, Mayhew M, Hoe M;
 XX DR WPI; 2001-663092/76.
 XX PT Anti cancer vaccine for the treatment of melanoma comprises a heat
 XX PT shock protein and a melanoma antigen i.e. tyrosinase -
 XX PS Disclosure; Page 19; 150pp; English.
 XX CC The invention relates to a method of induction of an immune response,
 XX CC comprising administration of an immunotherapeutic composition, comprising
 XX CC a heat shock protein, and a melanoma antigen, where the melanoma
 XX CC antigen is selected from tyrosinase, tyrosinase related protein 1,
 XX CC tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens,
 XX CC NYEs01, MART antigens, GM2, antigenic portions and combinations of these.
 XX CC The melanoma antigen is covalently bound to a javelin molecule, where the
 XX CC melanoma antigen bound to the javelin molecule is non-covalently bound to
 XX CC the heat shock protein. The composition is useful for inducing an immune
 XX CC response for the treatment of melanoma. AAU71980-AAU72481 represent
 XX CC melanoma antigen peptides of the invention.
 XX SQ Sequence 7 AA;
 Query Match 44.4%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YVPL 7
 DB 2 YVPL 5
 RESULT 22
 AAU80708
 ID AAU80708 standard; peptide; 7 AA.
 AC AAU80708;
 DT 26-MAR-2002 (first entry)
 DE Javelin peptide #138 for conjugation to multi-component viral particles.
 KW Immunogenic complex; non-pathogenic multi-component viral particle;
 KW javelin; heat shock protein; humoral immunity; cellular immunity;
 KW anti-viral immune response; viral infection; hepatitis; influenza;
 KW mumps; HIV infection; human immunodeficiency virus; polio;
 KW tick-borne encephalitis; ebola virus infection.
 OS Synthetic.
 XX WO200178772-A1.
 XX PD 25-OCT-2001.
 XX PF 17-APR-2001; 2001WO-US12568.
 XX PR 17-APR-2000; 2000US-197462P.
 XX PA (MOJA-) MOJAVE THERAPEUTICS INC.

PI Hoe M, Landsberger F;
 XX WPI; 2002-049177/06.
 XX PT New heat shock protein-based viral vaccines, useful for enhancing
 XX PT anti-viral immune response in an organism, particularly as a vaccine
 XX PT for preventing or ameliorating viral infections, e.g. hepatitis,
 XX PT influenza or HIV infection -
 XX PS Disclosure; Page 13; 75pp; English.
 XX CC The present invention relates to the use of an immunogenic complex
 XX CC comprising a non-pathogenic multi-component viral particle covalently
 XX CC linked to a javelin molecule (preferably a peptide) that selectively
 XX CC binds to a heat shock protein. The immunogenic complex is useful for
 XX CC inducing both humoral and cellular immunity, especially for enhancing
 XX CC the anti-viral immune response, in a human or non-human subject. The
 XX CC immunogenic complex is particularly useful as a vaccine for preventing
 XX CC or ameliorating viral infections, e.g. hepatitis, influenza, mumps,
 XX CC HIV (human immunodeficiency virus) infection, polio, tick-borne
 XX CC encephalitis or ebola virus infection. AAU80571-AAU80734 represent
 XX CC javelin peptides which may be covalently conjugated to multi-component
 XX CC viral particles.
 XX SQ Sequence 7 AA;
 Query Match 44.4%; Score 4; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YVPL 7
 DB 2 YVPL 5
 RESULT 23
 AAR58322
 ID AAR58322 standard; peptide; 8 AA.
 XX AC AAR58322;
 XX DT 22-SEP-1994 (first entry)
 XX DE Hypotensive polypeptide.
 XX KW Hypotensive; antioxidative; calcium absorption; salt; food;
 XX KW pharmaceuticals; physiologically active agents.
 XX OS Lactobacillus helveticus.
 XX PN JP06041191-A.
 XX PD 15-FEB-1994.
 XX PF 03-MAR-1993; 93JP-0043047.
 XX PR 04-MAR-1992; 92JP-0047340.
 XX PA (CALV) CALPIS SHOKUHN KOGYO KK.
 XX WPI; 1994-089332/11.
 XX PT New polypeptide - used in physiologically active agents having
 XX PT e.g. hypotensive antioxidative and calcium absorption promoting
 XX PT activity
 XX PS Claim 1-2; Page 7; 10pp; Japanese.
 XX CC Sequences (AAR58319-341) are used in conjunction with
 XX CC physiologically active agents showing a property such as
 XX CC hypotensive activity, calcium absorption promoting activity and
 XX CC antioxidative activity. The peptides are non-toxic and can be
 XX CC used in physiologically active agents.

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XX SQ Sequence 8 AA;
Query Match 44.4%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
    ||||
DB 5 YVPL 8

RESULT 24
AA116845
ID AA116845 standard; peptide; 8 AA.
AC AA116845;
XX
XX DT 20-JUL-1999 (first entry)
XX
XX DE Heat shock protein (hsp) binding peptide.
XX
XX KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;
XX KW surface protein; tethering peptide; chaperone process; cytokine; cancer;
XX KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
XX KW acquired immune deficiency; autoimmune disease.
XX
XX OS Synthetic.
XX
XX PN WO9922761-A1.
XX
XX PD 14-MAY-1999.
XX
XX PF 22-OCT-1998; 98WO-US22335.
XX
XX PR 31-OCT-1997; 97US-0961707.
XX
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
XX PI Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;
XX PI Querfelli O, Rothman JE;
XX
XX DR WPI; 1999-313177/26.
XX
XX DR N-PSDB; AAXG0745.
XX
XX PT Identifying peptides which bind heat shock proteins
XX
XX PS Disclosure; Fig 2H; 155pp; English.
XX
XX CC The invention relates to conjugate peptides engineered to noncovalently
XX CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
XX CC peptide comprises (a) contacting a phage display library having
XX CC bacteriophage expressing, in a surface protein, inserted peptides with a
XX CC hsp target, and bound to a benzoinone ansamycin antibiotic (BAA), in a
XX CC physiologic binding buffer; (b) isolating a phage binding to the hsp
XX CC target; and (c) identifying the inserted peptide expressed. The peptides
XX CC which bind to a hsp can be used as tethering peptides for a hsp which may
XX CC serve as an accessory in a chaperone process and/or may comprise a
XX CC cytokine. They can also be coupled to antigens to induce an immune
XX CC response. Such compositions can be used for treating neoplastic disease,
XX CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
XX CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
XX CC disease of the immune system, e.g. acquired immune deficiencies or
XX CC autoimmune diseases.
XX SQ Sequence 8 AA;
Query Match 44.4%; Score 4; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
    ||||
DB 5 YVPL 8

RESULT 25
ABB04380
ID ABB04380 standard; peptide; 8 AA.
XX
XX AC ABB04380;
XX
XX DT 02-MAY-2002 (first entry)
XX
XX DE Carrot partial antifreeze peptide D.
XX
XX KW Carrot; frozen food; anti-freeze peptide; AFP; confectionery; ice-cream;
XX KW Daucus carota; Autumn King.
XX
XX OS Daucus carota.
XX
XX PN WO9822591-A2.
XX
XX PD 28-MAY-1998.
XX
XX PF 06-NOV-1997; 97WO-EP06181.
XX
XX PR 19-NOV-1996; 96EP-0308362.
XX
XX PA (UNIL ) UNILEVER NV.
XX PA (UNIL ) UNILEVER PLC.
XX
XX PI Byass LJ, Doucet CJ, Fenn RA, McArthur AJ, Sidebottom CM;
XX PI Smallwood WF, Warrell D;
XX
XX DR WPI; 2001-227110/08.
XX
XX PT Frozen food product mfg. process - using anti-freeze peptides to
XX PT produce specific elongated ice crystals with desirable ice
XX PT recrystallisation properties and relatively hard and brittle texture
XX
XX PS Example 6; Page 25; 37pp; English.
XX
XX CC The invention relates to a process for the production of a frozen food
XX CC product comprising anti-freeze peptides (AFP), where the conditions are
XX CC chosen so that the ice crystals in the product have an aspect ratio of
XX CC 1.9 or greater. The process is used for preparing frozen confectionery
XX CC products and ice-cream mixes. The present sequence is part of a peptide
XX CC with antifreeze properties isolated from carrot (Daucus carota, cultivar
XX CC Autumn King).
XX SQ Sequence 8 AA;
Query Match 44.4%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8
    ||||
DB 3 VPLF 6

RESULT 26
AAB20475
ID AAB20475 standard; Peptide; 8 AA.
XX
XX AC AAB20475;
XX
XX DT 21-JUN-2001 (first entry)
XX
XX DE Mouse contactin precursor peptide isolated in database screening.
XX
XX KW Contactin; mouse; PSK; seizure related protein; epilepsy;
XX KW neurological disorder; diagnosis; therapy.
XX
XX OS Mus sp.

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XX PN WO200125268-A1.
 XX PD 12-APR-2001.
 XX PF 04-OCT-2000; 2000WO-DK00556.
 XX PR 04-OCT-1999; 99DK-0001420.
 XX PA (SCHR/) SCHROTZ-KING P.
 XX PA (KING/) KING A.
 XX PA (MANN/) MANN M.
 XX PA (ANDE/) ANDERSEN J.
 XX PA (KUES/) KUESTER B.
 XX PI Schrotz-King P, King A, Mann M, Andersen J, Kuester B;
 XX DR WPI; 2001-290605/30.
 XX PT Novel human seizure related proteins useful for controlling epileptic
 PT seizures and neurological disorders, and for identifying potential drug
 PT targets for use in diagnosis and/or prognosis of neurological disorders
 PT
 XX PS Disclosure; Page 59; 150pp; English.
 XX CC The present sequence is that of a mouse contactin precursor peptide
 CC identified during a proteomics screening approach for membrane
 CC receptors in the brain. 9 proteins from an RP-HPLC preparation
 CC from the mouse E16 brain plasma membrane were analyzed by
 CC nanoelectrospray tandem mass spectrometry. Peptide sequences were
 CC found by searching NRDB or EST databases with peptide sequence tags.
 CC Sample 9 was identified as contactin. Sample 7 was novel, and named
 CC PSK-1. Human PSKs (see AAB20446-48) were subsequently identified.
 CC These are novel transmembrane receptor or secreted proteins that
 CC are potentially involved in the control or generation of seizures
 CC such as epileptic seizures or other neurological disorders.
 CC PSK-1, -2 and -3 polynucleotides and polypeptides can be used to
 CC identify potential drug targets. They can also be used in the
 CC diagnosis of seizure related conditions or other neurodegeneration
 CC such as Alzheimer, Rasmussen's Encephalitis, Parkinson's disease,
 CC multiple sclerosis, cerebrovascular disorders (stroke syndromes),
 CC like ischaemia, Huntington's disease or schizophrenia (claimed),
 CC and in the treatment of conditions caused by PSK upregulation,
 CC deficiency or impaired function.
 XX SQ Sequence 8 AA;
 Query Match 44.4%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred.No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VESY 4
 Db |||||
 2 VESY 5
 RESULT 27
 ABG78590
 ID ABG78590 standard; Peptide; 8 AA.
 AC ABG78590;
 XX 29-NOV-2002 (first entry)
 XX Multiple sclerosis associated feature (MSF) tryptic digest peptide #78.
 XX Multiple sclerosis; MS; multiple sclerosis associated feature; MSF;
 KW human; multiple sclerosis-associated protein isoform; MSF;
 KW antiinflammatory; neuroprotective.
 XX Homo sapiens.
 OS

PN WO200259604-A2.
 XX 01-AUG-2002.
 XX PF 25-JAN-2002; 2002WO-GB00330.
 XX PR 26-JAN-2001; 2001US-264404P.
 XX PR 20-NOV-2001; 2001US-331647P.
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Herath HMAc, Perekh RB, Rohlf C;
 XX DR WPI; 2002-599812/64.
 XX PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.
 PT determining the stage or severity of MS, comprises detecting the
 PT presence of MS-associated features or protein isoforms by 2-dimensional
 PT electrophoresis -
 XX PS Disclosure; Page 22; 128pp; English.
 XX CC This invention relates to a novel method for screening or diagnosing
 CC multiple sclerosis (MS) in a subject to determine the stage or severity
 CC of MS, to identify a subject at risk of developing MS or to monitor the
 CC effect of a therapy administered. The method comprises analysing a
 CC sample body fluid from the subject by two-dimensional electrophoresis
 CC and detecting the presence of multiple sclerosis-associated features
 CC (MSFs), or multiple sclerosis-associated protein isoforms (MSPIs).
 CC The MSF's of the invention correspond to spots identified on a 2D gel
 CC these proteins may have antiinflammatory or neuroprotective activity.
 CC The methods of the invention and the compositions are useful for
 CC clinical screening, diagnosis and treatment of MS, for monitoring the
 CC effectiveness of MS treatment, for selecting participants in clinical
 CC trials, for identifying patients most likely to respond to a particular
 CC therapeutic treatment and for screening and developing drugs for
 CC treatment of MS. Agents that modulate the expression or activity of an
 CC MSPI are useful for treating MS, for preventing or delaying the onset or
 CC development of MS, to prevent or delay the progression of MS, or to
 CC ameliorate the symptoms MS. Nucleic acids comprising a sequence encoding
 CC an MSPI, MSPI-related polypeptide, or their fragments are useful for
 CC promoting MSPI function by gene therapy. The present sequence represents
 CC a human multiple sclerosis associated feature tryptic digest
 CC peptide of the invention.
 XX SQ Sequence 8 AA;
 Query Match 44.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred.No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VESY 4
 Db |||||
 2 VESY 5
 RESULT 28
 ABJ20030
 ID ABJ20030 standard; Peptide; 8 AA.
 XX AC ABJ20030;
 XX 10-APR-2003 (first entry)
 XX MHC binding peptide SEQ ID No 195.
 XX Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;
 KW antiinflammatory; major histocompatibility complex; MHC;
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
 KW inflammation; gene therapy; MHC binding peptide.
 OS Synthetic.

XX PN WO200294981-A2.
 XX PD 28-NOV-2002.
 XX PF 16-MAY-2002; 2002WO-IL00383.
 XX PR 16-MAY-2001; 2001US-290958P.
 XX PR 29-MAY-2001; 2001US-0865548.
 XX PA (TECR) TECHNION RES & DEV FOUND LTD.
 XX PI Barnea E, Beer I, Ziv T, Admon A, Daseau L, Buchsbaum S;
 XX PF WPI; 2003-210043/20.
 XX PT Identifying peptides that are capable of binding to major
 PT histocompatibility complex (MHC) molecules of a particular haplotype by
 PT analyzing peptides bound to the soluble and secreted form of the MHC
 PT molecules of the particular haplotype -
 XX Claim 37; Page 194; 238pp; English.
 XX The invention relates to a novel method for identifying peptides
 CC originating from a particular cell type, which are capable of binding to
 CC major histocompatibility complex (MHC) molecules of a particular
 CC haplotype. The method comprises analysing peptides bound to the soluble
 CC and secreted form of the MHC molecules of the particular haplotype. The
 CC method is useful for identifying peptides for treating an autoimmune
 CC disease, such as T or B cell and/or allergic disease or condition,
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
 CC sequences of the invention may be used in a gene therapy application.
 CC This sequence represents a peptide relating to the method for identifying
 CC MHC binding peptides of the invention.
 XX Sequence 8 AA;
 XX Query Match 44.4%; Score 4; DB 24; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YVPL 7
 Db ||||
 4 YVPL 7
 RESULT 29
 AAR46514
 ID AAR46514 standard; peptide; 9 AA.
 XX AAR46514;
 XX 25-MAR-2003 (updated)
 DT 30-MAR-1994 (first entry)
 XX Plasmodium yoelii CSP residues 276-288.
 XX Vaccine; polar lipid; targeting; immune response; antigenic
 KW peptide; antigen; circumsporozoite protein.
 XX Synthetic.
 OS US5256641-A.
 XX 26-OCT-1993.
 PD 09-JUL-1992; 92US-0911209.
 XX 01-NOV-1990; 90US-0607982.
 XX (OREG-) STATE OF OREGON.
 PA (UYOR-) UNIV OREGON HEALTH SCI.

XX Malkovsky M, Stowell MHB, Yatvin MB, Mcclard RW;
 PI Parks DW, Witteff;
 XX WPI; 1993-350862/44.
 XX New covalent conjugate of antigenic peptide and polar lipid e.g.
 PT sphingosine - useful in protective vaccines, treatment of
 PT auto-immune disease and preventing of transplant rejection
 XX Disclosure; Page 13; 15pp; English.
 XX The peptide is an example of an antigenic peptide which may be
 CC joined via a functional linker group, opt. at the two ends of a
 CC spacer group, to a polar lipid carrier, e.g. sphingosine, ceramide,
 CC phosphatidyl choline, ethanolamine, inositol or serine, cardiolipin
 CC or phosphatidic acid. The compsn. may be used as a vaccine against
 CC Plasmodium (malaria) infection. An advantage of the system is that
 CC when incorporated into the compsn. entry of the antigenic peptide into
 CC the cells of the immune system is facilitated (no need for endocytosis)
 CC and targeting to specific organelles becomes possible. Unlike known
 CC vaccines, intracellular synthesis of viral antigens is not necessary
 CC for presentation via the MHC class I antigen pathway, nor intracellular
 CC proteolysis for presentation via the MHC class II antigen pathway, so
 CC both humoral and cellular immunity is achieved. Also, when a spacer is
 CC present, the antigen release rate may be controlled.
 CC See also AAR46507-47
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX Sequence 9 AA;
 XX Query Match 44.4%; Score 4; DB 14; Length 9;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SYVP 6
 Db ||||
 1 SYVP 4
 RESULT 30
 AAW68359
 ID AAW68359 standard; peptide; 9 AA.
 XX AAW68359;
 XX 25-MAR-2003 (updated)
 DT 14-OCT-1998 (first entry)
 XX MHC binding peptide CSP 276-288.
 DE Antigen; major histocompatibility complex; MHC; lymphocyte; detection;
 XX immobilisation; cytotoxic T-cell; tumour; leukaemia; lymphoma;
 KW viral infection.
 XX Synthetic.
 OS Plasmodium yoelii.
 XX WO9744667-A2.
 PN 27-NOV-1997.
 PD 21-MAY-1997; 97WO-FR00892.
 XX 21-MAY-1996; 96US-0651925.
 XX (INRM) INERM INST NAT SANTE & RECH MEDICALE.
 PA (INSP) INST PASTEUR.
 XX Langladedemoyen P, Lone Y, Kourilsky P, Abastado J;
 PI WPI; 1998-018653/02.
 DR

XX	Detection, purification and elimination of antigen-specific lymphocytes - for producing cytotoxic T cells for immuno-therapy of cancers and viral infection
XX	Disclosure; Page 29; 222pp; French.
CC	Peptides AAW68301-W68384 are examples of antigens (Ag) which can be loaded onto recombinantly produced major histocompatibility complex (MHC) molecules in a method of detecting antigen-specific lymphocytes. The MHC-antigen complex is then immobilised on a solid support and a sample containing cells recognising the MHC-Ag complex may be isolated. This peptide is derived from amino acids 276-288 of the Plasmodium yoelii CSP protein. A similar method is used to isolate, purify or eliminate Ag-specific T-cells or to produce Ag-specific cytotoxic T-cells (CTL). The method is also used to detect and quantify tumour-specific T-cells and to generate CMC for specific killing of tumour cells (solid tumours, leukaemia or lymphoma) by injection into a human or animal, but also for treating viral infections.
CC	(Updated on 25-WAR-2003 to correct PI field.)
XX	Sequence 9 AA;
XX	Query Match 44.4%; Score 4; DB 19; Length 9; Best Local Similarity 100.0%; Pred.No. 9.3e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	3 SYVP 6
DB	1 SYVP 4
RESULT 31	
AAB23654	ID ID AAB23654 standard; Peptide; 9 AA.
XX	AAB23654;
XX	05-JAN-2001 (first entry)
XX	Cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:6.
DE	ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytotatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
KW	Homo sapiens.
OS	WO200049041-Al.
PN	24-AUG-2000.
PD	18-FEB-2000; 2000WO-JPO0941.
PF	19-FEB-1999; 99JP-0041535.
PP	(SUME) SUMITOMO ELECTRIC IND CO.
PR	Shinbara N, Udono H, Yui K;
PX	WPI; 2000-54374B/49.
XX	Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
XX	Claim 5; Page 52; 72pp; Japanese.
XX	The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ATPase domain of a heat shock protein. Also described are:(1) a drug composition containing (I)

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
|
|
|
Db 2 YVPL 5

RESULT 33

AA96776
ID AAY86776 standard; Peptide; 9 AA.

AC AAY86776;

DT 05-MAY-2000 (first entry)

DE Telomerase peptide #191.

XX Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
KW telomerase T lymphocyte.

XX Homo sapiens.

OS WO200002581-A1.

PN 20-JAN-2000.

PD 30-JUN-1999; 99WO-NO00220.

PF 08-JUL-1998; 98NO-0003141.

PR (NHSD) NORSK HYDRO AS.

XX Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
PI Saeboe-Larsen S;

XX WPI: 2000-145727/13.

XX Protein or peptide fragments useful in the treatment and prophylaxis of
PT cancer in mammals -

PS Claim 12; Page 35; 53pp; English.

XX This sequence represents a telomerase peptide of the invention, and can
CC be used in a method for the treatment or prophylaxis of cancer. The
CC sequences are useful in the treatment or prophylaxis of cancer
CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
CC tract carcinomas. They are useful for generating telomerase T lymphocytes
CC capable of recognising and destroying tumour cells in a mammal,
CC comprising culturing T lymphocytes obtained from the mammal with the
CC peptides. Telomerase protein is expressed only by tumour cells, hence,
CC other body cells are not targeted or destroyed by telomerase specific T
CC cells.
CC Note: This sequence was indexed from WO200002581, which is the first
CC major country equivalent to NO9803141.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
|
|
|
Db 5 YVPL 8

RESULT 34

AA968305
ID AAY68305 standard; Peptide; 9 AA.

XX AAY68305;

DT 13-APR-2000 (first entry)

DE Altered MHC determinant binding peptide SEQ ID NO:137.

XX MHC class I; major histocompatibility complex; microglobulin; antigen;
KW immune response; immunisation; AIDS; multiple sclerosis; toxic shock;
KW cancer; lupus erythematosus; snake bite; cytostatic; antiviral;
KW immunomodulatory; dermatological; immunosuppressive; antiinflammatory;
KW neuroprotective.

XX Plasmodium yoelii.

OS US6011146-A.

PN 04-JAN-2000.

PD 07-JUN-1995; 95US-0481985.

PF 15-NOV-1991; 91US-0792473.

PR 05-DEC-1991; 91US-0801818.

XX (INSP) INST PASTEUR.

PA (INRM) INST NAT SANTE & RECH MEDICALE.

PI Kourilsky P, Mottez E, Abastado J;

XX WPI: 2000-125951/11.

XX New recombinant DNA encoding covalently linked form of major
PT histocompatibility complex Class I determinant, used for immune system
PT stimulation, e.g. for treating cancer -

PS Disclosure; Column 11; 88pp; English.

XX The present invention describes a recombinant DNA molecule (I)
CC containing a sequence (Ia) that encodes an altered MHC (major
CC histocompatibility complex) Class I determinant (II) comprises a
CC polypeptide with alpha1, alpha2, alpha3 and beta2-microglobulin
CC domains, in which alpha3 and beta2 are covalently linked, thorough C-
CC and N-termini respectively, via a nucleotide spacer sequence encoding a
CC polypeptide. (III) includes an antigen-binding site and when (II) and
CC the antigen are associated they are recognized by a mammalian T cell
CC receptor (TCR). (I) are used to produce (II) which are used to study
CC functional interactions between the various MHC domains. They can also
CC be used to modulate (in vivo or in vitro) the immune system by inducing
CC an effector response (cytotoxicity, antibody synthesis, phagocytosis)
CC of immune system cells, typically for treating, or immunising against;
CC cancer, acquired immune deficiency syndrome, lupus erythematosus,
CC multiple sclerosis, toxic shock and snake bite, but also for selective
CC destruction of autoreactive cells, diagnostically to assay T cell
CC receptors and to raise specific antibodies (useful for diagnosis.
CC therapy, studying MHC-associated cellular processes and for affinity
CC purification). AA257558 and AAY68186 to AAY68316 are sequences used in
CC the exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
|
|
|
Db 1 SYVP 4

RESULT 35

AAV52959
ID AAV52959 standard; Peptide; 9 AA.
XX AC
XX AAV52959;
XX DT
XX 14-FEB-2000 (first entry)
XX DE
XX

Altered MHC determinant binding peptide SEQ ID NO:137.

Major histocompatibility complex; MHC class I; MHC class II; antigen; immune response; diagnosis; antibody; immunisation; autoimmune disease; acquired immune deficiency syndrome; AIDS; cytostatic; dermatological; anti-inflammatory; neuroprotective; immunosuppressive; antithyroid; vaccine; lupus erythematosus; multiple sclerosis; thyroiditis; toxic shock; tumour; snakebite.

Synthetic.
OS Plasmodium yoelii.

XX US5976551-A.

XX 02-NOV-1999.

XX 07-JUN-1995; 95US-0484905.

XX 05-DEC-1991; 91US-0801818.

XX 15-NOV-1991; 91US-0792473.

XX (INSP) INST PASTEUR.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Kourilsky P, Mottez E, Abastado J;

XX WPI; 2000-037081/03.

Composition containing an antigen and altered major histocompatibility Class II determinant, used to immunize against autoimmune diseases, e.g. acquired immune deficiency syndrome -

Claim 8; Column 11; 96pp; English.

The present invention describes a composition capable of eliciting anti-major histocompatibility (MHC) antibodies. The composition comprises an antigen associated with an altered MHC Class II determinant (I) comprising alpha1, alpha2, beta1 and beta2 polypeptide domains encoded by a mammalian MHC Class II locus covalently linked to form a polypeptide (I) containing beta2, alpha2, alpha1 and beta1 domains in sequence. The resulting Antigen-MHC complex is recognizable by the T cell receptor. The compositions are used for immunisation against, or treatment of, a wide range of autoimmune diseases, e.g. acquired immune deficiency syndrome (AIDS), lupus erythematosus, multiple sclerosis, thyroiditis, toxic shock, tumour and snakebite, depending on the nature of antigen. (I) is also used to analyse functional interactions between the various domains and for targeting lymphocyte receptors. Antibodies against (I) are produced by usual methods of immunisation or cell fusion, and may be humanised by standard methods. These antibodies are useful for diagnosis (detection or purification of MHC gene products), therapy (neutralising MHC on cell surfaces) and in the study of MHC and cellular processes. AAZ33240 to AAZ33242 and AAY52840 to AAY52970 represent sequences used in the exemplification of the present invention.

XX Sequence 9 AA;

Query Match 44.4%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6

Db 1 SYVP 4

RESULT 36

AAW98253

XX ID AAW98253 standard; Peptide; 9 AA.

XX AC AAW98253;

XX DT 24-JAN-2002 (first entry)

XX Human peptide #1528 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer; amyloid protein; angiotensin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -

Disclosure; Page 4003; 4143pp; English.

The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

XX Sequence 9 AA;

Query Match 44.4%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYV 5

Db 3 ESYV 6

RESULT 37

AAW63512

ID AAW63512 standard; peptide; 9 AA.

XX

AC AAG63512;
 XX DT 15-OCT-2001 (first entry)
 XX DE Amino acid sequence of an antigen derived from Plasmodium.
 XX DE
 XX KW Pseudopeptide; immunomodulation; adjuvant; antigen presenting cell;
 KW macrophage; dendritic cell; cytokine production; immunocompetent cell;
 KW autoimmune disease.
 XX OS Plasmodium sp.
 XX PN WO200146126-A1.
 XX PD 28-JUN-2001.
 XX PF 21-DEC-2000; 2000WO-FR03650.
 XX PR 22-DEC-1999; 99WO-IB02038.
 XX PA (OMPH-) OM-PHARMA.
 XX PI Bauer J, Martin OR, Rodriguez S;
 XX WI; 2001-496651/54.
 XX XX
 XX New amphiphilic acylated pseudopeptides having a functionalized
 PT auxiliary spacer, useful as immunomodulators, e.g. as adjuvants in
 PT vaccines -
 XX Disclosure; Page 34; 267pp; French.
 XX XX
 XX The specification describes N-Acylated pseudopeptides, which have
 CC a neutral or charged acidic group at one terminal and a functionalized
 CC auxiliary spacer at the other. The pseudopeptides show immunomodulatory
 CC and adjuvant action, based on activation of antigen presenting cells
 CC (e.g. macrophages or dendritic cells), induction of differentiation of
 CC dendritic cells, induction of cytokine production and induction of
 CC maturation of immunocompetent cell strains originating from hematopoietic
 CC and lymphoid organs. They reinforce humoral and cellular immunity. They
 CC can be grafted onto antigens (to modulate immune response) or onto
 CC drugs (to improve the therapeutic activity or targeting). The
 CC pseudopeptides are thus useful in human or veterinary medicine as
 CC immunizing or diagnostic agents. Typically, the pseudopeptides are used
 CC as adjuvants together with (or covalently bonded to) antigens for
 CC vaccination against viral, parasitic/protozoal, microbial or fungal
 CC infections; incubated with blood cells ex vivo, to render the cells
 CC immunocompetent before reintroduction in vivo; or used in therapy of
 CC certain autoimmune diseases. The present sequence represents a
 CC Plasmodium antigen, which may be used with the pseudopeptides of the
 CC invention.
 XX Sequence 9 AA;
 SQ
 Query Match 44.4%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SYVP 6
 Db |||||
 1 SYVP 4
 RESULT 38
 AAG63517
 ID AAG63517 standard; peptide; 9 AA.
 XX AC AAG63517;
 XX DT 15-OCT-2001 (first entry)
 XX DE Amino acid sequence of an antigen derived from Plasmodium.

KW Pseudopeptide; immunomodulation; adjuvant; antigen presenting cell;
 KW macrophage; dendritic cell; cytokine production; immunocompetent cell;
 KW autoimmune disease.
 XX OS Plasmodium sp.
 XX PN WO200146126-A1.
 XX PD 28-JUN-2001.
 XX PF 21-DEC-2000; 2000WO-FR03650.
 XX PR 22-DEC-1999; 99WO-IB02038.
 XX PA (OMPH-) OM-PHARMA.
 XX PI Bauer J, Martin OR, Rodriguez S;
 XX WI; 2001-496651/54.
 XX XX
 XX New amphiphilic acylated pseudopeptides having a functionalized
 PT auxiliary spacer, useful as immunomodulators, e.g. as adjuvants in
 PT vaccines -
 XX Example 3.5; Page 90; 267pp; French.
 XX XX
 XX The specification describes N-Acylated pseudopeptides, which have
 CC a neutral or charged acidic group at one terminal and a functionalized
 CC auxiliary spacer at the other. The pseudopeptides show immunomodulatory
 CC and adjuvant action, based on activation of antigen presenting cells
 CC (e.g. macrophages or dendritic cells), induction of differentiation of
 CC dendritic cells, induction of cytokine production and induction of
 CC maturation of immunocompetent cell strains originating from hematopoietic
 CC and lymphoid organs. They reinforce humoral and cellular immunity. They
 CC can be grafted onto antigens (to modulate immune response) or onto
 CC drugs (to improve the therapeutic activity or targeting). The
 CC pseudopeptides are thus useful in human or veterinary medicine as
 CC immunizing or diagnostic agents. Typically, the pseudopeptides are used
 CC as adjuvants together with (or covalently bonded to) antigens for
 CC vaccination against viral, parasitic/protozoal, microbial or fungal
 CC infections; incubated with blood cells ex vivo, to render the cells
 CC immunocompetent before reintroduction in vivo; or used in therapy of
 CC certain autoimmune diseases. The present sequence represents a
 CC Plasmodium antigen, which may be used with the pseudopeptides of the
 CC invention.
 XX Sequence 9 AA;
 SQ
 Query Match 44.4%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SYVP 6
 Db |||||
 1 SYVP 4
 RESULT 39
 AAG66424
 ID AAG66424 standard; Peptide; 9 AA.
 XX AC AAG66424;
 XX DT 23-OCT-2001 (first entry)
 XX DE Circumsporozoite protein, CSP, used as a peptide antigen.
 XX KW Immunomodulator; vaccine; immune response; immunogenic; CSP;
 KW Circumsporozoite protein.
 XX OS Plasmodium yoelii.
 XX PN WO200154720-A1.

XX PD 02-AUG-2001.
 XX PF 05-JAN-2001; 2001WO-EP00087.
 XX PR 28-JAN-2000; 2000AT-0000129.
 XX PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX PI Lingnau K, Mattner F, Schmidt W, Birnstiel M, Buschle M;
 XX DR WPI; 2001-536419/59.
 XX PT Pharmaceutical composition useful for inducing immune response
 PT comprises antigen, immunogenic oligodeoxynucleotide containing
 PT cytosine-guanine dinucleotide motifs and polycationic polymer -
 XX Example 2; Page 22; 39pp; English.
 XX CC The present invention relates to a pharmaceutical composition which
 CC comprises an antigen, an immunogenic oligodeoxynucleotide containing
 CC cytosine-guanine dinucleotide (CpG) motifs (CpG-ODN) and a polycationic
 CC polymer. The composition is useful for making a vaccine to induce potent
 CC immune responses, or to decrease or ablate undesired immune responses.
 CC The present sequence, CSP, is a peptide from the circumsporozoite protein
 CC of Plasmodium yoelii. This sequence was used as a peptide antigen in the
 CC method of the present invention.
 XX SQ Sequence 9 AA;
 Query Match 44.4%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 SYVP 6
 Db 1 SYVP 4
 RESULT 40
 AAG79591
 ID AAG79591 standard; Peptide; 9 AA.
 XX AC AAG79591;
 XX DT 09-JAN-2003 (first entry)
 XX DE Malarial epitope #3.
 XX KW Yellow fever; YF; virus; flavivirus; vector; antigen; envelope protein;
 KW E protein; immunization; immune response; parasite; vaccine; malaria;
 KW dengue; Japanese encephalitis; tick-borne encephalitis; fungi;
 KW monkey neurovirulence testing.
 XX OS Plasmodium malariae.
 XX PN GB2372991-A.
 XX PD 11-SEP-2002.
 XX PF 09-MAR-2001; 2001GB-0005877.
 XX PR 09-MAR-2001; 2001GB-0005877.
 XX PA (FIOC-) FIOCRUZ FUNDACAO CRUZ OSWALDO.
 XX PI Bonaldo MC, Galler R, Da Silva Freire M, Garrat RC;
 XX DR WPI; 2002-735136/80.
 XX PT Novel Flavivirus vector useful for expressing heterologous antigens,
 PT comprises foreign gene sequences inserted at sites in the level of its
 PT envelope protein -

XX PS Claim 18; Page 94; 96pp; English.
 XX CC The sequences given in AAG79596-91 are insertion sequences which
 CC may be inserted into the envelope protein derived from yellow
 CC fever virus (yF) in the vector of the invention. The vector
 CC has foreign gene sequences inserted at sites in the level of its
 CC envelope protein, where the sites are structurally apart from areas
 CC known to interfere with the overall Flavivirus E protein structure.
 CC Vectors such as these may be useful for immunization against Flavivirus
 CC and other infectious agents. It is useful for expressing heterologous
 CC antigens and for eliciting an immune response to foreign antigens.
 CC The vector of the invention is useful for eliciting an adequate immune
 CC response to cope with different parasite stages. Vaccines containing
 CC the vectors of the invention are useful for treating yellow fever
 CC and other diseases such as malaria, dengue, Japanese encephalitis,
 CC tick-borne encephalitis, and fungi infections. The vector of the
 CC invention is a safe and effective virus. It has several advantages
 CC such as well-defined and efficient production methodology,
 CC strict quality control including monkey neurovirulence testing, long
 CC lasting immunity, cheapness, single doses, and estimated use is over
 CC 200 million doses with excellent records of safety.
 XX SQ Sequence 9 AA;
 Query Match 44.4%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 SYVP 6
 Db 1 SYVP 4
 RESULT 41
 ABR06327
 ID ABR06327 standard; Peptide; 9 AA.
 XX AC ABR06327;
 XX DT 19-MAY-2003 (first entry)
 XX DE Human cancer-related protein 109PLD4 HLA peptide #262.
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX OS Homo sapiens.
 XX PN W0200283921-A2.
 XX PD 24-OCT-2002.
 XX PF 10-APR-2002; 2002WO-US11654.
 XX PR 10-APR-2001; 2001US-282739P.
 XX PR 10-APR-2001; 2001US-283112P.
 XX PR 25-APR-2001; 2001US-286630P.
 XX PA (AGEN-) AGENSYS INC.
 XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX DR WPI; 2003-075555/07.
 XX PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX PS Claim 13; Page 175; 1021pp; English.
 XX

CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLPP 9
 ||||
 Db 3 PLPP 6

RESULT 42
 ABR07074
 ID ABR07074 standard; Peptide; 9 AA.

XX ABR07074;

DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 109P1D4 HLA peptide #1009.

KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.

OS Homo sapiens.

PN WO200283921-A2.

XX 24-OCT-2002.

PF 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -

XX Claim 13; Page 183; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.

XX Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLPP 9
 ||||
 Db 2 PLPP 5

RESULT 43

ABR07293

ID ABR07293 standard; Peptide; 9 AA.

XX ABR07293;

DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 109P1D4 HLA peptide #1228.

KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.

OS Homo sapiens.

PN WO200283921-A2.

XX 24-OCT-2002.

PF 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -

XX Claim 13; Page 185; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.

XX Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLPP 9

XX 19-JUL-1995.
 XX 22-DEC-1994; 94EP-0203737.
 XX 23-DEC-1993; 93CU-0000125.
 XX (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
 XX Garcia LH, Gonzalez AC, Sosa GS, Sosa JGA;
 XX WPI; 1995-247529/33.
 XX New fructosyl:transferase from Acetobacter diazotrophicus - for the
 PT prodn. of fructo-oligosaccharide and fructan cpds. from sucrose, useful
 PT e.g. as low calorie sweeteners.
 XX Example 3; Page 7; 16pp; English.
 XX An extracellular Frase was isolated from A. diazotrophicus SRT4,
 CC and its N-terminal sequence (AAR79143) was determined.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 10 AA;
 QY Query Match 44.4%; Score 4; DB 16; Length 10;
 DB Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 6 PLFP 9
 ||||
 3 PLFP 6

RESULT 47
 AAG85227
 ID AAG85227 standard; Peptide; 10 AA.
 XX AAG85227;
 XX 11-SEP-2001 (first entry)
 DE Saccharomyces cerevisiae peptide, SEQ ID NO: 176.
 XX Saccharomyces cerevisiae;
 KW drug discovery; drug design.
 XX Saccharomyces cerevisiae.
 XX WO200142276-A1.
 XX 14-JUN-2001.
 XX 13-DEC-2000; 2000WO-GB04773.
 XX 13-DEC-1999; 99GB-0029471.
 XX (PROT-) PROTEOM LTD.
 XX Roberts GW, Heal JR;
 XX WPI; 2001-367863/38.
 XX Identifying complementary peptides by analysis of protein and
 PT nucleotide sequence databases, useful in drug design -
 XX Example 3; Page 54; 488pp; English.
 XX The invention relates to the identification of complementary peptides
 CC by analysis of protein and nucleotide sequence databases from higher
 CC eukaryotic genomes, excluding human and plants. The specific
 CC complementary peptides interact with their relevant target proteins
 CC encoded in the eukaryote genome. The peptides may be used as reagents

CC and drugs for drug discovery and as lead ligands for drug design and
 CC development. The present sequence is a complementary peptide from
 CC Saccharomyces cerevisiae.
 XX Sequence 10 AA;
 QY Query Match 44.4%; Score 4; DB 22; Length 10;
 DB Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 3 SYVP 6
 ||||
 6 SYVP 9

RESULT 48
 ABB83032
 ID ABB83032 standard; peptide; 10 AA.
 XX ABB83032;
 XX 27-AUG-2002 (first entry)
 DE Transferrin receptor gene mapped peptide #18.
 XX Peptide database; peptide characterisation; computer-mediated;
 KW exon identification; mutation; polymorphic; exon-intron boundary;
 KW post-translational modification; clinical diagnosis;
 KW transferrin receptor gene.
 XX Unidentified.
 XX WO200221139-A2.
 XX 14-MAR-2002.
 XX 10-SEP-2001; 2001WO-GB04034.
 XX 08-SEP-2000; 2000GB-0022136.
 XX 13-SEP-2000; 2000US-232273P.
 XX 28-NOV-2000; 2000US-0724405.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX (ROBY/) ROBINSON A W.
 XX Robinson AW, Townsend RR;
 XX WPI; 2002-393870/42.
 XX Computer-based method for the identification and characterization of a
 PT peptide sequence present in a peptide database that corresponds to an
 PT experimental peptide, involves using previously ordained criteria -
 XX Example 1; Page 53; 74pp; English.
 XX The invention relates to computer-based determination of whether a
 CC peptide database contains peptides corresponding to an experimental
 CC peptide. This functions by constituting a search string to determine a
 CC candidate that read sequences in the database, and computer-mediated
 CC back-reading of candidate sequences that fit in the data of peak list
 CC (sequences) that satisfy matching criteria are identified as corresponding
 CC in peptide or nucleotide databases for unambiguous identification of
 CC exons, determining a correct reading frame, identifying the artifacts
 CC and errors in sequences, identifying mutations and polymorphisms,
 CC identifying post-translational modifications, and identifying
 CC exon-intron boundaries. The method is also useful for detecting a variety
 CC of post-translational modifications relevant to basic research or to the
 CC clinical diagnosis of disease, and for detecting proteolytic processing
 CC or changes associated with transfection or genetic changes. The method
 CC identifies the corresponding sequence if it is present in the database,
 CC without the need for a skilled observer to choose from a list of possible
 CC matches. The current sequence represents a transferrin gene mapped

```

CC peptide.
XX
SQ Sequence 10 AA;

Query Match 44.4%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
    ||||
Db 6 SYVP 9

RESULT 49
ABR06228
ID ABR06228 standard; Peptide; 10 AA.
XX
AC ABR06228;
XX
DT 19-MAY-2003 (first entry)
DE Human cancer-related protein 109P1D4 HLA peptide #163.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
PS Claim 13; Page 174; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
SQ Sequence 10 AA;

Query Match 44.4%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
    ||||
Db 1 PLFP 4

RESULT 51
ABR06590
ID ABR06590 standard; Peptide; 10 AA.
XX
AC ABR06590;
XX
DT 19-MAY-2003 (first entry)

```

XX Human cancer-related protein 109P1D4 HLA peptide #525.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 XX Human leukocyte antigen.
 KW Homo sapiens.
 OS WO200283921-A2.
 XX
 PN 24-OCT-2002.
 XX
 PD 10-APR-2002; 2002WO-US11654.
 XX
 PF 10-APR-2001; 2001US-282739P.
 XX
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 PS Claim 13; Page 178; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 44.4%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PLFP 9
 DB 1 PLFP 4
 XX
 DE 19-MAY-2003 (first entry)
 XX
 DT Human cancer-related protein 109P1D4 HLA peptide #1189.
 XX
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 PS Claim 13; Page 178; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 44.4%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PLFP 9
 DB 1 PLFP 4
 XX
 DE 19-MAY-2003 (first entry)
 XX
 DT Human cancer-related protein 109P1D4 HLA peptide #1189.
 XX
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX

PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 PS Claim 13; Page 184; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 44.4%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PLFP 9
 DB 3 PLFP 6
 XX
 DE 19-MAY-2003 (first entry)
 XX
 DT Human cancer-related protein 109P1D4 HLA peptide #1377.
 XX
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX

PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX Claim 13; Page 186; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
XX Sequence 10 AA;
SQ
Query Match 44.4%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PLFP 9
Db 2 PLFP 5
|||||
RESULT 54
AAR72659
ID AAR72659 standard; peptide; 11 AA.
XX
AC AAR72659;
XX
XX 25-MAR-2003 (updated)
DT 25-OCT-1995 (first entry)
XX
DE Cladosporium herbarum allergen Clah22 B-cell epitope (141-151).
XX
XX Fungal spore; allergen; Clah22; allergy; yeast protein YCP4;
KW B-cell epitope; antigenic region.
XX
XX Cladosporium herbarum.
OS
XX WO9506121-A2.
PN
XX 02-MAR-1995.
PD
XX 24-AUG-1994; 94WO-AT00120.
PF
XX 27-AUG-1993; 93AT-0001725.
PR
XX
XX (BIOM-) BIOMAY PROD N & HANDELSGES MBH.
PA
XX Achatz G, Breitenbach M, Ebner C, Hirschwehr R;
PI Kraft D, Lechenauer E, Oberkofler H, Prillinger H;
PI Simon B, Unger A;
XX
XX WPI; 1995-106850/14.
DR
XX Allergens derived from Cladosporium herbarum spores - also
PT recombinant DNA for expressing the allergens, useful for in vitro
PT allergy detection
XX
XX Claim 1; Page 23; 35pp; German.

XX Spores of Cladosporium herbarum are the most common fungal spores
CC found in the air; they can cause allergic reactions. Various Clah
CC allergens and sequences encoding them have now been isolated. The
CC mature Clah22 allergen has mol. wt. 22 KD and is encoded by cDNA
CC sequence AAQ87845. The allergen has homology to the yeast protein
CC YCP4. Potential epitopic subfragments were identified by computer
CC analysis of the amino acid sequence. See AAR72653-R72661 for potential
CC B-cell epitopes and AAR72662-R72668 for potential T-cell epitopes.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 11 AA;
SQ
Query Match 44.4%; Score 4; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 YVPL 7
Db 2 YVPL 5
|||||
RESULT 55
AAE11116
ID AAE11116 standard; peptide; 11 AA.
XX
AC AAE11116;
XX
XX 18-DEC-2001 (first entry)
DT
DE Tryptic peptide #18 of phhAB fusion protein.
XX
XX Phenylalanine hydroxylase; PAH; phhA; 4a-carbinolamine dehydratase; phhB;
KW aromatic aminotransferase; phhC; milk protein; animal protein; casein;
KW proteinaceous food product; globulin; whey protein; phenylketonuria;
KW PKU; inherited metabolic disorder; impaired brain function; nootropic;
KW cell therapy; tryptic peptide.
XX
XX Unidentified.
OS
XX WO200168822-A2.
PN
XX 20-SEP-2001.
PD
XX 14-MAR-2001; 2001WO-DK00172.
PF
XX 14-MAR-2000; 2000US-0525116.
PR
XX (NILA-) NILAB APS.
PA
XX Johnsen M, Ravn P, Madsen SM, Vrang A, Israelsen H, Bredmose L;
PI Arnau J, Jensen SH, Gjetting T, Nielsen E;
XX
XX WPI; 2001-590055/66.
DR
XX Novel recombinant cells comprising a nucleic acid encoding a gene
PT product having phenylalanine hydroxylase activity, that is derived from
PT a prokaryotic organism, is useful for treating phenylketonuria in
PT mammals -
XX
XX Example 8; Page 47; 91pp; English.
XX
XX The patent discloses novel cells comprising a nucleic acid encoding
CC a gene product having phenylalanine hydroxylase (PAH) activity such
CC as phenylalanine hydroxylase (phhA), 4a-carbinolamine dehydratase
CC (phhB) and aromatic aminotransferase (phhC), which are derived
CC from a prokaryotic organism. The patent also relates to fusion
CC proteins comprising a protein enhancing and/or stabilising the
CC PAH activity in addition to PAH activity. The cells are useful
CC for producing PAH. The sequences of the invention are also useful
CC for preparing a proteinaceous food product (animal protein such
CC as a milk protein derived from casein, globulin or a whey protein)
CC having reduced content of phenylalanine. The method involves contacting

CC	disorders, e.g. immune deficiency, autoimmune states, hypersensitivity,
CC	allergy, graft rejection, infection, hormonal disorders and central
CC	nervous system diseases), also, where (I) is a MHC ligand (IIa), in
CC	vaccines for treatment or prevention of: (i) viral, bacterial, parasitic
CC	or fungal infections; or (ii) of cancers. A particular application is in
CC	anti-melanoma vaccines. (I) are also useful for in vitro diagnosis of
CC	diseases associated with interactions between MHC and (I), e.g. melanoma
CC	and human immunodeficiency virus infection. AAM98898 to AAM99592
CC	represent peptides which can be used in pharmaceutical compounds from
CC	the present invention.
XX	
XX	
SQ	Sequence 11 AA;
	Query Match 44.4%; Score 4; DB 22; Length 11;
	Best Local Similarity 100.0%; Pred. No. 2.7e-02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	3 SYVP 6
Dd	3 SYVP 6
RESULT 57	
AAG63527	
ID	AAG63527 standard; peptide; 11 AA.
XX	
AC	AAG63527;
XX	
DT	15-OCT-2001 (first entry)
XX	
DE	An epitope which may be conjugated to pseudopeptides.
KW	Pseudopeptide; immunomodulation; adjuvant; antigen presenting cell;
KW	macrophage; dendritic cell; cytokine production; immunocompetent cell;
KW	autoimmune disease.
XX	
OS	Synthetic.
XX	
PN	WO200146126-A1.
XX	
PD	28-JUN-2001.
XX	
PF	21-DEC-2000; 2000WO-FR03650.
XX	
PR	22-DEC-1999; 99WO-IB02038.
XX	
PA	(OMPH-) OM-PHARMA.
XX	
PI	Bauer J, Martin OR, Rodriguez S;
XX	
DR	WPI; 2001-496651/54.
XX	
PT	New amphiphilic acylated pseudopeptides having a functionalized
PT	auxiliary spacer, useful as immunomodulators, e.g. as adjuvants in
PT	vaccines -
XX	
PS	
XX	Example 3.9; Fig 67; 267pp; French.
CC	The specification describes N-Acylated pseudopeptides, which have
CC	a neutral or charged acidic group at one terminal and a functionalized
CC	auxiliary spacer at the other. The pseudopeptides show immunomodulatory
CC	and adjuvant action, based on activation of antigen presenting cells
CC	(e.g. macrophages or dendritic cells), induction of differentiation of
CC	dendritic cells, induction of cytokine production and induction of
CC	maturatation of immunocompetent cell strains originating from hematopoietic
CC	and lymphoid organs. They reinforce humoral and cellular immunity. They
CC	can be grafted onto antigens (to modulate immune response) or onto
CC	drugs (to improve the therapeutic activity or targeting). The
CC	pseudopeptides are thus useful in human or veterinary medicine as
CC	immunizing or diagnostic agents. Typically, the pseudopeptides are used
CC	as adjuvants together with (or covalently bonded to) antigens for
CC	vaccination against viral, parasitic/protozoal, microbial or fungal
CC	infections; incubated with blood cells ex vivo, to render the cells

CC immunocompetent before reintroduction in vivo; or used in therapy of
 CC certain autoimmune diseases. The present sequence represents an
 CC epitope which may be conjugated to pseudopeptides of the invention.

SQ Sequence 11 AA;

Query Match 44.4%; Score 4; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6
 ||||
 Db 3 SYVP 6

RESULT 58

ID ABP99426 standard; Peptide; 11 AA.

XX ABP99426;

DT 24-MAR-2003 (first entry)

XX Beta-amyloid binding D-form peptide 13.

XX Alzheimer's disease; beta amyloid; nootropic; neuroprotective;
 KW plaque.

XX Unidentified.

XX Key Location/Qualifiers

PH Misc-difference 1..11

FT /note= "D-form residue"

XX WO200281505-A2.

XX 17-OCT-2002.

XX 08-APR-2002; 2002WO-EP03862.

XX 06-APR-2001; 2001DE-1017281.

XX (IMBM-) IMB INST MOLEKULARE BIOTECHNOLOGIE EV.

XX Willbold D, Wiesehan K;

XX WPI; 2003-103321/09.

XX New D-amino acid peptide specific for beta-amyloid peptide, useful in
 PT diagnosis, prevention and treatment of Alzheimer's disease -
 XX Example; Fig 1; 28pp; German.

XX The invention relates to peptides (I) consisting essentially of D-amino
 CC acids and able to bind to monomeric, oligomeric and/or fibrils of
 CC beta-amyloid peptide (bAP) with dissociation constant (Kd) at most 10,
 CC preferably 4 micro M. (I) act by inhibiting the aggregation of bAP to
 CC plaques and dissolution of existing plaques. (I) or other peptides with
 CC high binding affinity for bAP, are used for diagnosis of Alzheimer's
 CC disease (AD) in living subjects, as contrast agents for detection of
 CC amyloid plaque, for prevention or treatment of AD and for investigating
 CC the relationship between pathological conditions and AD symptoms. (I)
 CC have no significant side effects, are more resistant to proteases than
 CC L-peptides, have low immunogenicity and are highly specific. The present
 CC sequence is that of a peptide of the invention.

SQ Sequence 11 AA;

Query Match 44.4%; Score 4; DB 24; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6

Db 6 SYVP 9
 ||||

RESULT 59

ID AAY67307 standard; peptide; 12 AA.

XX AAY67307;

DT 05-APR-2000 (first entry)

XX Malarial epitope of Plasmodium yoelii, used to alter viral proteins.

XX Malarial epitope; ME1; reduced lethal dose; attenuated influenza virus;
 KW nonstructural gene segment; NS1; tumour antigen expression; vaccine;
 KW HIV; HBV; herpes virus; polio virus; interferon.

XX Plasmodium yoelii.

XX WO9964571-A1.

XX 16-DEC-1999.

XX 11-JUN-1999; 99WO-US13139.

XX 12-JUN-1998; 98US-0089103.

XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.

PA (EGOR/) EGOROV A.

PA (MUST/) MUSTER T.

PI Egorov A, Muster T, Garcia-Sastre A, Palese P;

XX WPI; 2000-105886/09.

XX Novel interferon inducing genetically engineered attenuated viruses
 PT used. e.g. against polioviruses -
 XX Disclosure; Page 23; 48pp; English.

XX This peptide represents the malarial epitope (ME 1) of Plasmodium yoelii,
 CC which can be introduced into the antigenic site E of the haemagglutinin
 CC of the influenza virus. The resulting chimeric virus has a reduced lethal
 CC dose when compared to the wild type virus. The invention relates to novel
 CC genetically engineered attenuated viruses, which contain a modified viral
 CC nonstructural (NS) gene segment, which affects the ability of the virus
 CC to grow in interferon deficient substrates. The attenuated virus is
 CC genetically engineered Influenza A virus with an IFN-inducing phenotype
 CC containing a knockout of the NS1 segment. The attenuated virus can be
 CC used in a vaccine. The attenuated virus of the invention may also be used
 CC to express heterologous proteins, including tumour and viral antigens.
 CC Especially, the attenuated viruses are used as vaccines against a broad
 CC range of viruses and antigens from different species, e.g. epitopes of
 CC HIV such as gp120, HBV surface antigen; Herpes virus glycoproteins, VP1
 CC of polioviruses, etc. The attenuated viruses can also be used for the
 CC prophylaxis or treatment of infection (viral or nonviral pathogens) or
 CC tumour formation.

SQ Sequence 12 AA;

Query Match 44.4%; Score 4; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6
 ||||

Db 4 SYVP 7

RESULT 60

AAW99153 standard; Peptide; 12 AA.
 ID AAW99153

```

XX AC AAM99153;
XX AC
XX AC
XX AC
XX DT 07-DEC-2001 (first entry)
XX DE
XX DE Vaccine related MHC ligand peptide SEQ ID NO:256.
XX KW Glutamic acid; glutamine; vaccine; major histocompatibility complex;
XX KW MHC; immunomodulator; antiallergic; endocrine; neuroprotetant;
XX KW virucidal; bactericidal; antiparasitic; fungicidal; cytostatic;
XX KW medicine; pharmaceutical; immune disorder; immune deficiency;
XX KW autoimmune; hypersensitivity; allergy; graft rejection; infection;
XX KW hormonal disorder; central nervous system disease; cancer; melanoma;
XX KW anti-melanoma vaccine; human immunodeficiency virus.
XX OS
XX OS Homo sapiens.
XX PN WO20010772-A2.
XX PN
XX PD
XX PD 27-SEP-2001.
XX PF
XX PF 22-MAR-2001; 2001WO-FR00872.
XX PF
XX PR 23-MAR-2000; 2000FR-0003711.
XX PR
XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.
XX PA
XX PI Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
XX PI
XX DR WPI; 2001-611470/70.
XX DR
XX PT Stabilized pharmaceutical containing N-terminal glutamic acid or
XX PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
XX PT with strong acid -
XX PS
XX PS Claim 9; Page 75; 149pp; French.
XX CC
XX CC The present invention describes a pharmaceutical compound (I) that
XX CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue
XX CC in the form of an addition salt with a strong, physiologically
XX CC acceptable acid (II). Also described are: (a) a pharmaceutical
XX CC composition containing at least one (I); (b) a vaccine containing at
XX CC least one (I) where this is a major histocompatibility complex (MHC)
XX CC ligand (Ia); (c) a method for in vitro diagnosis of diseases associated
XX CC with the presence of (Ia); (d) a kit for method (c) that includes a (Ia);
XX CC and (e) a process for preparing (I). (I) has immunomodulator, endocrine,
XX CC antiallergic, neuroprotetant, virucidal, bactericidal, antiparasitic,
XX CC fungicidal and cytostatic activities. (I) are useful, in human or
XX CC veterinary medicine, in pharmaceutical compositions (for treating immune
XX CC disorders, e.g. immune deficiency, autoimmune states, hypersensitivity,
XX CC allergy, graft rejection, infection, hormonal disorders and central
XX CC nervous system diseases), also, where (I) is a MHC ligand (Ia), in
XX CC vaccines for treatment or prevention of: (i) viral, bacterial, parasitic
XX CC or fungal infections; or (ii) of cancers. A particular application is in
XX CC anti-melanoma vaccines. (I) are also useful for in vitro diagnosis of
XX CC diseases associated with interactions between MHC and (I). e.g. melanoma
XX CC and human immunodeficiency virus infection. AM98898 to AM99592
XX CC represent peptides which can be used in pharmaceutical compounds from
XX CC the present invention.
XX SQ Sequence 12 AA;
XX SQ
XX SQ Query Match 44.4%; Score 4; DB 22; Length 12;
XX SQ Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX SQ Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX SQ
XX QY 1 VESY 4
XX Db ||||
XX Db 7 VESY 10
XX Db
XX RESULT 61
XX AAG63518
XX ID AAG63518 standard; peptide; 12 AA.
XX AC AAG63518;
XX AC
XX DT 15-OCT-2001 (first entry)
XX DE
XX DE Amino acid sequence of a modified antigen derived from Plasmodium.
XX KW Pseudopeptide; immunomodulation; adjuvant; antigen presenting cell;
XX KW macrophage; dendritic cell; cytokine production; immunocompetent cell;
XX KW autoimmune disease.
XX KW Plasmodium sp.
XX OS
XX OS WO200146126-A1.
XX PN
XX PN 28-JUN-2001.
XX PD
XX PD 21-DEC-2000; 2000WO-FR03650.
XX PF
XX PF 22-DEC-1999; 99WO-IB02038.
XX PR
XX PR (OMPH-) OM-PHARMA.
XX PA
XX PI Bauer J, Martin OR, Rodriguez S;
XX PI
XX DR WPI; 2001-496651/54.
XX DR
XX PT New amphiphilic acylated pseudopeptides having a functionalized
XX PT auxiliary spacer, useful as immunomodulators, e.g. as adjuvants in
XX PT vaccines -
XX PS
XX PS Example 3.5; Page 90; 267pp; French.
XX CC
XX CC The specification describes N-Acylated pseudopeptides, which have
XX CC a neutral or charged acidic group at one terminal and a functionalized
XX CC auxiliary spacer at the other. The pseudopeptides show immunomodulatory
XX CC and adjuvant action, based on activation of antigen presenting cells
XX CC (e.g. macrophages or dendritic cells), induction of differentiation of
XX CC dendritic cells, induction of cytokine production and induction of
XX CC maturation of immunocompetent cell strains originating from hematopoietic
XX CC and lymphoid organs. They reinforce humoral and cellular immunity. They
XX CC can be grafted onto antigens (to modulate immune response) or onto
XX CC drugs (to improve the therapeutic activity or targeting). The
XX CC pseudopeptides are thus useful in human or veterinary medicine as
XX CC immunizing or diagnostic agents. Typically, the pseudopeptides are used
XX CC as adjuvants together with (or covalently bonded to) antigens for
XX CC vaccination against viral, parasitic/protozoal, microbial or fungal
XX CC infections; incubated with blood cells ex vivo, to render the cells
XX CC immunocompetent before reintroduction in vivo; or used in therapy of
XX CC certain autoimmune diseases. The present sequence represents a
XX CC Plasmodium antigen, which may be used with the pseudopeptides of the
XX CC invention.
XX SQ Sequence 12 AA;
XX SQ
XX SQ Query Match 44.4%; Score 4; DB 22; Length 12;
XX SQ Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX SQ Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX SQ
XX QY 3 SYVP 6
XX Db ||||
XX Db 4 SYVP 7
XX Db
XX RESULT 62
XX AAR21802
XX ID AAR21802 standard; Peptide; 13 AA.
XX AC
XX AC AAR21802;
XX DT
XX DT 25-MAR-2003 (updated)
XX DT 09-JUN-1992 (first entry)

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PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
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PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
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PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465460/50.
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders -
XX Claim 1; SEQ ID No 1240; 880pp; English.
XX The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia, myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative
CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
CC disorders (e.g. Alzheimer's disease and Parkinson's disease), chromosomal
CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
CC disorders (e.g. glomerulonephritis), cardiovascular disorders
CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
CC Addison's disease), reproductive system disorders, gastrointestinal
CC disorder (inflammatory disorders), liver disorders (cirrhosis),
CC as stimulators of B-cell responsiveness to pathogens, activators of
CC T-cells, to induce higher affinity antibodies, and as a means to induce
CC tumour proliferation in pathologies e.g. acquired immune deficiency
CC syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction
CC pathway protein, amino acid sequences of the invention.
XX Sequence 13 AA;
SQ
Query Match 44.4%; Score 4; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYVP 6
Db 1 SYVP 4
RESULT 64
AAB68132
ID AAB68132 standard; peptide; 13 AA.
XX AAB68132;
AC AAB68132;
XX 09-JUL-2001 (first entry)
XX Peptide derived from the beta4 part of alpha6beta4 integrin.
XX Gastrointestinal epithelial tumour cell; alpha6beta4 integrin;
KW tumour-associated antigen; metastatic disease; malignant disease;
KW tumour typing; tumour screening; tumour.
XX Homo sapiens.
OS
XX WO200130854-A2.
PN 03-MAY-2001.
XX 26-OCT-2000; 2000WO-SE02082.
XX 28-OCT-1999; 99SE-0003895.
XX (ACTI-) ACTIVE BIOTECH AB.
XX

PI Brodin TN, Karlstroem PJ, Ohlsson LG, Tordsson MJ, Kearney PP;
 PI Nilsson BHK;
 DR WPI; 2001-308619/32.
 XX
 PT Novel antibody for diagnosis, treatment of human metastatic and
 PT malignant diseases, has binding structure for target structure
 PT displayed on cell surface of human gastrointestinal epithelial tumour
 PT and normal cells -
 XX
 XX Claim 27; Page 27; 75pp; English.
 XX
 CC The present sequence is derived from the beta4 part of alpha6beta4
 CC integrin. The specification describes antibodies which bind to this
 CC protein. Alpha6beta4 integrin is displayed in and on the cell surface of
 CC human gastrointestinal epithelial tumour cells and in a subpopulation of
 CC normal human gastrointestinal epithelial cells. Alpha6beta4 integrin is
 CC a tumour-associated antigen. The antibody, and its fragments, are
 CC useful for treating conditions based on anti-angiogenic mechanism in
 CC humans. They are useful for treating human metastatic and malignant
 CC disease, for in vitro, in vivo diagnosis and prognosis of human malignant
 CC disease, comprising tumour typing, tumour screening, tumour diagnosis and
 CC prognosis and monitoring premalignant conditions. Quantitative in vivo
 CC diagnosis is carried out by determining the localization of antibody to
 CC tumour deposits in humans.
 XX
 SQ Sequence 13 AA;
 Query Match 44.4%; Score 4; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 VPLF 8
 DB 1 VPLF 4
 RESULT 65
 ID ABP53814 standard; Peptide; 13 AA.
 XX
 AC ABP53814;
 XX
 DT 06-JAN-2003 (first entry)
 XX
 DE Human CNTF potential MHC class II binding activity peptide #4.
 XX
 KW Human; ciliary neurotrophic factor; CNTF; reduced immunogenicity;
 KW immune response; major histocompatibility complex; MHC class II;
 KW T cell epitope; immunogenic.
 XX
 OS Homo sapiens.
 XX
 XX WO200270698-A2.
 FN
 PD 12-SEP-2002.
 XX
 PF 27-FEB-2002; 2002WO-EP02084.
 XX
 PR 02-MAR-2001; 2001EP-0105089.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Carr FJ, Carter G;
 XX
 DR WPI; 2003-018694/01.
 XX
 PT New modified human ciliary neurotrophic factor which is substantially
 PT non-immunogenic or less immunogenic than any non-modified molecule,
 PT useful for treating conditions in a mammal -
 XX
 PS Claim 6; Page 11; 33pp; English.

CC The present invention describes a modified molecule (I) with the
 CC biological activity of human ciliary neurotrophic factor (CNTF) which is
 CC substantially non-immunogenic or less immunogenic than any non-modified
 CC molecule with the same biological activity when used in vivo. Also
 CC described: (1) a DNA sequence (II) coding for (I); (2) a pharmaceutical
 CC carrier (III) comprising (I) and a carrier, diluent or excipient;
 CC (3) manufacturing (M1) (I); (4) a 13mer T cell epitope peptide (IV) with
 CC a potential MHC Class II binding activity and created from a non-modified
 CC CNTF selected from the 81 peptide sequences given in ABP53811 to
 CC ABP53891; and (5) a peptide sequence (V) consisting of at least 9
 CC consecutive amino acid residues of (IV). The modified CNTF molecule can
 CC be administered to humans for therapeutic purposes. The 13-mer T cell
 CC epitope peptide and the peptide sequence is useful in the manufacture of
 CC CNTF with substantially no or less immunogenic than any non-modified
 CC molecule with the same biological activity when used in vivo. The
 CC modified human CNTF can be substantially non-immunogenic or less
 CC immunogenic than any non-modified counterpart. The sequence given in
 CC ABP53810 represents the primary sequence of human CNTF, which is given
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 13 AA;
 Query Match 44.4%; Score 4; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ESYV 5
 DB 3 ESYV 6
 RESULT 66
 ID ABP53834 standard; Peptide; 13 AA.
 XX
 AC ABP53834;
 XX
 DT 06-JAN-2003 (first entry)
 XX
 DE Human CNTF potential MHC class II binding activity peptide #24.
 XX
 KW Human; ciliary neurotrophic factor; CNTF; reduced immunogenicity;
 KW immune response; major histocompatibility complex; MHC class II;
 KW T cell epitope; immunogenic.
 XX
 OS Homo sapiens.
 XX
 XX WO200270698-A2.
 FN
 PD 12-SEP-2002.
 XX
 PF 27-FEB-2002; 2002WO-EP02084.
 XX
 PR 02-MAR-2001; 2001EP-0105089.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Carr FJ, Carter G;
 XX
 DR WPI; 2003-018694/01.
 XX
 PT New modified human ciliary neurotrophic factor which is substantially
 PT non-immunogenic or less immunogenic than any non-modified molecule,
 PT useful for treating conditions in a mammal -
 XX
 PS Claim 6; Page 11; 33pp; English.
 XX
 CC The present invention describes a modified molecule (I) with the
 CC biological activity of human ciliary neurotrophic factor (CNTF) which is
 CC substantially non-immunogenic or less immunogenic than any non-modified
 CC molecule with the same biological activity when used in vivo. Also
 CC described: (1) a DNA sequence (II) coding for (I); (2) a pharmaceutical
 CC carrier (III) comprising (I) and a carrier, diluent or excipient;

CC (3) manufacturing (M1) (I); (4) a 13mer T cell epitope peptide (IV) with
 CC a potential MHC Class II binding activity and created from a non-modified
 CC CNTP selected from the 81 peptide sequences given in ABP53811 to
 CC ABP53891; and (5) a peptide sequence (V) consisting of at least 9
 CC consecutive amino acid residues of (IV). The modified CNTP molecule can
 CC be administered to humans for therapeutic purposes. The 13-mer T cell
 CC epitope peptide and the peptide sequence is useful in the manufacture of
 CC CNTP with substantially no or less immunogenic than any non-modified
 CC molecule with the same biological activity when used in vivo. The
 CC modified human CNTP can be substantially non-immunogenic or less
 CC immunogenic than any non-modified counterpart. The sequence given in
 CC ABP53810 represents the primary sequence of human CNTP, which is given
 CC in the exemplification of the present invention.

XX
 SQ Sequence 13 AA;

Query Match 44.4%; Score 4; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5
 Db |||||
 9 ESYV 12

RESULT 67
 ABP53835
 ID ABP53835 standard; Peptide; 13 AA.
 XX
 AC ABP53835;
 XX
 DT 06-JAN-2003 (first entry)
 XX
 DE Human CNTP potential MHC class II binding activity peptide #25.
 XX
 KW Human; ciliary neurotrophic factor; CNTP; reduced immunogenicity;
 KW immune response; major histocompatibility complex; MHC class II;
 KW T cell epitope; immunogenic.
 XX
 OS Homo sapiens.
 XX
 PN WO200270698-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 27-FEB-2002; 2002WO-EP02084.
 XX
 PR 02-MAR-2001; 2001EP-0105089.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Carr FJ, Carter G;
 XX
 DR WPI; 2003-018694/01.
 XX
 PT New modified human ciliary neurotrophic factor which is substantially
 PT non-immunogenic or less immunogenic than any non-modified molecule,
 PT useful for treating conditions in a mammal -
 XX
 PS Claim 6; Page 11; 33pp; English.

CC The present invention describes a modified molecule (I) with the
 CC biological activity of human ciliary neurotrophic factor (CNTP) which is
 CC substantially non-immunogenic or less immunogenic than any non-modified
 CC molecule with the same biological activity when used in vivo. Also
 CC described: (1) a DNA sequence (II) coding for (I); (2) a pharmaceutical
 CC carrier (III) comprising (I) and a carrier, diluent or excipient;
 CC (3) manufacturing (M1) (I); (4) a 13mer T cell epitope peptide (IV) with
 CC a potential MHC Class II binding activity and created from a non-modified
 CC CNTP selected from the 81 peptide sequences given in ABP53811 to
 CC ABP53891; and (5) a peptide sequence (V) consisting of at least 9
 CC consecutive amino acid residues of (IV). The modified CNTP molecule can
 CC be administered to humans for therapeutic purposes. The 13-mer T cell
 CC epitope peptide and the peptide sequence is useful in the manufacture of
 CC CNTP with substantially no or less immunogenic than any non-modified
 CC molecule with the same biological activity when used in vivo. The
 CC modified human CNTP can be substantially non-immunogenic or less
 CC immunogenic than any non-modified counterpart. The sequence given in
 CC ABP53810 represents the primary sequence of human CNTP, which is given
 CC in the exemplification of the present invention.

CC epitope peptide and the peptide sequence is useful in the manufacture of
 CC CNTP with substantially no or less immunogenic than any non-modified
 CC molecule with the same biological activity when used in vivo. The
 CC modified human CNTP can be substantially non-immunogenic or less
 CC immunogenic than any non-modified counterpart. The sequence given in
 CC ABP53810 represents the primary sequence of human CNTP, which is given
 CC in the exemplification of the present invention.

XX
 SQ Sequence 13 AA;

Query Match 44.4%; Score 4; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5
 Db |||||
 1 ESYV 4

RESULT 68
 ABP53854
 ID ABP53854 standard; Peptide; 13 AA.
 XX
 AC ABP53854;
 XX
 DT 06-JAN-2003 (first entry)
 XX
 DE Human CNTP potential MHC class II binding activity peptide #44.
 XX
 KW Human; ciliary neurotrophic factor; CNTP; reduced immunogenicity;
 KW immune response; major histocompatibility complex; MHC class II;
 KW T cell epitope; immunogenic.
 XX
 OS Homo sapiens.
 XX
 PN WO200270698-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 27-FEB-2002; 2002WO-EP02084.
 XX
 PR 02-MAR-2001; 2001EP-0105089.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Carr FJ, Carter G;
 XX
 DR WPI; 2003-018694/01.
 XX
 PT New modified human ciliary neurotrophic factor which is substantially
 PT non-immunogenic or less immunogenic than any non-modified molecule,
 PT useful for treating conditions in a mammal -
 XX
 PS Claim 6; Page 11; 33pp; English.

CC The present invention describes a modified molecule (I) with the
 CC biological activity of human ciliary neurotrophic factor (CNTP) which is
 CC substantially non-immunogenic or less immunogenic than any non-modified
 CC molecule with the same biological activity when used in vivo. Also
 CC described: (1) a DNA sequence (II) coding for (I); (2) a pharmaceutical
 CC carrier (III) comprising (I) and a carrier, diluent or excipient;
 CC (3) manufacturing (M1) (I); (4) a 13mer T cell epitope peptide (IV) with
 CC a potential MHC Class II binding activity and created from a non-modified
 CC CNTP selected from the 81 peptide sequences given in ABP53811 to
 CC ABP53891; and (5) a peptide sequence (V) consisting of at least 9
 CC consecutive amino acid residues of (IV). The modified CNTP molecule can
 CC be administered to humans for therapeutic purposes. The 13-mer T cell
 CC epitope peptide and the peptide sequence is useful in the manufacture of
 CC CNTP with substantially no or less immunogenic than any non-modified
 CC molecule with the same biological activity when used in vivo. The
 CC modified human CNTP can be substantially non-immunogenic or less
 CC immunogenic than any non-modified counterpart. The sequence given in
 CC ABP53810 represents the primary sequence of human CNTP, which is given
 CC in the exemplification of the present invention.

CC in the exemplification of the present invention.

XX SQ Sequence 13 AA;

Query Match 44.4%; Score 4; DB 24; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5
Db 8 ESYV 11

RESULT 69

ID ABP53874 standard; Peptide; 13 AA.

XX AC ABP53874;

DT 06-JAN-2003 (first entry)

XX Human CNTF potential MHC class II binding activity peptide #64.

XX Human; ciliary neurotrophic factor; CNTF; reduced immunogenicity;
KW immune response; major histocompatibility complex; MHC class II;
KW T cell epitope; immunogenic.

XX OS Homo sapiens.

XX PN W0200270698-A2.

XX PD 12-SEP-2002.

XX PF 27-FEB-2002; 2002WO-EP02084.

XX PR 02-MAR-2001; 2001EP-0105089.

XX (MERE) MERCK PATENT GMBH.

XX Carr FJ, Carter G;

XX WPI; 2003-019694/01.

XX New modified human ciliary neurotrophic factor which is substantially
PT non-immunogenic or less immunogenic than any non-modified molecule,
PT useful for treating conditions in a mammal -

XX Claim 6; Page 11; 33pp; English.

XX The present invention describes a modified molecule (I) with the
CC biological activity of human ciliary neurotrophic factor (CNTF) which is
CC substantially non-immunogenic or less immunogenic than any non-modified
CC molecule with the same biological activity when used in vivo. Also
CC described: (1) a DNA sequence (II) coding for (I); (2) a pharmaceutical
CC carrier (III) comprising (I) and a carrier, diluent or excipient;
CC (3) manufacturing (M1) (I); (4) a 13mer T cell epitope peptide (IV) with
CC a potential MHC Class II binding activity and created from a non-modified
CC CNTF selected from the 81 peptide sequences given in ABP53811 to
CC ABP53891; and (5) a peptide sequence (V) consisting of at least 9
CC consecutive amino acid residues of (IV). The modified CNTF molecule can
CC be administered to humans for therapeutic purposes. The 13-mer T cell
CC epitope peptide and the peptide sequence is useful in the manufacture of
CC CNTF with substantially no or less immunogenic than any non-modified
CC molecule with the same biological activity when used in vivo. The
CC modified human CNTF can be substantially non-immunogenic or less
CC immunogenic than any non-modified counterpart. The sequence given in
CC ABP53810 represents the primary sequence of human CNTF, which is given
CC in the exemplification of the present invention.

XX SQ Sequence 13 AA;

Query Match 44.4%; Score 4; DB 24; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5
Db 5 ESYV 8

RESULT 70

ID AAR83142 standard; peptide; 14 AA.

XX AC AAR83142;

DT 14-DEC-1995 (first entry)

XX [4-Leu, 12-D-Arg, 13-Leu] motilin-(1-14) peptide (porcine).

XX motilin; gastrointestinal; diabetic gastroparesis; paralytic ileus.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 12

FT /note= "D-Arg"

FT Modified-site 14

FT /note= "Gln-OH or Gln-NH2"

XX AU9455967-A.

XX PD 16-FEB-1995.

XX PF 24-JUN-1994; 94AU-0065967.

XX PR 06-AUG-1993; 93US-0103490.

XX (OHME-) OHMEDA PHARM PROD DIV INC.

XX Dharanipragada R, Florance JR, Galdes A, Macielag MJ;
PI Marvin MS;

XX WPI; 1995-107112/15.

XX New motilin-like polypeptide(s) - with gastrointestinal motor
PT stimulating activity

XX Disclosure; Page 14; 50pp; English.

XX New motilin-like polypeptides are disclosed which have gastrointestinal
CC motor stimulating activity and which bind with high affinity to the
CC motilin receptor and mimic the peristaltic effects of motilin on
CC gastrointestinal tissue. The peptides are 12-22 amino acids in length
CC and (with reference to motilin) contain one or more of (a) Leu instead
CC of Met at position 13 for greater chemical stability, (b) D-Arg instead
CC of L-Arg at position 12 for greater potency and (c) an N-alkylated Phe
CC at position 1 for increased stability to biodegradation. The peptides
CC are useful clinically for the treatment of diabetic gastroparesis,
CC paralytic ileus and post-operative ileus.
CC The present sequence is a specific example of the new peptides.

XX SQ Sequence 14 AA;

Query Match 44.4%; Score 4; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8
Db 2 VPLF 5

RESULT 71

ABB56665
ID ABB56665 standard; Peptide; 14 AA.

XX ABB56665;
 XX 05-MAR-2002 (first entry)
 XX Human SNP related amino acid sequence SEQ ID NO:1230.
 XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
 KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
 KW autoimmune disease; inflammation; cancer; nervous system disease;
 KW infection; polymorphic protein.
 XX
 OS Homo sapiens.
 XX
 XX WO200138586-A2.
 XX
 XX 31-MAY-2001.
 XX
 XX 22-NOV-2000; 2000WO-US32311.
 XX
 XX 24-NOV-1999; 99US-0167383.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Shimkets RA, Leach M;
 XX
 XX WPI; 2001-355949/37.
 XX
 XX Isolated human nucleic acids comprising one or more single nucleotide
 PT polymorphisms, useful for treating a subject suffering from a
 PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
 PT sequence polymorphism -
 XX
 PS Claim 1; Page 616; 674pp; English.
 XX
 XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
 CC to ABB56903 represent human peptides encoded by some of the SNP
 CC oligonucleotides. The sequences from the present invention can have
 CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
 CC and antibodies from the present invention can be used for treating a
 CC subject suffering from, at risk for, or suspected of, suffering from a
 CC pathology ascribed to the presence of a sequence polymorphism. The
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs
 CC are also useful for determining which forms of a characterised
 CC polymorphism are present in individuals. The antibodies may be used in
 CC the detection, quantitation and/or cellular or tissue localisation of a
 CC polymorphic protein (e.g., for use in measuring levels of the
 CC polymorphic protein within appropriate physiological samples).
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 44.4%; Score 4; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YVPL 7
 Db 6 YVPL 9
 XX
 RESULT 72
 AAM97755
 ID AAM97755 standard; Peptide; 14 AA.
 XX
 AC AAM97755;
 XX
 XX 24-JAN-2002 (first entry)
 XX
 XX Human peptide #1030 encoded by a SNP oligonucleotide.

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 XX Homo sapiens.
 OS
 XX WO200147944-A2.
 XX
 XX 05-JUL-2001.
 PD
 XX 28-DEC-2000; 2000WO-US35498.
 PF
 XX 28-DEC-1999; 99US-0173419.
 PR
 XX 27-DEC-2000; 2000US-0173419.
 PR
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shimkets RA, Leach M;
 XX
 XX WPI; 2001-465210/50.
 DR
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 PT
 XX Disclosure; Page 3893; 4143pp; English.
 PS
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.
 CC
 XX Sequence 14 AA;
 SQ
 Query Match 44.4%; Score 4; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 VPLF 8
 Db 1 VPLF 4
 XX
 RESULT 73
 AAM99155
 ID AAM99155 standard; Peptide; 14 AA.
 XX
 AC AAM99155;
 XX
 XX 07-DEC-2001 (first entry)
 DT
 XX Vaccine related MHC ligand peptide SEQ ID NO:258.
 DE
 XX Glutamic acid; glutamine; vaccine; major histocompatibility complex;
 KW MHC; immunomodulator; antiallergic; endocrine; neuroprotectant;
 KW virucidal; bactericidal; antiparasitic; fungicidal; cytostatic;

KW medicine; pharmaceutical; immune disorder; immune deficiency;
 KW autoimmunity; hypersensitivity; allergy; graft rejection; infection;
 KW hormonal disorder; central nervous system disease; cancer; melanoma;
 KW anti-melanoma vaccine; human immunodeficiency virus.
 XX
 OS Homo sapiens.
 XX
 XX WO200170772-A2.
 XX
 XX 27-SEP-2001.
 XX
 XX 22-MAR-2001; 2001WO-FR00872.
 XX
 XX 23-MAR-2000; 2000FR-0003711.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 XX Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
 XX WPI; 2001-611470/70.
 XX
 XX Stabilized pharmaceutical containing N-terminal glutamic acid or
 XX glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
 XX with strong acid .
 XX
 XX Claim 9; Page 75; 149pp; French.
 XX
 XX The present invention describes a pharmaceutical compound (I) that
 XX contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue
 XX in the form of an addition salt with a strong, physiologically
 XX acceptable acid (II). Also described are: (a) a pharmaceutical
 XX composition containing at least one (I); (b) a vaccine containing at
 XX least one (I) where this is a major histocompatibility complex (MHC)
 XX ligand (Ia); (c) a method for in vitro diagnosis of diseases associated
 XX with the presence of (Ia); (d) a kit for method (c) that includes a (Ia);
 XX and (e) a process for preparing (I). (I) has immunomodulator, endocrine,
 XX antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic,
 XX fungicidal and cytostatic activities. (I) are useful in human or
 XX veterinary medicine, in pharmaceutical compositions (for treating immune
 XX disorders, e.g. immune deficiency, autoimmune states, hypersensitivity,
 XX allergy, graft rejection, infection, hormonal disorders and central
 XX nervous system diseases), also, where (I) is a MHC ligand (Ia), in
 XX vaccines for treatment or prevention of: (i) viral, bacterial, parasitic
 XX or fungal infections; or (ii) of cancers. A particular application is in
 XX anti-melanoma vaccines. (I) are also useful for in vitro diagnosis of
 XX diseases associated with interactions between MHC and (I), e.g. melanoma
 XX and human immunodeficiency virus infection. AAM98898 to AAM99592
 XX represent peptides which can be used in pharmaceutical compounds from
 XX the present invention.
 XX
 XX SQ Sequence 14 AA;
 XX
 XX Query Match 44.4%; Score 4; DB 22; Length 14;
 XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 XX ||||
 XX 7 VESY 10
 XX
 XX Db
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 XX RESULT 74
 XX AAB70401
 XX ID AAB70401 standard; Peptide; 14 AA.
 XX
 XX AC AAB70401;
 XX
 XX 02-MAY-2001 (first entry)
 XX
 XX DE Rabies matrix protein derived peptide SEQ ID NO:35.
 XX
 XX KW Identification; antiviral; viral protein; viral replication; NP;
 XX viral infection; nucleoprotein.

XX. Rabies virus.
 XX WO200111335-A2.
 XX
 XX 15-FEB-2001.
 XX
 XX 11-AUG-2000; 2000WO-US222257.
 XX
 XX 11-AUG-1999; 99US-0148263.
 XX
 XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX
 XX O'Neill R, Harty R, Palese PM;
 XX WPI; 2001-168816/17.
 XX
 XX Identifying a substance that inhibits the interaction between a viral
 XX protein and a host cell protein, useful for the discovery of new
 XX antiviral compounds -
 XX
 XX Example; Page 77; 147pp; English.
 XX
 XX The present invention describes a method (M1) for identifying a
 XX substance that inhibits the interaction of a viral protein (VP) with a
 XX host cell protein (HP). The method comprises: (a) contacting HP with VP
 XX in the presence of a test substance; and (b) detecting complex formation,
 XX where the ability of the test substance to inhibit HP/VP interaction is
 XX indicated by a decrease in complex formation. The antiviral compounds
 XX that inhibit the interaction between a host protein (NS1-BP or NPI-1)
 XX and a viral protein (NS1) are useful for treating or inhibiting viral
 XX infection, preferably influenza and rhinovirus infection, in humans.
 XX Antiviral compounds include peptides and antibodies. In particular
 XX compositions comprising a polypeptide containing an amino acid sequence
 XX corresponding to the NP-NLS domain of the influenza virus NP protein,
 XX which inhibits the specific interaction of the NPI-1 protein with the
 XX influenza virus NP protein are useful for treating or inhibiting
 XX influenza viral infection in humans. The present sequence represents
 XX a peptide, which is used in an example from the present invention.
 XX
 XX SQ Sequence 14 AA;
 XX
 XX Query Match 44.4%; Score 4; DB 22; Length 14;
 XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 XX Qy 4 YVPL 7
 XX ||||
 XX 9 YVPL 12
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 XX Db
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 XX RESULT 75
 XX ABP46338
 XX ID ABP46338 standard; peptide; 14 AA.
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 XX AC ABP46338;
 XX
 XX 19-AUG-2002 (first entry)
 XX
 XX DE Human BlyS binding scFv VH CDR3 SEQ ID 2349.
 XX
 XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;
 XX immunosuppressive; immunostimulant; immunomodulatory; antitumoric;
 XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 XX OS Homo sapiens.
 XX
 XX WO200202641-A1.
 XX
 XX 10-JAN-2002.

```

XX 15-JUN-2001; 2001WO-US19110.
XX
XX 16-JUN-2000; 2000US-212210P.
XX
XX 17-OCT-2000; 2000US-240816P.
XX
XX 16-MAR-2001; 2001US-276248P.
XX
XX 21-MAR-2001; 2001US-277379P.
XX
XX 25-MAY-2001; 2001US-293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
XX Claim 2; Page 2975; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
XX SQ Sequence 14 AA;
XX
XX Query Match 44.4%; Score 4; DB 23; Length 14;
XX Best Local Similarity 100.0%; Pred.No. 3.4e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Qy 6 PLFP 9
XX Db 11 PLFP 14

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 Job time : 24.9709 secs

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Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVLPFP 9

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Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

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Maximum DB seq length: 20

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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	5	55.6	15	11	US-09-880-748-2310
3	5	55.6	16	11	US-09-880-748-2263
4	4	44.4	7	9	US-09-833-067-26
5	4	44.4	7	10	US-09-758-128-45
6	4	44.4	7	10	US-09-758-426-45
7	4	44.4	7	10	US-09-758-198-45
8	4	44.4	7	11	US-09-861-661-45
9	4	44.4	7	12	US-10-052-578-286
10	4	44.4	7	12	US-10-053-520-286
11	4	44.4	7	12	US-10-286-457-308
12	4	44.4	7	12	US-10-053-498B-286
13	4	44.4	8	11	US-09-865-548A-195
14	4	44.4	8	12	US-10-052-578-82
15	4	44.4	8	12	US-10-053-520-82

8	12	US-10-053-498B-82	Sequence 82, Appl
8	16	US-10-305-346-10	Sequence 10, Appl
9	12	US-10-206-155-2	Sequence 2, Appl
9	12	US-10-360-836-1	Sequence 1, Appl
9	12	US-10-275-707-9	Sequence 9, Appl
9	14	US-10-205-150-3	Sequence 3, Appl
10	10	US-09-950-313-40	Sequence 40, Appl
10	12	US-10-360-836-81	Sequence 81, Appl
10	15	US-10-062-710-208	Sequence 208, Appl
11	12	US-10-239-313A-268	Sequence 268, Appl
12	12	US-10-239-313A-256	Sequence 256, Appl
13	10	US-09-764-868-1240	Sequence 1240, Ap
13	11	US-09-955-999-120	Sequence 120, App
14	11	US-09-880-748-2349	Sequence 2349, Ap
14	11	US-09-880-748-2388	Sequence 2388, Ap
14	11	US-09-880-748-2423	Sequence 2423, Ap
14	11	US-09-880-748-2447	Sequence 2447, Ap
14	11	US-09-880-748-2467	Sequence 2467, Ap
14	11	US-09-880-748-2533	Sequence 2533, Ap
14	11	US-09-880-748-2640	Sequence 2640, Ap
14	11	US-09-880-748-2657	Sequence 2657, Ap
14	11	US-09-880-748-2689	Sequence 2689, Ap
14	12	US-10-239-313A-258	Sequence 258, App
15	11	US-09-880-748-2267	Sequence 2267, Ap
15	11	US-09-880-748-2269	Sequence 2269, Ap
15	11	US-09-880-748-2270	Sequence 2270, Ap
15	11	US-09-880-748-2286	Sequence 2286, Ap
15	11	US-09-880-748-2292	Sequence 2292, Ap
15	12	US-10-161-791-379	Sequence 379, App
15	12	US-10-275-707-16	Sequence 16, Appl
16	10	US-09-947-258-1	Sequence 1, Appl
16	11	US-09-947-258-4	Sequence 4, Appl
16	11	US-09-880-748-2261	Sequence 2261, Ap
16	11	US-09-880-748-2266	Sequence 2266, Ap
16	12	US-10-239-313A-259	Sequence 259, App
18	9	US-09-789-561-189	Sequence 189, App
18	14	US-10-038-612-76	Sequence 76, Appl
19	9	US-09-823-936-18	Sequence 18, Appl
19	10	US-09-755-836-23	Sequence 23, Appl
19	11	US-09-880-748-2793	Sequence 2793, Ap
19	12	US-10-236-508-28	Sequence 28, Appl
19	15	US-10-072-438-42	Sequence 42, Appl
19	15	US-10-137-765-41	Sequence 41, Appl
19	15	US-10-146-337-41	Sequence 41, Appl
19	15	US-10-286-140-18	Sequence 18, Appl
20	15	US-10-225-567A-1293	Sequence 1293, Ap
4	8	US-08-424-550B-343	Sequence 343, App
4	9	US-09-834-765-735	Sequence 735, App
4	10	US-09-922-261-399	Sequence 399, App
4	10	US-09-742-096-26	Sequence 26, Appl
4	12	US-10-293-086-39	Sequence 39, Appl
4	12	US-10-331-907-48	Sequence 48, Appl
4	15	US-10-006-869-157	Sequence 157, App
5	10	US-09-185-908-35	Sequence 35, Appl
5	10	US-09-185-908-156	Sequence 156, App
5	12	US-10-281-479A-25	Sequence 25, Appl
5	12	US-10-275-180A-25	Sequence 25, Appl
5	12	US-10-286-132A-25	Sequence 25, Appl
5	15	US-10-006-869-160	Sequence 160, App
5	15	US-10-006-869-1282	Sequence 1282, Ap
5	15	US-10-235-483-28	Sequence 28, Appl
5	15	US-10-235-483-29	Sequence 29, Appl
5	15	US-10-283-349-40	Sequence 40, Appl
5	15	US-10-288-986-12	Sequence 12, Appl
6	8	US-08-859-699-23	Sequence 23, Appl
6	9	US-09-761-636A-12	Sequence 12, Appl
6	10	US-09-953-657-1	Sequence 1, Appl
6	10	US-09-953-657-2	Sequence 2, Appl
6	10	US-09-953-657-3	Sequence 3, Appl
6	10	US-09-953-657-6	Sequence 6, Appl
6	10	US-09-953-657-7	Sequence 7, Appl
6	10	US-09-953-657-8	Sequence 8, Appl
6	10	US-09-727-963A-85	Sequence 85, Appl

89 3 33.3 6 10 US-09-185-908-36 Sequence 36, Appl
90 3 33.3 6 10 US-09-185-908-38 Sequence 38, Appl
91 3 33.3 6 10 US-09-185-908-157 Sequence 157, App
92 3 33.3 6 10 US-09-185-908-159 Sequence 159, App
93 3 33.3 6 12 US-09-969-748C-21 Sequence 21, Appl
94 3 33.3 6 12 US-09-949-039-17 Sequence 17, Appl
95 3 33.3 6 12 US-10-272-497-47 Sequence 47, Appl
96 3 33.3 6 12 US-10-272-497-51 Sequence 51, Appl
97 3 33.3 6 12 US-10-315-515-143 Sequence 143, App
98 3 33.3 6 12 US-10-031-874A-60 Sequence 60, Appl
99 3 33.3 6 12 US-10-277-292-697 Sequence 697, App
100 3 33.3 6 12 US-10-280-340-697 Sequence 697, App

ALIGNMENTS

RESULT 1
US-10-281-652-31
; Sequence 31, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101 ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-31

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Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 VESYVPLFP 9
Db 1 VESYVPLFP 9

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; Sequence 2310, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2310
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
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Db 8 SYVPL 12

RESULT 3
US-09-880-748-2263
; Sequence 2263, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
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; ORGANISM: Homo sapiens
US-09-880-748-2263

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Db 8 SYVPL 12

RESULT 4
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; Sequence 26, Application US/09833067
; Patent No. US20020054888A1
; GENERAL INFORMATION:
; APPLICANT: O'HANLEY, PETER
; APPLICANT: DENICH, KENNETH
; TITLE OF INVENTION: DISSOCIATED PILI, THEIR PRODUCTION AND USE
; FILE REFERENCE: 050939/0102
; CURRENT APPLICATION NUMBER: US/09/833,067
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/196,493
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 26
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; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT

; ORGANISM: Unknown Sequence
; FEATURE:
; OTHER INFORMATION: Description of Unknown Sequence: highly hydrophobic region
; OTHER INFORMATION: of amino acids
US-09-833-067-26

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Best Local Similarity 100.0%; Pred. No. 6e+05;
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Qy 5 VPLF 8
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RESULT 5
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; Sequence 45, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-128-45

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Qy 6 PLFP 9
Db 3 PLFP 6

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; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-426-45

Query Match 44.4%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9
Db 3 PLFP 6

RESULT 7
US-09-758-198-45
; Sequence 45, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020187925A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-198-45

Query Match 44.4%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9
Db 3 PLFP 6

RESULT 8
US-09-861-661-45
; Sequence 45, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-861-661-45

Query Match 44.4%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
| | | |
Db 3 PLFP 6

RESULT 9
US-10-052-578-286
; Sequence 286, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-052-578-286

Query Match 44.4%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
| | | |
Db 2 YVPL 5

RESULT 10
US-10-053-520-286
; Sequence 286, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-520-286

Query Match 44.4%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
| | | |
Db 2 YVPL 5

RESULT 11
US-10-286-457-308
; Sequence 308, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 308
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, bas
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-308

Query Match 44.4%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8
| | | |
Db 4 VPLF 7

RESULT 12
US-10-053-498B-286
; Sequence 286, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-286

Query Match 44.4%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7
|
|
|
|
Db 2 YVPL 5

RESULT 13

US-09-865-548A-195
; Sequence 195, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 195
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-195

Query Match 44.4%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7
|
|
|
|
Db 4 YVPL 7

RESULT 14

US-10-052-578-82
; Sequence 82, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-052-578-82

Query Match 44.4%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7
|
|
|
|
Db 2 YVPL 5

RESULT 15

US-10-053-520-82
; Sequence 82, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-520-82

Query Match 44.4%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7
|
|
|
|
Db 2 YVPL 5

RESULT 16

US-10-053-498B-82
; Sequence 82, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-82

Query Match 44.4%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
Db 2 YVPL 5

RESULT 17

US-10-305-346-10
; Sequence 10, Application US/10305346
; Publication No. US20030130195A1
; GENERAL INFORMATION:
; APPLICANT: AMIOT, Jean
; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS
; FILE REFERENCE: 6013-57/US-1
; CURRENT APPLICATION NUMBER: US/10/305,346
; CURRENT FILING DATE: 2002-11-27
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk proteins
US-10-305-346-10

Query Match 44.4%; Score 4; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
Db 1 YVPL 4

RESULT 18

US-10-206-155-2
; Sequence 2, Application US/10206155
; Publication No. US20030157135A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Moriya
; APPLICANT: Gonzalez-Assequinolaza, Gloria
; APPLICANT: Nussenzweig, Ruth S.
; APPLICANT: Koezuka, Yasuhiko
; TITLE OF INVENTION: USE OF GLYCOSYLCERAMIDES AS ADJUVANTS
; FILE REFERENCE: 5986/1H958US1
; CURRENT APPLICATION NUMBER: US/10/206,155
; CURRENT FILING DATE: 2002-07-25
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: P. yoelii
US-10-206-155-2

Query Match 44.4%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 19

US-10-360-836-1
; Sequence 1, Application US/10360836
; Publication No. US20030185854A1
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; CURRENT FILING DATE: 2003-02-07
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-1

Query Match 44.4%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 20

US-10-275-707-9
; Sequence 9, Application US/10275707
; Publication No. US20030194801A1
; GENERAL INFORMATION:
; APPLICANT: BONALDO, MIRNA C.
; APPLICANT: GALLER, RICARDO
; APPLICANT: FREIRE, MARCOS DA SILVA
; APPLICANT: GARRAT, RICHARD C.
; TITLE OF INVENTION: USE OF FLAVIVIRUS FOR THE EXPRESSION OF PROTEIN EPITOPES
; TITLE OF INVENTION: AND DEVELOPMENT OF NEW LIVE ATTENUATED VACCINE VIRUS TO
; FILE REFERENCE: 3673-21
; CURRENT APPLICATION NUMBER: US/10/275,707
; CURRENT FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2002-03-08
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Plasmodium yoelii
US-10-275-707-9

Query Match 44.4%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 21

US-10-205-150-3
; Sequence 3, Application US/10205150
; Publication No. US20020197269A1
; GENERAL INFORMATION:

```
; APPLICANT: LINGNAU, KAREN ET AL.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR IMMUNOMODULATION AND PREPARATION
; OF VACCINES COMPRISING AN ANTIGEN AND AN IMMUNOGENIC OLIGODEOXYN
; TITLE OF INVENTION: AND A POLYCATIONIC POLYMER AS ADJUVANTS
; FILE REFERENCE: SONN:018US
; CURRENT APPLICATION NUMBER: US/10/205,150
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: PCT/EP01/00087
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-205-150-3

Query Match      44.4%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYVP 6
Db      1 SYVP 4

RESULT 22
US-09-950-313-40
; Sequence 40, Application US/09950313
; Patent No. US20020102610A1
; GENERAL INFORMATION:
; APPLICANT: TOWNSEND, ROBERT
; APPLICANT: ROBINSON, ANDREW
; TITLE OF INVENTION: AUTOMATED IDENTIFICATION OF PEPTIDES
; FILE REFERENCE: 9195-064
; CURRENT APPLICATION NUMBER: US/09/950,313
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: UK 0022,136.6
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,273
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-313-40

Query Match      44.4%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYVP 6
Db      6 SYVP 9

RESULT 23
US-10-360-836-81
; Sequence 81, Application US/10360836
; Publication No. US200301858541
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALIGNANCIES
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
```

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; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmidial CS T cell epitope sequence inserted
; OTHER INFORMATION: into V7 constructs
US-10-360-836-81

Query Match      44.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYVP 6
Db      2 SYVP 5

RESULT 24
US-10-062-710-208
; Sequence 208, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis B
US-10-062-710-208

Query Match      44.4%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYVP 6
Db      6 SYVP 9

RESULT 25
US-10-239-313A-268
; Sequence 268, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Lilliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
```

; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 268
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Plasmodium yoelii
US-10-239-313A-268

Query Match 44.4%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
|||
Db 3 SYVP 6

RESULT 26

US-10-239-313A-256
; Sequence 256, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 256
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-256

Query Match 44.4%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESY 4
|||
Db 7 VESY 10

RESULT 27

US-09-764-868-1240
; Sequence 1240, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1240
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-1240

Query Match 44.4%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
|||
Db 1 SYVP 4

RESULT 28

US-09-955-999-120
; Sequence 120, Application US/09955999
; Publication No. US20030036505A1
; GENERAL INFORMATION:
; APPLICANT: Barash et al.
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypept
; TITLE OF INVENTION: Antibodies, and Methods Based Thereon
; FILE REFERENCE: PT086Pl
; CURRENT APPLICATION NUMBER: US/09/955,999
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-999-120

Query Match 44.4%; Score 4; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
|||
Db 1 SYVP 4

RESULT 29

US-09-880-748-2349
; Sequence 2349, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2349
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2349

Query Match 44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9

```
Db          11 PLFP 14
|||||
RESULT 30
US-09-880-748-2388
; Sequence 2388, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2388
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2388

Query Match          44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 PLFP 9
|||||
Db          11 PLFP 14

Query Match          44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 PLFP 9
|||||
Db          11 PLFP 14

RESULT 31
US-09-880-748-2423
; Sequence 2423, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2423
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2423

Query Match          44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 PLFP 9
|||||
Db          11 PLFP 14

RESULT 32
US-09-880-748-2447
; Sequence 2447, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2447
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2447

Query Match          44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 PLFP 9
|||||
Db          11 PLFP 14

RESULT 33
US-09-880-748-2467
; Sequence 2467, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2467
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2467

Query Match          44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
   |||
Db 11 PLFP 14

RESULT 34
US-09-880-748-2533
; Sequence 2533, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2533
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2533

Query Match 44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
   |||
Db 11 PLFP 14

RESULT 35
US-09-880-748-2640
; Sequence 2640, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2640
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2640

Query Match 44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
   |||
Db 11 PLFP 14

RESULT 36
US-09-880-748-2657
; Sequence 2657, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2657
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2657

Query Match 44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
   |||
Db 11 PLFP 14

RESULT 37
US-09-880-748-2689
; Sequence 2689, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2689
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2689

Query Match 44.4%; Score 4; DB 11; Length 14;
```

```
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9
Db 11 PLFP 14

RESULT 38
US-10-239-313A-258
; Sequence 258, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIRA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-258

Query Match 44.4%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESY 4
Db 7 VESY 10

RESULT 39
US-09-880-748-2267
; Sequence 2267, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2267
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2267

Query Match 44.4%; Score 4; DB 11; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6
Db 8 SYVP 11

RESULT 40
US-09-880-748-2269
; Sequence 2269, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2269
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2269

Query Match 44.4%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6
Db 8 SYVP 11

RESULT 41
US-09-880-748-2270
; Sequence 2270, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2270
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2270
```

Query Match 44.4%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
| | | |
Db 8 SYVP 11

RESULT 42

US-09-880-748-2286
; Sequence 2286, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2286
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2286

Query Match 44.4%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
| | | |
Db 8 SYVP 11

RESULT 43

US-09-880-748-2292
; Sequence 2292, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2292
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2292

Query Match 44.4%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
| | | |
Db 8 SYVP 11

RESULT 44

US-10-161-791-379
; Sequence 379, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWKES, Dana E.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-379

Query Match 44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
| | | |
Db 8 PLFP 11

RESULT 45

US-10-275-707-16
; Sequence 16, Application US/10275707
; Publication No. US20030194801A1

```
; GENERAL INFORMATION:
; APPLICANT: BONALDO, MIRNA C.
; APPLICANT: GALLER, RICARDO
; APPLICANT: FREIRE, MARCOS DA SILVA
; APPLICANT: GARRAT, RICHARD C.
; TITLE OF INVENTION: USE OF FLAVIVIRUS FOR THE EXPRESSION OF PROTEIN EPIPTOPES
; TITLE OF INVENTION: AND DEVELOPMENT OF NEW LIVE ATTENUATED VACCINE VIRUS TO
; TITLE OF INVENTION: IMMUNIZE AGAINST FLAVIVIRUS AND OTHER INFECTIOUS AGENTS
; FILE REFERENCE: 3673-21
; CURRENT APPLICATION NUMBER: US/10/275,707
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/BR02/00036
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: GB 0105877.5
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Plasmodium yoelii
US-10-275-707-16

Query Match      44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYVP 6
      ||||
Db      4 SYVP 7

RESULT 46
US-09-947-258-1
; Sequence 1, Application US/09947258
; Patent No. US20020102248A1
; GENERAL INFORMATION:
; APPLICANT: Chung, J.H.
; TITLE OF INVENTION: Modulating Response to Genotoxic Stress
; FILE REFERENCE: 4239-61084
; CURRENT APPLICATION NUMBER: US/09/947,258
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-947-258-1

Query Match      44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLFP 9
      ||||
Db      5 PLFP 8

RESULT 47
US-09-947-258-4
; Sequence 4, Application US/09947258
; Patent No. US20020102248A1
; GENERAL INFORMATION:
; APPLICANT: Chung, J.H.
; TITLE OF INVENTION: Modulating Response to Genotoxic Stress
; FILE REFERENCE: 4239-61084
; CURRENT APPLICATION NUMBER: US/09/947,258
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 16
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-947-258-4

Query Match      44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLFP 9
      ||||
Db      5 PLFP 8

RESULT 48
US-09-880-748-2261
; Sequence 2261, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2261
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2261

Query Match      44.4%; Score 4; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYVP 6
      ||||
Db      8 SYVP 11

RESULT 49
US-09-880-748-2266
; Sequence 2266, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2266
```



```
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2266

Query Match      44.4%; Score 4; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6
    ||||
Db 8 SYVP 11

RESULT 50
US-10-239-313A-259
; Sequence 259, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 259
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-259

Query Match      44.4%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESY 4
    ||||
Db 7 VESY 10

RESULT 51
US-09-789-561-189
; Sequence 189, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043P1
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 189
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-561-189

Query Match      44.4%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9
    ||||
Db 6 PLFP 9

RESULT 52
US-10-038-612-76
; Sequence 76, Application US/10038612
; Publication No. US20020160478A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; TITLE OF INVENTION: Modulate the Activity of Protein Kinases
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 18
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: Tyk2
US-10-038-612-76

Query Match      44.4%; Score 4; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7
    ||||
Db 3 YVPL 6

RESULT 53
US-09-823-936-18
; Sequence 18, Application US/09823936
; Patent No. US20020061309A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, Stephen J.
; APPLICANT: GROSS, Cynthia
; APPLICANT: LINDBO, John A.
; APPLICANT: FOGUE, Gregory P.
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS
; TITLE OF INVENTION: N-TERMINAL VIRAL COAT PROTEIN FUSIONS
; FILE REFERENCE: 008010087CPUS05
; CURRENT APPLICATION NUMBER: US/09/823,936
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 09/ 520,967
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Tobacco mosaic virus
US-09-823-936-18

Query Match      44.4%; Score 4; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6
    ||||
Db 1 SYVP 4
```

RESULT 54
US-09-755-836-23
; Sequence 23, Application US/09755836
; Patent No. US20020107387A1
; GENERAL INFORMATION:
; APPLICANT: Turpen, Thomas H.
; Reinl, Stephen
; Grill, Laurence K.
; TITLE OF INVENTION: Production of Peptides in Plants as
; Viral Coat Protein Fusions
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/755,836
; FILING DATE: 05-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,003
; FILING DATE: 14-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8129-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-755-836-23

Query Match 44.4%; Score 4; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 55
US-09-880-748-2793
; Sequence 2793, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2793
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2793

Query Match 44.4%; Score 4; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
Db 6 PLFP 9

RESULT 56
US-10-236-508-28
; Sequence 28, Application US/10236508
; Publication No. US20030167512A1
; GENERAL INFORMATION:
; APPLICANT: Monto H. Kumagai
; APPLICANT: Guy R. della-Cioppa
; APPLICANT: Robert L. Erwin
; APPLICANT: David R. McGee
; TITLE OF INVENTION: METHOD OF DETERMINING THE PRESENCE OF A TRAIT IN A PLANT BY
; TITLE OF INVENTION: TRANSPECTING A NUCLEIC ACID SEQUENCE OF A DONOR PLANT INTO A
; FILE OF INVENTION: DIFFERENT HOST PLANT IN A POSITIVE ORIENTATION
; FILE REFERENCE: 08010137US05
; CURRENT APPLICATION NUMBER: US/10/236,508
; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 19
; TYPE: PRT
; ORGANISM: P. yoelii
US-10-236-508-28

Query Match 44.4%; Score 4; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 57
US-10-072-438-42
; Sequence 42, Application US/10072438
; Publication No. US20030027173A1
; GENERAL INFORMATION:
; APPLICANT: della-Cioppa, Guy
; APPLICANT: Erwin, Robert L.
; APPLICANT: Fitzmaurice, Wayne P.
; APPLICANT: Hanley, Kathleen M.
; APPLICANT: Kumagai, Monto H.
; APPLICANT: Lindbo, John A.
; APPLICANT: McGee, David R.
; APPLICANT: Padgett, Hal S.
; APPLICANT: Pogue, Gregory P.
; TITLE OF INVENTION: METHOD OF DETERMINING THE FUNCTION OF
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND THE PROTEINS THEY ENCODE BY
; TITLE OF INVENTION: TRANSPECTING THE SAME INTO A HOST
; FILE REFERENCE: 08010137US01

; CURRENT APPLICATION NUMBER: US/10/072,438
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US/09/232,170
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 19
; TYPE: PRT
; ORGANISM: VIRAL
US-10-072-438-42

Query Match 44.4%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 58
US-10-137-765-41
; Sequence 41, Application US/10137765
; Publication No. US20030028926A1
; GENERAL INFORMATION:
; APPLICANT: KUMAGAI, Monto H.
; APPLICANT: DELLA-CIOPPA, Guy R.
; APPLICANT: ERWIN, Robert L.
; APPLICANT: MCGEE, David R.
; TITLE OF INVENTION: METHOD OF COMPILING A FUNCTIONAL GENE PROFILE BY
; TITLE OF INVENTION: TRANSFECTING A NUCLEIC
; TITLE OF INVENTION: ACID SEQUENCE OF A NON-PLANT DONOR INTO A HOST PLANT IN A POSITIVE
; TITLE OF INVENTION: ORIENTATION
; FILE REFERENCE: 008010137US07
; CURRENT APPLICATION NUMBER: US/10/137,765
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/359,300A
; PRIOR FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 19
; TYPE: PRT
; ORGANISM: P yoelii
US-10-137-765-41

Query Match 44.4%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 59
US-10-146-337-41
; Sequence 41, Application US/10146337
; Publication No. US20030041355A1
; GENERAL INFORMATION:
; APPLICANT: KUMAGAI, Monto H.
; APPLICANT: DELLA-CIOPPA, Guy R.
; APPLICANT: ERWIN, Robert L.
; APPLICANT: MCGEE, David R.
; TITLE OF INVENTION: METHOD OF COMPILING A FUNCTIONAL GENE PROFILE BY
; TITLE OF INVENTION: TRANSFECTING A NUCLEIC
; TITLE OF INVENTION: ACID SEQUENCE OF A NON-PLANT DONOR INTO A HOST PLANT IN A POSITIVE
; TITLE OF INVENTION: ORIENTATION
; FILE REFERENCE: 008010137US07
; CURRENT APPLICATION NUMBER: US/10/146,337
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/359,300

; PRIOR FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 19
; TYPE: PRT
; ORGANISM: P yoelii
US-10-146-337-41

Query Match 44.4%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 60
US-10-286-140-18
; Sequence 18, Application US/10286140
; Publication No. US20030108557A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, Stephen J.
; APPLICANT: GROSS, Cynthia
; APPLICANT: LINDBO, John A.
; APPLICANT: FOGUE, Gregory P.
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS
; TITLE OF INVENTION: N-TERMINAL VIRAL COAT PROTEIN FUSIONS
; FILE REFERENCE: 008010087CPUS05
; CURRENT APPLICATION NUMBER: US/10/286,140
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/823,936
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 09/ 520,967
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Tobacco mosaic virus
US-10-286-140-18

Query Match 44.4%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 61
US-10-225-567A-1293
; Sequence 1293, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTO
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1293
; LENGTH: 20
; TYPE: PRT

```
; ORGANISM: Homo sapiens
US-08-424-550B-1293

Query Match      44.4%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VPLF 8
DB      9 VPLF 12

RESULT 62
US-08-424-550B-343
; Sequence 343, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-343

Query Match      33.3%; Score 3; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VES 3
DB      1 VES 3

RESULT 63
US-09-834-765-735
; Sequence 735, Application US/09834765

Query Match      33.3%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LFP 9
DB      2 LFP 4

RESULT 65
US-09-742-096-26
; Sequence 26, Application US/09742096
; Patent No. US20020155441A1

; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Paris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 735
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-735

Query Match      33.3%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYV 5
DB      1 SYV 3

RESULT 64
US-09-922-261-399
; Sequence 399, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 399
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-261-399

Query Match      33.3%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LFP 9
DB      2 LFP 4

RESULT 65
US-09-742-096-26
; Sequence 26, Application US/09742096
; Patent No. US20020155441A1
```

```
;
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 20073US01V
; CURRENT APPLICATION NUMBER: US/09/742,096
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 08/973,642
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: PCT/FR96/00894
; PRIOR FILING DATE: 1996-06-12
; PRIOR APPLICATION NUMBER: FR 95/07007
; PRIOR FILING DATE: 1995-06-13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-742-096-26

Query Match      33.3%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VES 3
      |||
Db      2 VES 4

RESULT 66
US-10-293-086-39
; Sequence 39, Application US/10293086
; Publication No. US20030134310A1
; GENERAL INFORMATION:
; APPLICANT: Cujec, Thomas P.
; TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors,
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 50036/048002
; CURRENT APPLICATION NUMBER: US/10/293,086
; CURRENT FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/337,990
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-086-39

Query Match      33.3%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YVP 6
      |||
Db      2 YVP 4

RESULT 67
US-10-331-907-48
; Sequence 48, Application US/10331907
; Publication No. US20030181660A1
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
```

```
;
; Hey, Patricia
; Kawaguchi, Yoshihiko
; Merriman, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/331,907
; FILING DATE: 31-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J. Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4091
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-331-907-48

Query Match      33.3%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 VPL 7
      |||
Db      1 VPL 3

RESULT 68
US-10-086-869-157
; Sequence 157, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

;
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-10-006-869-157

Query Match 33.3%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
|||
DB 1 VES 3

RESULT 69
US-09-185-908-35
; Sequence 35, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
US-09-185-908-35

Query Match 33.3%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYV 5
|||
DB 3 SYV 5

RESULT 70
US-09-185-908-156
; Sequence 156, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-156

Query Match 33.3%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYV 5
|||
DB 3 SYV 5

RESULT 71
US-10-281-479A-25
; Sequence 25, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Koopman, Robert P.
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THI
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.0029U6
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030133932A1e = Synt
US-10-281-479A-25

Query Match 33.3%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYV 5
|||
DB 1 SYV 3

RESULT 72
US-10-275-180A-25
; Sequence 25, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Koopman, Robert P.
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPT
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U5
; CURRENT APPLICATION NUMBER: US/10/275,180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
US-10-275-180A-25

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
; OTHER INFORMATION: Synthetic Construct
US-10-275-180A-25

```

```

Query Match      33.3%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 SYV 5
      |||
Db      1 SYV 3

```

RESULT 73

```

US-10-286-132A-25
; Sequence 25, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Loeuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U7
; CURRENT APPLICATION NUMBER: US/10/286.132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-25

```

```

Query Match      33.3%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 SYV 5
      |||
Db      1 SYV 3

```

RESULT 74

```

US-10-006-869-160
; Sequence 160, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 5
; TYPE: PRT

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-10-006-869-160

```

```

Query Match      33.3%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 VES 3
      |||
Db      2 VES 4

```

RESULT 75

```

US-10-006-869-1282
; Sequence 1282, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1282
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-10-006-869-1282

```

```

Query Match      33.3%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 VES 3
      |||
Db      2 VES 4

```

Search completed: November 25, 2003, 20:37:07
Job time : 14.4419 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 7.27326 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVLP 9

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCITUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	9	4	US-09-641-803-31
2	4	44.4	7	2	US-08-837-593-13
3	4	44.4	8	4	US-09-492-766-10
4	4	44.4	9	1	US-08-146-145-11
5	4	44.4	9	3	US-08-481-985B-137
6	4	44.4	9	4	US-09-266-764-16
7	4	44.4	10	1	US-08-362-232-3
8	4	44.4	10	1	US-08-814-196-3
9	4	44.4	11	3	US-08-652-877-72
10	4	44.4	11	3	US-08-476-515A-72
11	4	44.4	12	3	US-08-318-794-1
12	4	44.4	12	4	US-08-470-106-1
13	4	44.4	14	1	US-08-103-490A-23
14	4	44.4	14	1	US-08-103-490A-20
15	4	44.4	14	4	US-09-636-791A-35
16	4	44.4	15	3	US-08-602-999A-379
17	4	44.4	15	3	US-08-743-168B-26
18	4	44.4	15	3	US-08-743-168B-27
19	4	44.4	15	4	US-09-117-460-11
20	4	44.4	15	4	US-09-500-124-379
21	4	44.4	15	5	PCT-US96-10435-26
22	4	44.4	15	5	PCT-US96-10435-27
23	4	44.4	16	1	US-08-002-466-2
24	4	44.4	17	1	US-08-002-466-3
25	4	44.4	17	3	US-08-318-794-23
26	4	44.4	17	4	US-08-470-106-23
27	4	44.4	19	2	US-08-324-003A-23

ALIGNMENTS

```
RESULT 1
US-09-641-803-31
; Sequence 31, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-31

Query Match 100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9
Db 1 VESYVPLFP 9

RESULT 2
US-08-837-593-13
; Sequence 13, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; APPLICANT: Zhang Zhuqun
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
```

```
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-837-593-13

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9
Db 2 PLFP 5

RESULT 3
US-09-492-766-10
; Sequence 10, Application US/09492766
; Patent No. 6506732
; GENERAL INFORMATION:
; APPLICANT: AMTOT, Jean
; TITLE OF INVENTION: ENZYMTIC HYDROLYSATE OF MILK PROTEINS
; FILE REFERENCE: 6013-57"US"
; CURRENT APPLICATION NUMBER: US/09/492,766
; CURRENT FILING DATE: 2000-01-27
; EARLIER APPLICATION NUMBER: 60/117,661
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk
; OTHER INFORMATION: proteins
US-09-492-766-10

Query Match 44.4%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7
Db 1 YVPL 4

RESULT 4
US-08-146-145-11
; Sequence 11, Application US/08146145
; Patent No. 5747269
; GENERAL INFORMATION:
; APPLICANT: Rammensee, Hans-Georg
; APPLICANT: Falk, Kirsten
; APPLICANT: R tzsckke, Olaf
; APPLICANT: Stevanovic, Stefan
; APPLICANT: Jung, G nther
; TITLE OF INVENTION: DETERMINATION OF PEPTIDE MOTIFS ON MHC
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,145
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-146-145-11

Query Match 44.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 5
US-08-481-985B-137
; Sequence 137, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-137

Query Match 44.4%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 6
US-09-266-764-16
; Sequence 16, Application US/09266764
; Patent No. 6545139
; GENERAL INFORMATION:
; APPLICANT: Baylor College of Medicine
; TITLE OF INVENTION: Compositions and Methods For the Treatment and
; TITLE OF INVENTION: Prevention of Metastatic Disorders
; FILE REFERENCE: 00A146.0122
; CURRENT APPLICATION NUMBER: US/09/266,764
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/077,934
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-266-764-16

Query Match 44.4%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
Db 6 PLFP 9

RESULT 7
US-08-362-232-3
; Sequence 3, Application US/08362232
; Patent No. 5641667
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Fructosyltransferase Enzyme, Method
; TITLE OF INVENTION: For its Production and DNA Encoding the Enzyme.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11758
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.0 for DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,232
; FILING DATE: 22-December-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CU 125/93
; FILING DATE: 23-December-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 294-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-362-232-3

Query Match 44.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLPP 9
Db 3 PLPP 6

RESULT 8

US-08-814-196-3
; Sequence 3, Application US/08814196
; Patent No. 5731173
; GENERAL INFORMATION:

; APPLICANT:
; TITLE OF INVENTION: Fructosyltransferase Enzyme, Method
; TITLE OF INVENTION: For its Production and DNA Encoding the Enzyme.

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hoffmann & Baron

; STREET: 350 Jericho Turnpike

; CITY: Jericho

; STATE: New York

; COUNTRY: United States of America

; ZIP: 11758

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect 6.0 for DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/814,196

; FILING DATE: 10-MAR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/362,232

; FILING DATE: 22-December-1994

; APPLICATION NUMBER: CU 125/93

; FILING DATE: 23-December-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Baron, Ronald J.

; REGISTRATION NUMBER: 29,281

; REFERENCE/DOCKET NUMBER: 294-29

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 822-3550

; TELEFAX: (516) 822-3582

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-814-196-3

Query Match 44.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLPP 9
Db 3 PLPP 6

RESULT 9

US-08-652-877-72

; Sequence 72, Application US/08652877

; Patent No. 6187548

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjaln, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rofer Inc.

; STREET: 500 Arcola Rd., 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.5.1

; SOFTWARE: Word 6.0 (patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,877

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/15203

; FILING DATE: 22-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/487,314

; FILING DATE: 07-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: A1355E-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-454-3816

; TELEFAX: 610-454-3808

; INFORMATION FOR SEQ ID NO: 72:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: internal
US-08-652-877-72

Query Match 44.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESY 4
Db 3 VESY 6

RESULT 10

US-08-476-515A-72
; Sequence 72, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-476-515A-72

Query Match 44.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VESY 4
Db 3 VESY 6

RESULT 11

US-08-318-794-1
; Sequence 1, Application US/08318794
; Patent No. 6022726
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: GENETICALLY ENGINEERED ATTENUATED
; TITLE OF INVENTION: VIRUSES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,794
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-318-794-1

Query Match 44.4%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6
Db 4 SYVP 7

RESULT 12

US-08-470-106-1
; Sequence 1, Application US/08470106
; Patent No. 6316243
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: GENETICALLY ENGINEERED ATTENUATED
; VIRUSES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/470,106
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-470-106-1

Query Match 44.4%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
DB 4 SYVP 7

RESULT 13
US-08-103-490A-23
; Sequence 23, Application US/08103490A
; Patent No. 5422341
; GENERAL INFORMATION:
; APPLICANT: Macielag, Mark J.
; TITLE OF INVENTION: Motilin-Like Polypeptides With
; TITLE OF INVENTION: Gastrointestinal Motor Stimulating Activity
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The BOC Group, Inc.
; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/103,490A
; FILING DATE: 06-AUG-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R. Hain
; REGISTRATION NUMBER: 24,864
; REFERENCE/DOCKET NUMBER: 92H817
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-771-6292
; TELEFAX: 908-771-6159
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-08-103-490A-23

Query Match 44.4%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8
DB 2 VPLF 5

RESULT 14
US-08-103-490A-40
; Sequence 40, Application US/08103490A
; Patent No. 5422341
; GENERAL INFORMATION:
; APPLICANT: Macielag, Mark J.
; TITLE OF INVENTION: Motilin-Like Polypeptides With
; TITLE OF INVENTION: Gastrointestinal Motor Stimulating Activity
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The BOC Group, Inc.
; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/103,490A
; FILING DATE: 06-AUG-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R. Hain
; REGISTRATION NUMBER: 24,864
; REFERENCE/DOCKET NUMBER: 92H817
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-771-6292
; TELEFAX: 908-771-6159
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-103-490A-40

Query Match 44.4%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8
DB 2 VPLF 5

RESULT 15
US-09-636-791A-35
; Sequence 35, Application US/09636791A
; Patent No. 6503703
; GENERAL INFORMATION:
; APPLICANT: Palese et al
; TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS THAT
; TITLE OF INVENTION: INHIBIT INTERACTION OF HOST CELL PROTEINS AND VIRAL
; TITLE OF INVENTION: PROTEINS REQUIRED FOR VIRAL REPLICATION
; FILE REFERENCE: 6923-077-999
; CURRENT APPLICATION NUMBER: US/09/636,791A

; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,263
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Rabies virus
US-09-636-791A-35

Query Match 44.4%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
|||||
DB 9 YVPL 12

RESULT 16
US-08-602-999A-379
; Sequence 379, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PSNNJE
; INFORMATION FOR SEQ ID NO: 379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-379

Query Match 44.4%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
|||||

DB 8 PLFP 11

RESULT 17
US-08-743-168B-26
; Sequence 26, Application US/08743168B
; Patent No. 6271015
; GENERAL INFORMATION:
; APPLICANT: Gilula, No. 6271015ton B
; APPLICANT: Cravatt, Benjamin F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10550 No. 6271015th Torrey Pines Road
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,168B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/489,535
; FILING DATE: 12-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 485.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-743-168B-26

Query Match 44.4%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
|||||
DB 12 PLFP 15

RESULT 18
US-08-743-168B-27
; Sequence 27, Application US/08743168B
; Patent No. 6271015
; GENERAL INFORMATION:
; APPLICANT: Gilula, No. 6271015ton B
; APPLICANT: Cravatt, Benjamin F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10550 No. 6271015th Torrey Pines Road
; CITY: La Jolla
; STATE: California
; COUNTRY: US

```
;
;
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,168B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/489,535
; FILING DATE: 12-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 485.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-743-168B-27

Query Match 44.4%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 PLFP 9
DB 2 PLFP 5

RESULT 19
US-09-117-860-11
; Sequence 11, Application US/09117860A
; Patent No. 6338955
; GENERAL INFORMATION:
; APPLICANT: OGURI, Suguru
; APPLICANT: MINOWA, Mari
; APPLICANT: YOSHIDA, Aruto
; APPLICANT: TANIGUCHI, Naoyuki
; APPLICANT: TAKEUCHI, Nakoto
; TITLE OF INVENTION: NOVEL 1-4 N-ACETYLGLUCOSAMINYLTRANSFERASE AND GENE
; FILE REFERENCE: 081356/0119
; CURRENT APPLICATION NUMBER: US/09/117,860A
; CURRENT FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: WO PCT/JP97/04546
; EARLIER FILING DATE: 1997-12-10
; EARLIER APPLICATION NUMBER: JP 161462/1997
; EARLIER FILING DATE: 1997-06-18
; EARLIER APPLICATION NUMBER: JP 332411/1996
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bovine
; US-09-117-860-11

Query Match 44.4%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 VESY 4
|||
```

```
DB 6 VESY 9

RESULT 20
US-09-500-124-379
; Sequence 379, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-379

Query Match 44.4%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 PLFP 9
DB 8 PLFP 11

RESULT 21
PCT-US96-10435-26
; Sequence 26, Application PC/TUS9610435
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: CIS-9, 10-OCTADECENAMIDASE
; NUMBER OF SEQUENCES: 32
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10435
; FILING DATE: 12-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/489,535
; FILING DATE: 12-JUN-1995
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
PCT-US96-10435-26

Query Match 44.4%; Score 4; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9
Db 12 PLFP 15

RESULT 22
PCT-US96-10435-27
; Sequence 27, Application PC/TUS9610435
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: CIS-9, 10-OCTADECENOAMIDASE
; NUMBER OF SEQUENCES: 32
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10435
; FILING DATE: 12-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/489,535
; FILING DATE: 12-JUN-1995
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
PCT-US96-10435-27

Query Match 44.4%; Score 4; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9
Db 2 PLFP 5

RESULT 23
US-08-002-466-2
; Sequence 2, Application US/08002466
; Patent No. 5580561
; GENERAL INFORMATION:
; APPLICANT: Cercek, Boris
; TITLE OF INVENTION: Inhibition of Suppression of Immune
; Defense Caused by Peptides Active in the Structuredness of
; the Cytoplasmic Matrix (SCM) Assay

; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,466
; FILING DATE: 19930108
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/539,686
; FILING DATE: 18-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/167/007
; FILING DATE: 03-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/022,759
; FILING DATE: 06-MAR-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Farber, Michael B
; REGISTRATION NUMBER: 32,612
; REFERENCE/DOCKET NUMBER: 8941
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (818) 796-4000
; TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-002-466-2

Query Match 44.4%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPLF 8
Db 10 VPLF 13

RESULT 24
US-08-002-466-3
; Sequence 3, Application US/08002466
; Patent No. 5580561
; GENERAL INFORMATION:
; APPLICANT: Cercek, Boris
; TITLE OF INVENTION: Inhibition of Suppression of Immune
; Defense Caused by Peptides Active in the Structuredness of
; the Cytoplasmic Matrix (SCM) Assay
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91001
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19930108
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,686
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: US 07/167/007
FILING DATE: 03-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/022,759
FILING DATE: 06-MAR-1987
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 8941
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-002-466-3

Query Match 44.4%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8
DB 10 VPLF 13

RESULT 25
US-08-318-794-23
Sequence 23, Application US/08318794
Patent No. 6022726
GENERAL INFORMATION:
APPLICANT: Palese, Peter
TITLE OF INVENTION: GENETICALLY ENGINEERED ATTENUATED
TITLE OF INVENTION: VIRUSES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,794
FILING DATE: 20-DEC-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7682-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-318-794-23

Query Match 44.4%; Score 4; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
DB 5 SYVP 8

RESULT 26
US-08-470-106-23
Sequence 23, Application US/08470106
Patent No. 6316243
GENERAL INFORMATION:
APPLICANT: Palese, Peter
TITLE OF INVENTION: GENETICALLY ENGINEERED ATTENUATED
VIRUSES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,106
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-470-106-23

Query Match 44.4%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
DB 5 SYVP 8

RESULT 27

US-08-324-003A-23
; Sequence 23, Application US/08324003A
; Patent No. 5977438
; GENERAL INFORMATION:
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Reini, Stephen
; APPLICANT: Grill, Laurence K.
; TITLE OF INVENTION: Production of Peptides in Plants as
; TITLE OF INVENTION: Viral Coat Protein Fusions
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,003A
; FILING DATE: 14-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8129-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-324-003A-23

Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
DB 1 SYVP 4

RESULT 28

US-09-174-060-20
; Sequence 20, Application US/09174060
; Patent No. 5989554
; GENERAL INFORMATION:
; APPLICANT: Knuth, Mark W
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Shultz, John W
; APPLICANT: Lesley, Scott A
; APPLICANT: Villars, Catherine E
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
; TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
; TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: 1 South Pinckney St.
; CITY: Madison
; STATE: WI
; COUNTRY: USA

; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/174,060
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/338,382
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-174-060-20

Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
DB 6 YVPL 9

RESULT 29

US-08-338-382-20
; Sequence 20, Application US/08338382
; Patent No. 6069230
; GENERAL INFORMATION:
; APPLICANT: Knuth, Mark W
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Shultz, John W
; APPLICANT: Lesley, Scott A
; APPLICANT: Villars, Catherine E
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
; TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
; TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: 1 South Pinckney St.
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,382
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.024
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-257-5353
TELEFAX: 608-257-9175
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-338-382-20

Query Match 44.4%; Score 4; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 4 YVPL 7
Db 6 YVPL 9

RESULT 30
US-07-798-776-10
; Sequence 10, Application US/07798776
; Patent No. 5434074
; GENERAL INFORMATION:
; APPLICANT: GIBSON, D. WADE
; APPLICANT: WELCH, ANTHONY R.
; TITLE OF INVENTION: HERPES VIRUS PROTEINASE AND METHOD OF
; TITLE OF INVENTION: ASSAYING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W., Eleventh Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/798,776
FILING DATE: 19911127
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: FOULKE, CYNTHIA L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: 1107.07080
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 508-9100
TELEFAX: (202) 508-9299
TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Simian cytomegalovirus
STRAIN: Colburn

US-07-798-776-10
Query Match 44.4%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 4 YVPL 7
Db 6 YVPL 9

Qy 2 ESYV 5
Db 5 ESYV 8

RESULT 31
US-07-798-776-11
; Sequence 11, Application US/07798776
; Patent No. 5434074
; GENERAL INFORMATION:
; APPLICANT: GIBSON, D. WADE
; APPLICANT: WELCH, ANTHONY R.
; TITLE OF INVENTION: HERPES VIRUS PROTEINASE AND METHOD OF
; TITLE OF INVENTION: ASSAYING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W., Eleventh Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/798,776
FILING DATE: 19911127
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: FOULKE, CYNTHIA L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: 1107.07080
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 508-9100
TELEFAX: (202) 508-9299
TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human cytomegalovirus

US-07-798-776-11
Query Match 44.4%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 ESYV 5
Db 5 ESYV 8

RESULT 32
US-08-251-288A-10
; Sequence 10, Application US/08251288A
; Patent No. 6001967
; GENERAL INFORMATION:
; APPLICANT: Gibson, Wade
; APPLICANT: Welch, Anthony
; TITLE OF INVENTION: HERPES PROTEINASE AND METHOD
; TITLE OF INVENTION: OF ASSAYING
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:

Qy 2 ESYV 5
Db 5 ESYV 8

US-07-798-776-11
Query Match 44.4%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 ESYV 5
Db 5 ESYV 8

ADDRESSSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/251,288A
FILING DATE: 31-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.46284
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6001967e
US-08-251-288A-10
Query Match 44.4%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 2 ESYV 5
Db 5 ESYV 8
|||||
RESULT 33
US-08-251-288A-11
Sequence 11, Application US/08251288A
Patent No. 6001967
GENERAL INFORMATION:
APPLICANT: Gibson, Wade
TITLE OF INVENTION: HERPES PROTEINASE AND METHOD
OF ASSAYING
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/251,288A
FILING DATE: 31-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.46284
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6001967e
US-08-251-288A-11
Query Match 44.4%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 2 ESYV 5
Db 5 ESYV 8
|||||
RESULT 34
US-09-298-819A-10
Sequence 10, Application US/09298819A
Patent No. 6077679
GENERAL INFORMATION:
APPLICANT: Gibson, Wade
APPLICANT: Welch, Anthony
TITLE OF INVENTION: HERPES PROTEINASE AND METHOD
OF ASSAYING
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,819A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/251,288
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.46284
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6077679e
US-09-298-819A-10
Query Match 44.4%; Score 4; DB 3; Length 20;

```
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 2 ESYV 5
Db 5 ESYV 8

RESULT 35
US-09-298-819A-11
; Sequence 11, Application US/09298819A
; Patent No. 6077679
; GENERAL INFORMATION:
; APPLICANT: Gibson, Wade
; APPLICANT: Welch, Anthony
; TITLE OF INVENTION: HERPES PROTEINASE AND METHOD
; TITLE OF INVENTION: OF ASSAYING
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,819A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/251,288
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.46284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6077679e
; US-09-298-819A-11

Query Match 44.4%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5
Db 5 ESYV 8

RESULT 36
US-09-586-563C-10
; Sequence 10, Application US/09586563C
; Patent No. 6406902
; GENERAL INFORMATION:
; APPLICANT: Gibson, Wade
; APPLICANT: Welch, Anthony
; TITLE OF INVENTION: Herpes Proteinase and Method of Assaying
; FILE REFERENCE: Gibson Herpes Proteinase Matter 00003
; CURRENT APPLICATION NUMBER: US/09/586,563C

Query Match 44.4%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5
Db 5 ESYV 8

RESULT 37
US-09-586-563C-11
; Sequence 11, Application US/09586563C
; Patent No. 6406902
; GENERAL INFORMATION:
; APPLICANT: Gibson, Wade
; APPLICANT: Welch, Anthony
; TITLE OF INVENTION: Herpes Proteinase and Method of Assaying
; FILE REFERENCE: Gibson Herpes Proteinase Matter 00003
; CURRENT APPLICATION NUMBER: US/09/586,563C
; CURRENT FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/298,819
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian cytomegalovirus
; US-09-586-563C-11

Query Match 44.4%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5
Db 5 ESYV 8

RESULT 38
US-09-586-562C-10
; Sequence 10, Application US/09586562C
; Patent No. 6410296
; GENERAL INFORMATION:
; APPLICANT: Gibson, Wade
; APPLICANT: Welch, Anthony
; TITLE OF INVENTION: Herpes Proteinase and Method of Assaying
; FILE REFERENCE: Gibson Herpes Proteinase Matter 00003
; CURRENT APPLICATION NUMBER: US/09/586,562C
; CURRENT FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/298,819
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian cytomegalovirus
; US-09-586-562C-10

Query Match 44.4%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5
 ||||
Db 5 ESYV 8

RESULT 39
US-09-586-562C-11
; Sequence 11, Application US/09586562C
; Patent No. 6410296
; GENERAL INFORMATION:
; APPLICANT: Gibson, Wade
; APPLICANT: Welch, Anthony
; TITLE OF INVENTION: Herpes Proteinase and Method of Assaying
; FILE REFERENCE: Gibson Herpes Proteinase Matter 00003
; CURRENT APPLICATION NUMBER: US/09/586,562C
; CURRENT FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/298,819
; PRIOR FILING DATE: 1998-04-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian cytomegalovirus
US-09-586-562C-11

Query Match 44.4%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 ESYV 5
 ||||
Db 5 ESYV 8

RESULT 40
US-08-459-568-33
; Sequence 33, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-568-33

Query Match 33.3%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6
 |||
Db 1 YVP 3

RESULT 41
US-08-399-411-33
; Sequence 33, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,411
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-399-411-33

Query Match 33.3%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6
 |||
Db 1 YVP 3

RESULT 42
US-08-803-899-22
; Sequence 22, Application US/08803899
; Patent No. 5912224
; GENERAL INFORMATION:
; APPLICANT: DONAHOE, PATRICIA K.
; APPLICANT: WANG, TONGWEN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
; TITLE OF INVENTION: CELLULAR RESPONSE TO TGF-BETA LIGANDS
; NUMBER OF SEQUENCES: 26

;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
;/ STREET: 1100 NEW YORK AVENUE, SUITE 600
;/ CITY: WASHINGTON
;/ STATE: DC
;/ COUNTRY: USA
;/ ZIP: 20005
;/ COMPUTER READABLE FORM: disk
;/ MEDIUM TYPE: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/803,899
;/ FILING DATE: 02/21/1997
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 60/012,054
;/ FILING DATE: 02/22/1996
;/ CLASSIFICATION: 514
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: STEFFE, ERIC K.
;/ REGISTRATION NUMBER: 36,688
;/ REFERENCE/DOCKET NUMBER: 0609.4240001
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (202)371-2600
;/ TELEFAX: (202)371-2540
;/ INFORMATION FOR SEQ ID NO: 22:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 4 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS:
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-803-899-22

Query Match 33.3%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
|||
Db 2 PLF 4

RESULT 43
US-08-789-347A-16
;/ Sequence 16, Application US/08789347A
;/ Patent No. 5922837
;/ GENERAL INFORMATION:
;/ APPLICANT: MEINKE, PETER T.
;/ APPLICANT: RATTRAY, SANDRA J.
;/ APPLICANT: SCHMATZ, DENNIS M.
;/ TITLE OF INVENTION: ANTIPROTOZOAL CYCLIC TETR
;/ TITLE OF INVENTION: APEPTIDES
;/ NUMBER OF SEQUENCES: 29
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Merck & Co., Inc.
;/ STREET: P.O. Box 2000, 126 E. Lincoln Ave.
;/ CITY: Rahway
;/ STATE: NJ
;/ COUNTRY: USA
;/ ZIP: 07065-0900
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette
;/ COMPUTER: IBM Compatible
;/ OPERATING SYSTEM: Windows
;/ SOFTWARE: FastSeq for Windows Version 2.0b
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/789,347A
;/ FILING DATE: 27-JAN-1997
;/ CLASSIFICATION: 530
;/ PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: 60/010,931
;/ FILING DATE: 31-JAN-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Yang, Mollie M
;/ REGISTRATION NUMBER: 32,718
;/ REFERENCE/DOCKET NUMBER: 19628
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 908-594-6343
;/ TELEFAX: 908-594-4720
;/ TELEX:
;/ INFORMATION FOR SEQ ID NO: 16:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 4 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: circular
;/ MOLECULE TYPE: peptide
;/ US-08-789-347A-16

Query Match 33.3%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
|||
Db 1 PLF 3

RESULT 44
US-08-789-347A-17
;/ Sequence 17, Application US/08789347A
;/ Patent No. 5922837
;/ GENERAL INFORMATION:
;/ APPLICANT: MEINKE, PETER T.
;/ APPLICANT: RATTRAY, SANDRA J.
;/ APPLICANT: SCHMATZ, DENNIS M.
;/ TITLE OF INVENTION: ANTIPROTOZOAL CYCLIC TETR
;/ TITLE OF INVENTION: APEPTIDES
;/ NUMBER OF SEQUENCES: 29
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Merck & Co., Inc.
;/ STREET: P.O. Box 2000, 126 E. Lincoln Ave.
;/ CITY: Rahway
;/ STATE: NJ
;/ COUNTRY: USA
;/ ZIP: 07065-0900
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette
;/ COMPUTER: IBM Compatible
;/ OPERATING SYSTEM: Windows
;/ SOFTWARE: FastSeq for Windows Version 2.0b
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/789,347A
;/ FILING DATE: 27-JAN-1997
;/ CLASSIFICATION: 530
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 60/010,931
;/ FILING DATE: 31-JAN-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Yang, Mollie M
;/ REGISTRATION NUMBER: 32,718
;/ REFERENCE/DOCKET NUMBER: 19628
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 908-594-6343
;/ TELEFAX: 908-594-4720
;/ TELEX:
;/ INFORMATION FOR SEQ ID NO: 17:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 4 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: circular
;/ MOLECULE TYPE: peptide

US-08-789-347A-17

Query Match 33.3%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8
|||
Db 1 PLF 3
|||

RESULT 45

US-08-516-859A-33
; Sequence 33, Application US/08516859A
; Patent No. 6069231
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/516,859A
; FILING DATE: 18-AUG-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-516-859A-33

Query Match 33.3%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6
|||
Db 1 YVP 3
|||

RESULT 46

US-08-973-462-26
; Sequence 26, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSTES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES

; FILE REFERENCE: 0660-0125-0 PCT
; CURRENT APPLICATION NUMBER: US/08/973,462B
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: PCT/FR96/00894
; EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: FR 95/07007
; EARLIER FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-08-973-462-26

Query Match 33.3%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3
|||
Db 2 VES 4
|||

RESULT 47

US-09-461-697-399
; Sequence 399, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 399
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-399

Query Match 33.3%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9
|||
Db 2 LFP 4
|||

RESULT 48

US-09-586-472-33
; Sequence 33, Application US/09586472
; Patent No. 6323335
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-586-472-33

Query Match 33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6
Db 1 YVP 3

RESULT 49
US-09-187-859-157
Sequence 157, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 157
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative linear modulating agent based on
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-187-859-157

Query Match 33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3
Db 1 VES 3

RESULT 50
US-08-469-260A-343
Sequence 343, Application US/08469260A
Patent No. 6451578
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJUK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-260A-343

Query Match 33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3
Db 1 VES 3

RESULT 51
US-09-528-706-33
Sequence 33, Application US/09528706
Patent No. 6468985
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting

```

; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; CLASSIFICATION:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-528-706-33

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```

Query Match 33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

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```

Qy 4 YVP 6
Db 1 YVP 3

```

```

RESULT 52
US-09-060-299-48
; Sequence 48, Application US/09060299
; Patent No. 6545137
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. 6545137el Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,299
; FILING DATE: 15-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B. J. Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-35
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4091
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-060-299-48

```

```

Query Match 33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

```

```

Qy 5 VPL 7
Db 1 VPL 3

```

```

RESULT 53
US-09-402-923A-48
; Sequence 48, Application US/09402923A
; Patent No. 655654
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. 655654el LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 655654th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740

```

```

; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-402-923A-48
;
Query Match          33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VPL 7
Db      1 VPL 3

RESULT 54
US-08-488-446-343
; Sequence 343, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-446-343
;
Query Match          33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VES 3
Db      1 VES 3

RESULT 55
US-09-839-542B-157
; Sequence 157, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-839-542B-157
;
Query Match          33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VES 3
Db      1 VES 3

RESULT 56
US-08-467-344A-343
; Sequence 343, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467.344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE DESCRIPTION: SEQ ID NO: 343:
US-08-467-344A-343

Query Match 33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 VES 3
|||
Db 1 VES 3

RESULT 57
US-08-170-360-14
; Sequence 14, Application US/08170360
; Patent No. 5656602
; GENERAL INFORMATION:
; APPLICANT: Tseng, Albert P. S.
; APPLICANT: Inglis, Adam
; TITLE OF INVENTION: FLA2 INHIBITORY COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,360
; FILING DATE: 03-MAR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PCT/AU92/00333
; FILING DATE: 06-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 7058
; FILING DATE: 04-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1871-104A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-170-360-14

Query Match 33.3%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 2 ESY 4
|||
Db 2 ESY 4

RESULT 58
US-08-358-160-195
; Sequence 195, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; ; DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528


```
Db          1 VES 3
||||
RESULT 61
US-08-836-561-40
; Sequence 40, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masanichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-561-40

Query Match          33.3%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 SYV 5
Db          1 SYV 3
||||

RESULT 62
US-09-171-554-12
; Sequence 12, Application US/09171554
; Patent No. 6291640
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: PEPTIDOMIMETIC INHIBITORS OF THE HUMAN CYTOMEGALOVIRUS
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: Response of OA

Query Match          33.3%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 SYV 5
Db          1 SYV 3
||||

US-09-171-554-12
; CURRENT APPLICATION NUMBER: US/09/171,554
; CURRENT FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: 60/034,041
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: 60/052,860
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059,806
; PRIOR FILING DATE: 1997-09-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)
; OTHER INFORMATION: N-terminal is capped with acetyl
; NAME/KEY: PEPTIDE
; LOCATION: (5)
; OTHER INFORMATION: C-terminal is modified with activated carbonyl;
; OTHER INFORMATION: C(O)-NH-CH2-phenyl
; OTHER INFORMATION: Description of Artificial Sequence:peptidomimetic
; OTHER INFORMATION: inhibitor
US-09-171-554-12

Query Match          33.3%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 SYV 5
Db          1 SYV 3
||||

RESULT 63
US-09-187-859-160
; Sequence 160, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-187-859-160

Query Match          33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 VES 3
Db          2 VES 4
||||

RESULT 64
US-09-187-859-1282
; Sequence 1282, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
```

APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1282
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-187-859-1282

Query Match 33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
DB 2 VES 4
|||

RESULT 65
US-09-646-154-11
Sequence 11, Application US/09646154
Patent No. 6429024
GENERAL INFORMATION:
APPLICANT: KOKUBO, TOHRU
APPLICANT: ARAI, KENJI
TITLE OF INVENTION: TEST METHOD FOR IGA NEPHROPATHY
FILE REFERENCE: KP-8821
CURRENT APPLICATION NUMBER: US/09/646,154
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/JP99/01525
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 5
TYPE: PRT
ORGANISM: Bovine sp.
US-09-646-154-11

Query Match 33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
DB 3 VES 5
|||

RESULT 66
US-08-766-596A-28
Sequence 28, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-28

Query Match 33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
DB 1 LFP 3
|||

RESULT 67
US-08-766-596A-29
Sequence 29, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-29

Query Match 33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8
Db 1 PLF 3

RESULT 68
US-09-434-122-40
; Sequence 40, Application US/09434122
; Patent No. 6538111
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihiro
; ANAZAWA, Hideharu
; HANAI, No. 6538111uo
; TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/434,122
; FILING DATE: 05-NO. 6538111-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-434-122-40

Query Match 33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5
Db 1 SYV 3

RESULT 69
US-09-839-542B-160
; Sequence 160, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-839-542B-160

Query Match 33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3
Db 2 VES 4

RESULT 70
US-09-839-542B-1282
; Sequence 1282, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1282
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:


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; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-839-542B-1282

Query Match          33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 2 VES 4

RESULT 71
US-08-205-938A-3
; Sequence 3, Application US/08205938A
; Patent No. 5466671
; GENERAL INFORMATION:
; APPLICANT: TEMPST, PAUL
; APPLICANT: CASTEELS, PETER
; TITLE OF INVENTION: APIDAECIN-TYPE PEPTIDE ANTIBIOTICS WITH
; TITLE OF INVENTION: IMPROVED ACTIVITIES AND/OR DIFFERENT
; TITLE OF INVENTION: ANTIBACTERIAL SPECTRUM
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSES: COOPER & DUNHAM LLP
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,938A
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45061
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212) 394-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-205-938A-3

Query Match          33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6
Db 4 YVP 6

RESULT 72
US-08-282-758B-40
; Sequence 40, Application US/08282758B
; Patent No. 5670310
; GENERAL INFORMATION:
; APPLICANT: Fields, Howard A.
; APPLICANT: Khudyakov, Yuri E.
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Differential Diagnosis of Chronic and Acute Hepatitis C
```

```
; TITLE OF INVENTION: Virus Infection
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,758B
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Jamie L.
; REGISTRATION NUMBER: 32,467
; REFERENCE/DOCKET NUMBER: 03063-0100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 818-3700
; TELEFAX: (404) 818-3799
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-282-758B-40

Query Match          33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6
Db 2 YVP 4

RESULT 73
US-08-405-230-2
; Sequence 2, Application US/08405230
; Patent No. 5707846
; GENERAL INFORMATION:
; APPLICANT: TANIGUCHI, Naoyuki
; APPLICANT: NISHIKAWA, Atsushi
; APPLICANT: YAMAGUCHI, No. 5707846omi
; TITLE OF INVENTION: NOVEL N-ACETYLGLUCOSAMINYL TRANSFERASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,230
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: US 08/110,736
; FILING DATE: 23-AUG-1993
; APPLICATION NUMBER: JP 4-245950
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-237118
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 001560-215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-405-230-2

Query Match 33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5
Db 4 SYV 6

RESULT 74
US-08-595-718A-1
; Sequence 1, Application US/08595718A
; Patent No. 5723579
; GENERAL INFORMATION:
; APPLICANT: Buettner, Joseph A.
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Fibrinogen Binding Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,718A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6

APPLICATION NUMBER: US 08/110,736
FILING DATE: 23-AUG-1993
APPLICATION NUMBER: JP 4-245950
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-237118
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 001560-215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-405-230-2

Query Match 33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5
Db 4 SYV 6

RESULT 74
US-08-595-718A-1
; Sequence 1, Application US/08595718A
; Patent No. 5723579
; GENERAL INFORMATION:
; APPLICANT: Buettner, Joseph A.
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Fibrinogen Binding Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,718A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
```

```
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
; US-08-595-718A-1

Query Match 33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 4 VPL 6

RESULT 75
US-08-595-718A-2
; Sequence 2, Application US/08595718A
; Patent No. 5723579
; GENERAL INFORMATION:
; APPLICANT: Buettner, Joseph A.
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Fibrinogen Binding Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,718A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
; US-08-595-718A-2

Query Match 33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 4 VPL 6
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Search completed: November 25, 2003, 20:30:07
Job time : 8.27326 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 8.9186 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLLYQEPVLGVR 13

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR_76:*

1: Pirl1.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	46.2	18	2	S49026
2	5	38.5	14	2	A60737
3	4	30.8	17	2	S50742
4	4	30.8	20	2	B44581
5	3	23.1	3	3	A33802
6	3	23.1	6	2	PT0560
7	3	23.1	7	2	S70335
8	3	23.1	7	2	A33098
9	3	23.1	7	2	PT0246
10	3	23.1	7	2	A39690
11	3	23.1	7	2	S29735
12	3	23.1	8	2	A39308
13	3	23.1	8	4	I54017
14	3	23.1	10	2	B33710
15	3	23.1	10	2	PX0030
16	3	23.1	10	2	PH1345
17	3	23.1	10	2	B45482
18	3	23.1	11	2	C35652
19	3	23.1	11	2	F58501
20	3	23.1	11	2	B41835
21	3	23.1	11	2	A55149
22	3	23.1	11	2	C51497
23	3	23.1	11	2	C37196
24	3	23.1	11	2	I52980
25	3	23.1	11	2	PH1583
26	3	23.1	12	2	S01749
27	3	23.1	12	2	S45629
28	3	23.1	12	2	PN0162
29	3	23.1	12	2	A60528

30	3	23.1	12	2	C20907	Ig kappa-1 chain J
31	3	23.1	12	2	A33520	inhibitory diffusi
32	3	23.1	13	2	A32734	enkephalin precurs
33	3	23.1	13	2	S70723	lipamide dehydrog
34	3	23.1	13	2	PH1316	Ig heavy chain DJ
35	3	23.1	13	2	B47415	mannose-1-phosphat
36	3	23.1	13	2	S03063	Ig lambda chain J
37	3	23.1	13	4	I70075	glycophorin B (mis
38	3	23.1	14	2	S22336	lipoygenase (BC 1
39	3	23.1	14	2	S27140	hypothetical prote
40	3	23.1	14	2	PA0111	protein QA100054 -
41	3	23.1	14	2	S33802	chaperone, TCP1-re
42	3	23.1	14	2	A28018	very late antigen-
43	3	23.1	14	2	B61597	cytochrome P450 AL
44	3	23.1	14	2	C59137	protein Pfl3 - gold
45	3	23.1	15	1	LFTWL	leu leader peptide
46	3	23.1	15	1	PW0004	chlorophyll a/b-bi
47	3	23.1	15	2	C37765	hypothetical prote
48	3	23.1	15	2	PA0079	malate dehydrogena
49	3	23.1	15	2	FA0088	Ig heavy chain DJ
50	3	23.1	15	2	PH1342	acidic fibroblast
51	3	23.1	15	2	S03955	collagen alpha 2(X
52	3	23.1	15	2	E56978	thyrotropin-releas
53	3	23.1	15	2	A45096	protein Pfl1 - gold
54	3	23.1	16	2	B59137	cytochrome P450 IF
55	3	23.1	16	2	E41425	hydrogenase (EC 1.
56	3	23.1	16	2	S03405	gene c-fms protein
57	3	23.1	16	2	I57530	phospholipase A2 (
58	3	23.1	16	2	S65520	hypothetical prote
59	3	23.1	16	2	A39109	protein p12E - Fri
60	3	23.1	16	2	S66613	shikimate 5-dehydr
61	3	23.1	16	2	I40065	photosystem I prot
62	3	23.1	16	2	S09732	chymotrypsin (EC 3
63	3	23.1	16	2	C61414	Ig heavy chain CDR
64	3	23.1	16	2	PT0224	Ig heavy chain DJ
65	3	23.1	16	2	PH1302	T-cell-receptor be
66	3	23.1	16	2	E49855	bleomycin-binding
67	3	23.1	16	2	S68730	pyrogallol hydroxy
68	3	23.1	16	2	S65430	NADH2 dehydrogenas
69	3	23.1	16	2	T14224	chorion class A pr
70	3	23.1	17	2	S05917	chorion class A pr
71	3	23.1	17	2	S05913	chorion class A pr
72	3	23.1	17	2	S05919	chorion class A pr
73	3	23.1	17	2	S05921	41K stone protein
74	3	23.1	17	2	F58502	41K non-reducing-
75	3	23.1	17	2	S41207	hypothetical prote
76	3	23.1	17	2	S71327	major merozoite su
77	3	23.1	17	2	A61557	bombolitin IV - Am
78	3	23.1	17	2	D22595	bombolitin V - Ame
79	3	23.1	17	2	E22595	chymotrypsin (EC 3
80	3	23.1	17	2	B61414	Ig mu heavy chain
81	3	23.1	17	2	A60570	thyroid hormone re
82	3	23.1	17	2	I55612	insulin-like growt
83	3	23.1	17	2	E23734	glutathione transf
84	3	23.1	18	2	E24735	epoxide hydrolase
85	3	23.1	18	2	S74195	proteasome chain 5
86	3	23.1	18	2	S09086	kidney stone prote
87	3	23.1	18	2	D56049	NTL1 protein - cur
88	3	23.1	18	2	S46418	cyclin C - mouse (
89	3	23.1	18	2	S48863	pylin - Vibrio par
90	3	23.1	18	2	A60277	45K protein - pig
91	3	23.1	18	2	S23950	myosin heavy chain
92	3	23.1	18	2	I50389	carboxylesterase (
93	3	23.1	18	2	S09026	Ig heavy chain DJ
94	3	23.1	18	2	PH1350	mammary-derived gr
95	3	23.1	18	2	A42016	serine proteinase
96	3	23.1	18	2	S71592	glutathione transf
97	3	23.1	19	2	S32548	calreticulin - rab
98	3	23.1	19	2	S13046	shikimate 5-dehydr
99	3	23.1	19	2	I40063	thionin, soluble -
100	3	23.1	19	2	B33708	

ALIGNMENTS

```

RESULT 1
S49026
C:Species: Haloarcula marismortui
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C:Accession: S49026; S63967
R:Engemann, S.; Herfurth, E.; Briesemeister, U.; Grelle, G.; Wittmann-Liebold, B.
submitted to the Protein Sequence Database, November 1994
A:Description: Cartography of ribosomal proteins of the 30S subunit from the halophilic
A:Reference number: S49023
A:Accession: S49026
A:Molecule type: protein
A:Residues: 1-18 <ENG>
R:Engemann, S.; Herfurth, E.; Briesemeister, U.; Grelle, G.; Wittmann-Liebold
Eur. J. Biochem. 234, 24-31, 1995
A:Title: Cartography of ribosomal proteins of the 30S subunit from the halophilic Haloar
A:Reference number: S63964; MUID:96096717; PMID:8529646
A:Accession: S63967
A:Molecule type: protein
A:Residues: 1-18 <ENW>
C:Keywords: blocked amino end; protein biosynthesis; ribosome

Query Match      46.2%; Score 6; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VLGPVR 13
      |||||
Db      12 VLGPVR 17

RESULT 2
A60737
pollen allergen Lol p IV - perennial ryegrass (fragments)
C:Species: Lolium perenne (perennial ryegrass)
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 17-Mar-1999
C:Accession: A60737
R:Jaggi, K.S.; Ekramoddoullah, A.K.M.; Kisil, F.T.
Int. Arch. Allergy Appl. Immunol. 89, 342-348, 1989
A:Title: Allergenic fragments of ryegrass (Lolium perenne) pollen allergen Lol p IV.
A:Reference number: A60737; MUID:90007726; PMID:2793222
A:Accession: A60737
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <JAG>
C:Keywords: pollen

Query Match      38.5%; Score 5; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 EPVLG 10
      |||||
Db      3 EPVLG 7

RESULT 3
S50742
proteinase inhibitor (Kunitz-type) 1-related protein - potato (fragment)
N:Alternate names: PKPI minor protein
C:Species: Solanum tuberosum (potato)
C:Date: 14-Jul-1995 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C:Accession: S50742
R:Mitsumori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.
Plant Mol. Biol. 26, 961-969, 1994
A:Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibitor
A:Reference number: S50741; MUID:95093035; PMID:8000008
A:Accession: S50742
A:Molecule type: protein
A:Residues: 1-17 <MIT>

Query Match      30.8%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PVLG 10
      |||||
Db      7 PVLG 10

RESULT 4
B44581
bombinin H Met-8 - yellow-bellied toad
C:Species: Bombina variegata (yellow-bellied toad)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
C:Accession: B44581
R:Mignogna, G.; Simmaco, M.; Kreil, G.; Barra, D.
EMBO J. 12, 4829-4832, 1993
A:Title: Antibacterial and haemolytic peptides containing D-alloisoleucine from the s
A:Reference number: S39612; MUID:94038967; PMID:8223491
A:Accession: B44581
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <MIG>
C:Superfamily: bombinin H precursor
C:Keywords: amidated carboxyl end; D-amino acid
F:2/Modified site: D-allo-isoleucine (Ile) #status experimental
F:20/Modified site: amidated carboxyl end (Ile) #status predicted

Query Match      30.8%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PVLG 10
      |||||
Db      4 PVLG 7

RESULT 5
A33802
thyrotropin-releasing hormone-like peptide - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A33802
R:Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.
J. Biol. Chem. 264, 7788-7791, 1989
A:Title: A novel peptide, pyroglutamylglutamylproline amide, in the rabbit prostate c
A:Reference number: A33802; MUID:89255196; PMID:2498305
A:Accession: A33802
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <COC>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match      23.1%; Score 3; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QEP 7
      |||
Db      1 QEP 3

RESULT 6
PT0560
T-cell receptor beta chain V-D-J region (126-1CE) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0560
R:Feeney, A.J.

```

J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: P70509; MUID:91277601; PMID:1711558
A:Accession: P70560
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <PEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 23.1%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
|||
Db 3 VLG 5

RESULT 7
S70335
endosperm protein, 40K - rye (fragment)
C:Species: Secale cereale (rye)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C:Accession: S70335
R:Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.
Biochim. Biophys. Acta 1295, 13-22, 1996
A:Title: Identification of major rye scalins as coeliac immunoreactive proteins.
A:Reference number: S70327; MUID:96283789; PMID:8679669
A:Accession: S70335
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <ROC>

Query Match 23.1%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
|||
Db 2 VLG 4

RESULT 8
A33098
244K exantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: A33098
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: A33098
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <NIC>

Query Match 23.1%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11
|||
Db 2 LGP 4

RESULT 9
PT0246
Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0246
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0246
A:Molecule type: DNA
A:Residues: 1-7 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
|||
Db 3 VLG 5

RESULT 10
A39690
neural cell adhesion molecule, cardiac splice form -, -, -, - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: A39690
R:Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: A39690
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual t
A:Molecule type: mRNA
A:Residues: 1-7 <BEY>
A:Cross-references: GB:M63970
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 23.1%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PVR 13
|||
Db 2 PVR 4

RESULT 11
S29735
polysphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichii
C:Species: Propionibacterium freudenreichii subsp. shermanii
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
C:Accession: S29735
R:Phillips, N.F.B.; Horn, P.J.; Wood, H.G.
Arch. Biochem. Biophys. 300, 309-319, 1993
A:Title: The polysphosphate- and ATP-dependent glucokinase from Propionibacterium shermanii
A:Reference number: S29735; MUID:93143332; PMID:8380966
A:Accession: S29735
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <PHI>
C:Keywords: phosphotransferase

Query Match 23.1%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
|||
Db 3 VLG 5

RESULT 12
A39308
glycine reductase (EC 1.4.99.-) sulphydryl protein C, alpha chain - Clostridium sticklandii
C:Species: Clostridium sticklandii

C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997

C:Accession: A39308

R:Stadman, T.C.; Davis, J.N.

J. Biol. Chem. 266, 22147-22153, 1991

A:Title: Glycine reductase protein C. Properties and characterization of its role in the

A:Reference number: A39308; MUID:92042141; PMID:1939235

A:Accession: A39308

A>Status: Preliminary

A:Molecule type: protein

A:Residues: 1-8 <STA>

C:Function:

A:Description: glycine reductase complex catalyzes the reductive deamination of glycine

C:Keywords: ATP; oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVL 9

Db 3 PVL 5

RESULT 13

I54017

C:Species: synthetic

A:Note: human gene engineered and expressed in *Echerichia coli*

C:Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000

C:Accession: I54017

R:Devlin, P.E.; Drummond, R.J.; Toy, P.; Mark, D.F.; Watt, K.W.; Devlin, J.J.

Gene 65, 13-22, 1988

A:Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fac

i.

A:Reference number: I54017; MUID:88284374; PMID:2456256

A:Accession: I54017

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-8 <DEV>

A:Cross-references: GB:M20922; NID:9806638; PIDN:AAA66353.1; PID:g183043

Query Match

Best Local Similarity 23.1%; Score 3; DB 4; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11

Db 4 LGP 6

RESULT 14

B33710

C:Species: Rattus norvegicus - rat

C:Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 24-Sep-1999

C:Accession: B33710

R:Wen, L.; Huang, J.K.; Blackshear, P.J.

J. Biol. Chem. 264, 9016-9021, 1989

A:Title: Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory ele

A:Reference number: A33710; MUID:89255378; PMID:2722815

A:Accession: B33710

A>Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-10 <WEN>

A:Cross-references: GB:J04791; NID:9205807; PIDN:AAA66163.1; PID:g806309

C:Superfamily: unassigned leader peptides

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVL 9

Db 3 PVL 5

Db 8 PVL 10

RESULT 15

PX0030

C:Species: *Geotrichum candidum*

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 30-Sep-1993

C:Accession: PX0030

R:Sugihara, A.; Shimada, Y.; Tominaga, Y.

J. Biochem. 107, 426-430, 1990

A:Title: Separation and characterization of two molecular forms of *Geotrichum candidu*

A:Reference number: PX0030; MUID:90256718; PMID:2341377

A:Accession: PX0030

A:Molecule type: protein

A:Residues: 1-10 <SUG>

C:Comment: Lipase catalyzes the hydrolysis of triacylglycerols. This fungus contains

C:Keywords: carboxylic ester hydrolase

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLY 4

Db 7 LLY 9

RESULT 16

PH1345

C:Species: *Homo sapiens* (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1345

R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor ly

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1345

A:Molecule type: DNA

A:Residues: 1-10 <WAS>

A:Note: the authors translated the stop codon for residue 4 as X

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11

Db 6 LGP 8

RESULT 17

B45482

C:Species: *Homo sapiens* (man)

C:Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 05-May-1995

C:Accession: B45482

R:Stafforini, D.M.; Rollins, E.N.; Prescott, S.M.; McIntyre, T.M.

J. Biol. Chem. 268, 3857-3865, 1993

A:Title: The platelet-activating factor acetylhydrolase from human erythrocytes. Puri

A:Reference number: A45482; MUID:93179380; PMID:8440681

A:Accession: B45482

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <STA>

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10

Db 7 VLG 9
|||

RESULT 18
C53652
rhlR protein - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Aug-1998
C;Accession: C53652
R;Ochsner, U.A.; Flechter, A.; Reiser, J.
J. Biol. Chem. 269, 19787-19795, 1994
A;Title: Isolation, characterization, and expression in Escherichia coli of the Pseudomonas
A;Reference number: A53652; MUID:94327521; PMID:8051059
A;Accession: C53652
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <OCH>
A;Cross-references: GB:L28170
C;Superfamily: sdia regulatory protein

Query Match 23.1%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
|||

Db 7 FLL 9
|||

RESULT 19
F58501
43.5K bile stone protein - unidentified bacterium (fragment)
C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: F58501
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: F58501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <BIN>
A;Experimental source: human bile with stones
A;Note: 6-Asn and 8-Ala were also found

Query Match 23.1%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12
|||

Db 8 GPV 10
|||

RESULT 20
B41835
translation elongation factor EF-G homolog - Bacillus subtilis (fragment)
C;Species: Bacillus subtilis
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Dec-1997
C;Accession: B41835
R;Mitchell, C.; Morris, P.W.; Vary, J.C.
J. Bacteriol. 174, 2474-2477, 1992
A;Title: Identification of proteins phosphorylated by ATP during sporulation of Bacillus
A;Reference number: A41835; MUID:92210489; PMID:1556067
A;Accession: B41835
A;Molecule type: protein
A;Residues: 1-11 <MIT>
A;Note: this protein is phosphorylated during stationary phase but not during exponential
C;Keywords: phosphoprotein

Query Match 23.1%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
|||

Db 1 FLL 3
|||

RESULT 21
A55149
tetracenomycin A2 oxygenase (BC 1.-.-.-) - Streptomyces glaucescens (fragment)
N;Alternate names: tcma2 oxygenase; tcmg
C;Species: Streptomyces glaucescens
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Mar-1996
C;Accession: A55149
R;Shen, B.; Hutchinson, C.R.
J. Biol. Chem. 269, 30726-30733, 1994
A;Title: Triple hydroxylation of tetracenomycin A2 to tetracenomycin C in Streptomyces
A2 oxygenase.
A;Reference number: A55149; MUID:95074090; PMID:7982994
A;Accession: A55149
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <SHE>
C;Genetics:
A;Start codon: TTG
C;Keywords: antibiotic biosynthesis; FAD; monomer; oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVL 9
|||

Db 7 PVL 9
|||

RESULT 22
C61497
seed protein ws-18 - winged bean (fragment)
C;Species: Psophocarpus tetragonolobus (winged bean)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: C61497
R;Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-c
A;Reference number: A61491; MUID:89351606; PMID:2765119
A;Accession: C61497
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HIR>
C;Keywords: glycoprotein; seed

Query Match 23.1%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVL 9
|||

Db 7 PVL 9
|||

RESULT 23
C37196
bradykinin-potentiating peptide 3 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: C37196
R;Gintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: C37196

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <CIN>
C:Keywords: pyroglutamic acid
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 23.1%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
|||
Db 2 LGP 4

RESULT 24

I52980
glucocerebrosidase - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
A:Accession: I52980; MUID:88195776; PMID:335914
R:Reiner, O.; Wigderson, M.; Horowitz, M.
DNA 7, 107-116, 1988

A>Title: Structural analysis of the human glucocerebrosidase genes.

A:Reference number: I52980; MUID:88195776; PMID:335914

A:Accession: I52980

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 <RES>

A:Cross-references: GB:M18916; NID:g183023; PIDN:AAA35878.1; PID:g183024

A:Accession: I65971

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 <RE2>

A:Cross-references: GB:M18917; NID:g183025; PIDN:AAA35879.1; PID:g183026

Query Match

Best Local Similarity 100.0%; Score 3; DB 2; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13
|||
Db 6 PVR 8

RESULT 25

PH1583
Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1583
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993

A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1583

A:Molecule type: DNA

A:Residues: 1-11 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match

Best Local Similarity 100.0%; Score 3; DB 2; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
|||
Db 5 LGP 7

RESULT 26

S01749
collagen alpha 1(I) chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999

C:Accession: S01749; S21415

R:Mooslehner, K.; Harbers, K.

Nucleic Acids Res. 16, 773, 1988

A>Title: Two mRNAs of mouse pro alpha-1(I) collagen gene differ in the size of the 3' untranslated region.

A:Reference number: S01749; MUID:88124276; PMID:3340560

A:Accession: S01749

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-12 <MOO>

A:Cross-references: EMBL:X06753; NID:g50499; PIDN:CRA29927.1; PID:g50500

R:Mooslehner, K.; Harbers, K.

submitted to the EMBL Data Library, July 1989

A:Reference number: S21415

A:Accession: S21415

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-12 <MO2>

A:Cross-references: EMBL:X15896; NID:g50497; PIDN:CAA33904.1; PID:g50498

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo

Query Match

Best Local Similarity 100.0%; Score 3; DB 2; Length 12;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
|||
Db 7 GPV 9

RESULT 27

S65629

protoporphyrinogen oxidase (EC 1.3.3.4) - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-May-2000

C:Accession: S65629

R:Taketani, S.; Yoshinaga, T.; Furukawa, T.; Kohnno, H.; Tokunaga, R.; Nishimura, K.;

Eur. J. Biochem. 230, 760-765, 1995

A>Title: Induction of terminal enzymes for heme biosynthesis during differentiation o

A:Reference number: S65629; MUID:95331315; PMID:7607249

A:Accession: S65629

A:Molecule type: protein

A:Residues: 1-12 <TAK>

C:Genetics:

C:Genome: nuclear

C:Function:

A:Pathway: heme biosynthesis; porphyrin biosynthesis

C:Superfamily: phycoene dehydrogenase

C:Keywords: heme biosynthesis; mitochondrion; oxidoreductase; porphyrin biosynthesis

Query Match

Best Local Similarity 100.0%; Score 3; DB 2; Length 12;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
|||
Db 6 VLG 8

RESULT 28

PN0162

malate dehydrogenase (EC 1.1.1.37) - fungus (Fusarium sporotrichioides) (fragment)

C:Species: Fusarium sporotrichioides

C>Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994

C:Accession: PN0162

R:Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.

submitted to JIPID, May 1994

A>Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr

A:Reference number: PN0160

A:Accession: PN0162

A:Molecule type: protein

A:Residues: 1-12 <FUK>

C;Keywords: oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
 |||
 Db 5 VLG 7

RESULT 29

A60528
 insulin-like growth factor-binding protein, serum - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
 C;Accession: A60528

R;Walton, P.E.; Baxter, R.C.; Burlleigh, B.D.; Etherton, T.D.

Comp. Biochem. Physiol. B 92, 561-567, 1989

A;Title: Purification of the serum acid-stable insulin-like growth factor binding protein

A;Reference number: A60528; MUID:89209787; PMID:2469442

A;Accession: A60528

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <WAL>

Query Match 23.1%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12
 |||
 Db 8 GPV 10

RESULT 30

C20907

Ig kappa-1 chain J3 region - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 16-Aug-1996
 C;Accession: C20907

R;Emorine, L.; Max, E.E.

Nucleic Acids Res. 11, 8877-8890, 1983

A;Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple

A;Reference number: A20907; MUID:84169523; PMID:6324107

A;Accession: C20907

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 <EMO>

C;Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11
 |||
 Db 3 LGP 5

RESULT 31

A33520

inhibitory diffusible factor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 30-Sep-1993
 C;Accession: A33520

R;Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.

J. Biol. Chem. 264, 6021-6024, 1989

A;Title: Isolation and amino-terminal sequence of a novel cellular growth inhibitor (inh)

A;Reference number: A33520; MUID:89197888; PMID:2703477

A;Accession: A33520

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <WAL>

A;Keywords: heterotetramer; immunoglobulin

A;Residues: 1-12 <WAL>

A;Keywords: heterotetramer; immunoglobulin

A;Residues: 1-12 <WAL>

A;Keywords: heterotetramer; immunoglobulin

A;Residues: 1-12 <WAL>

A;Residues: 1-12 <BLA>

Query Match 23.1%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12
 |||
 Db 8 GPV 10

RESULT 32

A32734

enkephalin precursor - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jan-2000
 C;Accession: A32734

R;Micancovic, R.; Ray, P.; Kruggel, W.; Lewis, R.V.

Biochem. Biophys. Res. Commun. 118, 299-303, 1984

A;Title: Purification and sequence of an opioid peptide derived from ovine proenkephala

A;Reference number: A32734; MUID:84128045; PMID:6546517

A;Accession: A32734

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <MIC>

C;Superfamily: proenkephalin

C;Keywords: neuropeptide; opioid peptide

Query Match 23.1%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
 |||
 Db 4 VLG 6

RESULT 33

S70723

lipamide dehydrogenase homolog - Salmonella typhimurium (fragment)

C;Species: Salmonella typhimurium

C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998

C;Accession: S70723

R;Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.

Mol. Microbiol. 17, 523-531, 1995

A;Title: Salmonella typhimurium responses to a bactericidal protein from human neutro

A;Reference number: S70719; MUID:96100451; PMID:8559071

A;Accession: S70723

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <QIS>

A;Experimental source: strain SL1344

Query Match 23.1%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
 |||
 Db 10 VLG 12

RESULT 34

PH1316

Ig heavy chain DJ region (clone C388-107) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1316

R;Wasserman, R.; Gailli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lym

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1316

A:Molecule type: DNA
A:Residues: 1-13 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
|||
DB 8 LGP 10

RESULT 35

B47415

mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment)

N;Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996

C;Accession: B47415

R;Szumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.

J. Biol. Chem. 268, 17943-17950, 1993

A;Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and uti

A;Reference number: A47415; MUID:93352609; PMID:7688733

A;Accession: B47415

A:Molecule type: protein

A:Residues: 1-13 <SZU>

A;Experimental source: liver

A;Complex: The enzyme appears to be a heterodimer of alpha and beta chains.

C;Function:

A;Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP

C;Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ad

C;Keywords: blocked amino end; nucleotidyltransferase

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
|||
DB 11 FLL 13

RESULT 36

S03063

Ig lambda chain J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 11-Jan-2002

C;Accession: S03063

R;Udey, J.A.; Blomberg, B.B.

Nucleic Acids Res. 16, 2959-2969, 1988

A;Title: Intergenic exchange maintains identity between two human lambda light chain imm

A;Reference number: S03063; MUID:88217512; PMID:3130611

A;Accession: S03063

A:Molecule type: DNA

A:Residues: 1-13 <UDE>

A;Cross-references: EMBL:X06877; NID:g33357; PIDN:CAA29996.1; PID:g1335162

C;Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
|||
DB 11 VLG 13

RESULT 37

I70075

Glycophorin B (mistranslated) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Feb-1997 #sequence_revision 14-Aug-1997 #text_change 20-Apr-2000

C;Accession: I70075

R;Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.

J. Biol. Chem. 265, 9259-9263, 1990

A;Title: Identification of the crossing-over point of a hybrid gene encoding human g1

A;Reference number: I55334; MUID:90264417; PMID:1971625

A;Accession: I70075

A;Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-13 <REA>

A;Cross-references: GB:M33505; GB:J05465; NID:g183726; PIDN:AAA53152.1; PID:g442425

A;Note: this sequence was not determined in this report; the translation is from an i

C;Genetics:

A;Gene: GDB:GYPB

A;Cross-references: GDB:118891

A;Map position: 4q28-4q31

Query Match

Best Local Similarity 23.1%; Score 3; DB 4; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 5
|||
DB 11 LYQ 13

RESULT 38

S22236

lipoxxygenase (EC 1.13.11.12) 1 - barley (fragment)

C;Species: Hordeum vulgare (barley)

C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

A;Accession: S22236

R;Doderer, A.; Kokkelink, I.; van der Veen, S.; Valk, B.E.; Schram, A.W.; Douma, A.C.

Biochim. Biophys. Acta 1120, 97-104, 1992

A;Title: Purification and characterization of two lipoxxygenase isoenzymes from germin

A;Reference number: S21772; MUID:92207997; PMID:1554746

A;Accession: S22236

A:Molecule type: protein

A:Residues: 1-14 <BOD>

A;Experimental source: var. Triumph, seed

C;Function:

A;Description: catalyzes the peroxidation of polyunsaturated fatty acids to their cor

C;Superfamily: lipoxxygenase

C;Keywords: monomer; oxidoreductase; seed

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4
|||
DB 5 LLY 7

RESULT 39

S27140

hypothetical protein 1 estrogen receptor 5'-region - human

C;Species: Homo sapiens (man)

C;Date: 05-Mar-1994 #sequence_revision 12-May-1995 #text_change 18-Aug-2000

C;Accession: S27140

R;Keaveney, M.; Klug, J.; Gannon, F.

DNA Seq. 2, 347-359, 1992

A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor 9

A;Reference number: S27140; MUID:93075998; PMID:1476547

A;Accession: S27140

A;Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-14 <KEA>

A;Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44319.1; PID:g31202

C;Superfamily: unassigned leader peptides

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11
|||
Db 12 LGP 14

RESULT 40

PA0111
protein QA100054 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 06-Jun-1997
C:Accession: PA0111
R:Kano, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A:Reference number: PA0109
A:Accession: PA0111
A:Molecule type: protein
A:Residues: 1-14 <KAM>
A:Experimental source: root

Query Match 23.1%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12
|||
Db 2 GPV 4

RESULT 41

S33802
Chaperone, TCPI-related - oat
C:Species: Avena sativa (oat)
C>Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999
C:Accession: S33802
R:Mummet, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Schaefer
Nature 363, 644-648, 1993
A:Title: A TCPI-related molecular chaperone from plants refolds phytochrome to its photo
A:Reference number: S33800; MUID:93288140; PMID:8099715
A:Accession: S33802
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <MDM>

Query Match 23.1%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11
|||
Db 7 LGP 9

RESULT 42

A28018
very late antigen-1 alpha chain - human (fragment)
N:Alternate names: VLA-1 alpha chain
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994
C:Accession: A28018
R:Takada, Y.; Strominger, J.L.; Henler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
A:Title: The very late antigen family of heterodimers is part of a superfamily of molecu
A:Reference number: A94151; MUID:87204112; PMID:3033641
A:Accession: A28018
A:Molecule type: protein
A:Residues: 1-14 <RAK>
C:Keywords: duplication; heterodimer; membrane protein

Query Match 23.1%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11
|||
Db 12 LGP 14

RESULT 43

B61597
cytochrome P450 AL-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: B61597
R:Shimono, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
Drug Metab. Dispos. 19, 291-297, 1991
A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto
A:Reference number: A61597; MUID:91292910; PMID:1676625
A:Accession: B61597
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SHI>

Query Match 23.1%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
|||
Db 9 FLL 11

RESULT 44

C59137
protein Pf3 - golden needle mushroom (fragment)
C:Species: Flammulina velutipes (golden needle mushroom)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: C59137
R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
submitted to the Protein Sequence Database, November 1999
A:Description: Differences of proteins expressed in the fruiting dikaryon and the non
A:Reference number: A59137
A:Accession: C59137
A:Molecule type: protein
A:Residues: 1-14 <SAK>

Query Match 23.1%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
|||
Db 3 VLG 5

RESULT 45

LFTWL
leu leader peptide - Thermus aquaticus
C:Species: Thermus aquaticus
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C:Accession: S00901
R:Croft, J.E.; Love, D.R.; Bergquist, P.L.
Mol. Gen. Genet. 210, 490-497, 1987
A:Title: Expression of leucine genes from an extremely thermophilic bacterium in Esche
A:Reference number: S00901; MUID:88121725; PMID:3323845
A:Accession: S00901
A:Molecule type: DNA
A:Residues: 1-15 <CRO>
A:Cross-references: EMBL:X06604; NID:948244; PIDN:CAA29823.1; PID:948245
A:Note: the source is designated as Thermus thermophilus
C:Superfamily: Thermus aquaticus leu leader peptide

Query Match 23.1%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
|||
Db 13 GPV 15

RESULT 46

PM0004
Chlorophyll a/b-binding protein 24.5K - green alga (*Dunaliella tertiolecta*) (fragment)
N:Alternate names: photosystem II light-harvesting chlorophyll 24.5K protein
C:Species: *Dunaliella tertiolecta*
C>Date: 04-Sep-1998 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
C:Accession: PM0004
R:Chow, L.P.; Bennett, J.; Falkowski, P.G.
Gene 95, 165-171, 1990
A:Title: Characterization of a cDNA encoding for the 28.5-kDa LHCII apoprotein from the
A:Reference number: JW0040; MUID:91065528; PMID:2449775
A:Accession: PM0004
A:Molecule type: protein
A:Residues: 1-15 <LAR>
C:Superfamily: chlorophyll a/b-binding protein
C:Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane pr

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
|||
Db 12 LGP 14

RESULT 47

C37765
Hypothetical protein (csma 3' region) - *Chloroflexus aurantiacus* (fragment)
C:Species: *Chloroflexus aurantiacus*
C>Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 30-Sep-1993
C:Accession: C37765
R:Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.
J. Bacteriol. 172, 4497-4504, 1990
A:Title: Gene encoding the 5.7-kilodalton chlorosome protein of *Chloroflexus aurantiacus*
A:Reference number: A37765; MUID:90330558; PMID:2376566
A:Accession: C37765
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <THE>
A:Cross-references: GB:M33964

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4
|||
Db 4 LLY 6

RESULT 48

PM0079
Malate dehydrogenase (EC 1.1.1.37) II - fungus (*Fusarium sporotrichioides*) (fragment)
C:Species: *Fusarium sporotrichioides*
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0079
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*
A:Reference number: PA0051
A:Accession: PA0079
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
|||
Db 5 VLG 7

RESULT 49

PM0088
Protein QP200051 - fungus (*Fusarium sporotrichioides*) (fragment)
C:Species: *Fusarium sporotrichioides*
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0088
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*
A:Reference number: PA0051
A:Accession: PA0088
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
|||
Db 13 PVL 15

RESULT 50

PHI342
Ig heavy chain DJ region (clone C507-95) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PHI342
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PHI302; MUID:93094761; PMID:1460419
A:Accession: PHI342
A:Molecule type: DNA
A:Residues: 1-15 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
|||
Db 10 LGP 12

RESULT 51

S03955
acidic fibroblast growth factor - dog (fragment)
N:Alternate names: alpha-endothelial cell growth factor
C:Species: *Canis lupus familiaris* (dog)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: S03955
R:Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Schur, J. Biochem. 181, 67-73, 1989
A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine
A:Reference number: S03953; MUID:89231704; PMID:2714282
A:Accession: S03955
A:Molecule type: protein
A:Residues: 1-15 <QUI>
C:Keywords: growth factor

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLY 4
|||
Db 7 LLY 9

RESULT 52

E56978
collagen alpha 2(XI) chain - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
C:Accession: B56978
R:Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ins
A:Reference number: A56978; MUID:95370194; PMID:7642541
A:Accession: B56978
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <WUA>
A>Note: the residue designated 'X' is modified lysine cross-linked to 1(XI) Lys-23 in FS

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12
|||
Db 10 GPV 12

RESULT 53

A45096
thyrotropin-releasing hormone receptor, splice form 387 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A45096
R:de la Pena, P.; Delgado, L.M.; del Camino, D.; Barros, F.
J. Biol. Chem. 267, 25703-25708, 1992
A:Title: Two isoforms of the thyrotropin-releasing hormone receptor generated by alterna
A:Reference number: A45096; MUID:93100278; PMID:1334485
A:Accession: A45096
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-15 <DEI>
A:Cross-references: GB:S51512; NID:g261982; PIDN:AAR24549.1; PID:g261983
A:Experimental source: GH3 anterior pituitary cells
A>Note: sequence extracted from NCBI backbone (NCBIP:120927)

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVL 9
|||
Db 7 PVL 9

RESULT 54

B59137
Protein Pfl - golden needle mushroom (fragment)
C:Species: Flammulina velutipes (golden needle mushroom)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: B59137
R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
submitted to the Protein Sequence Database, November 1999
A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
A:Reference number: A59137
A:Accession: B59137
A:Molecule type: protein
A:Residues: 1-15 <SAK>
A:Experimental source: strain FV-4

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
|||
Db 3 VLG 5

RESULT 55

E41425
cytochrome P450 1F-6 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 05-Mar-1999
C:Accession: E41425
R:Imaoka, S.; Kamataki, T.; Funae, Y.
J. Biochem. 102, 843-851, 1987
A:Title: Purification and characterization of six cytochromes P-450 from hepatic micr
A:Reference number: A41425; MUID:88139237; PMID:3436956
A:Accession: E41425
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <IMA>
C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C:Keywords: heme

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11
|||
Db 7 LGP 9

RESULT 56

S03405
hydrogenase (EC 1.18.99.1) small chain - Alcaligenes eutrophus (fragment)
C:Species: Alcaligenes eutrophus
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Sep-1998
C:Accession: S03405
R:Lorenz, B.; Schneider, K.; Kratzin, H.; Schlegel, H.G.
Biochim. Biophys. Acta 995, 1-9, 1989
A:Title: Immunological comparison of subunits isolated from various hydrogenases of a
A:Reference number: S03404; MUID:89166625; PMID:2493816
A:Accession: S03405
A:Molecule type: protein
A:Residues: 1-16 <LOR>
A:Experimental source: strain H16, DMS 541
C:Superfamily: hydrogenase (NiFe) small chain
C:Keywords: hydrogen metabolism; iron-sulfur protein; membrane bound; metalloprotein;

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVL 9
|||
Db 8 PVL 10

RESULT 57

157530
gene c-fms protein - mouse (fragment)
C:Species: Mus sp. (mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-May-1997
C:Accession: 157530
R:Yue, X.; Favot, P.; Dunn, T.L.; Cassidy, A.I.; Hume, D.A.
Mol. Cell. Biol. 13, 3191-3201, 1993
A:Title: Expression of mRNA encoding the macrophage colony-stimulating factor recepto
A:Reference number: 157530; MUID:93268269; PMID:8497248
A:Accession: 157530
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:S62219; NID:g986001
C:Genetics:
A:Gene: C-fms
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
|||
Db 3 LGP 5

RESULT 58
S65520
phospholipase A2 (EC 3.1.1.4) - Malayan spitting cobra (fragment)
N:Contains: muscarinic acetylcholine receptor inhibitor
C:Species: Naja naja sputatrix (Malayan spitting cobra)
C>Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 17-Mar-2000
C:Accession: S65520
R:Miyoshi, S.; Tu, A. T.
Arch. Biochem. Biophys. 328, 17-25, 1996
A:Title: Phospholipase A(2) from Naja naja sputatrix venom is a muscarinic acetylcholine
A:Reference number: S65520; MUID:9619575; PMID:8638927
A:Accession: S65520
A:Molecule type: protein
A:Residues: 1-16 <MIY>
C:Superfamily: phospholipase A2
C:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 5
|||
Db 2 LYQ 4

RESULT 59
A39109
Hypothetical protein 1 - hepatitis C virus
C:Species: hepatitis C virus
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1993
C:Accession: A39109
R:Han, J.-H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A:Reference number: A39109; MUID:91156678; PMID:1705704
A:Accession: A39109
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <HAN>
A:Cross-references: GB:M58406

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13
|||
Db 5 PVR 7

RESULT 60
S66613
protein p12E - Friend murine leukemia virus (fragments)
C:Species: Friend murine leukemia virus
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S66613

R:Hensel, J.; Hintz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.
Eur. J. Biochem. 232, 373-380, 1995
A:Title: Localization of the palmitoylation site in the transmembrane protein p12E of
A:Reference number: S66613; MUID:96035869; PMID:7556184
A:Accession: S66613
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9;10-16 <HEN>

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPV 8
|||
Db 1 EPV 3

RESULT 61

I40065
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C:Species: Buchnera aphidicola
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C:Accession: I40065
R:Roubakish, D.; Baumann, P.
Gene 155, 107-112, 1995
A:Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (en
A:Reference number: I40061; MUID:95212914; PMID:7535281
A:Accession: I40065
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: EMBL:U10499; NID:g854717; PIDN:AAA79128.1; PID:g854718
C:Genetics:
A:Gene: aroE
C:Keywords: oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPV 8
|||
Db 13 EPV 15

RESULT 62

S03732
Photosystem I protein psaJ - spinach chloroplast (fragment)
C:Species: chloroplast Spinacia oleracea (spinach)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Feb-1997
C:Accession: S03732
R:Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.
FEBS Lett. 263, 274-278, 1990
A:Title: Polypeptide composition of higher plant photosystem I complex. Identificati
A:Reference number: S03730; MUID:90242987; PMID:2185953
A:Accession: S03732
A:Molecule type: protein
A:Residues: 1-16 <IKE>
C:Genetics:
A:Gene: psaJ
A:Genome: chloroplast
C:Keywords: chloroplast; photosynthesis; photosystem I; transmembrane protein

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
|||
Db 12 PVL 14

RESULT 63

C61414
chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)
C:Species: Pseudemys scripta (slider)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
C:Accession: C61414
R:Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A:Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determined
A:Reference number: A61414; PMID:76146602; PMID:4807189
A:Accession: C61414
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <BHA>
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
|||
DB 8 PVL 10

RESULT 64

PT0224
Ig heavy chain CDR3 region (clone 1-91) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0224
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; PMID:91108337; PMID:1899102
A:Accession: PT0224
A:Molecule type: DNA
A:Residues: 1-16 <YAM>
A:Experimental source: B lymphocyte
A:Note: the authors translated the stop codon for residue 9 as X
C:Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
|||
DB 11 LGP 13

RESULT 65

PH1302
Ig heavy chain DJ region (clone C76-105) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1302
R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; PMID:93094761; PMID:1460419
A:Accession: PH1302
A:Molecule type: DNA
A:Residues: 1-16 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
|||
DB 11 LGP 13

RESULT 66

E49655
T-cell-receptor beta chain variable region, TCR V beta (clone 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: E49655
R:Grom, A.A.; Thompson, S.D.; Luyrink, L.; Passo, M.; Choi, E.; Glass, D.N.
Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993
A:Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juv
A:Reference number: A49655; MUID:94068553; PMID:8248215
A:Accession: E49655
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-16 <GRO>
A:Experimental source: peripheral blood lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIP:140450)
C:Keywords: T-cell receptor

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13
|||
DB 5 PVR 7

RESULT 67

S68730
bleomycin-binding protein - Streptomyces verticillus (fragment)
C:Species: Streptomyces verticillus
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
C:Accession: S68730
R:Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Na
PEBS Lett. 362, 80-84, 1995
A:Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing St
al characterisation.

A:Reference number: S68730; MUID:95212588; PMID:7535252
A:Accession: S68730
A:Molecule type: protein
A:Residues: 1-16 <SUG>
A:Experimental source: ATCC 15003
C:Keywords: antibiotic resistance

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
|||
DB 9 PVL 11

RESULT 68

S65430
pyrogallol hydroxyltransferase (EC 1.97.1.2) large chain - Pelobacter acidigallici (f
C:Species: Pelobacter acidigallici
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 07-May-1999
C:Accession: S65430
R:Reichenbecher, W.; Ruediger, A.; Kroneck, P.M.H.; Schink, B.
Eur. J. Biochem. 237, 406-413, 1996
A:Title: One molecule of molybdopterin guanine dinucleotide is associated with each s
and mass spectrometry.

A:Reference number: S65429; MUID:96215436; PMID:8647079
A:Accession: S65430
A:Molecule type: protein
A:Residues: 1-16 <REI>
C:Keywords: oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12
|||
Db 13 GPV 15

RESULT 69
Tl4224
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - Euhadra herklotsi mitochondrion
C:Species: mitochondrion Euhadra herklotsi
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: Tl4224
R;Yamazaki, N.; Ueshima, R.; Terrett, J.A.; Yokobori, S.; Kaifu, M.; Segawa, R.; Kobayashi, N.; et al. 1996
A:Submitted to the EMBL Data Library, May 1996
A:Description: Evolution of pulmonate gastropod mitochondrial genomes: Comparisons of cytochrome b and 16S rRNA sequences.
A:Reference number: Z17932
A:Accession: Tl4224
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <YAM>
A:Cross-references: EMBL:Z171694; NID:e912660; PID:e244560; PIDN:CAA96364.1
A:Experimental source: adult; hepatopancreas
C:Genetics:
A:Genome: mitochondrion
C:Keywords: mitochondrion; NAD; oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
|||
Db 10 FLL 12

RESULT 70
S05917
chorion class A protein L4 precursor - silkworm (fragment)
C:Species: Bombyx mori (silkworm)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C:Accession: S05917
R;Sporel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.
J. Mol. Biol. 209, 1-19, 1989
A:Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridization of Bombyx mori chorion DNA with Bombyx mori chorion DNA.
A:Reference number: S05913; MUID:90040707; PMID:2810362
A:Accession: S05917
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-17 <SPO>
A:Cross-references: EMBL:X15560; NID:g5781; PIDN:CAA33571.1; PID:g5782
A:Note: this sequence was submitted to the EMBL Data Library, Jun-1989
C:Genetics:
A:Map position: 2
C:Superfamily: chorion class A protein pc292

Query Match 23.1%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
|||
Db 6 FLL 8

RESULT 71
S05913
chorion class A protein L2 precursor - silkworm (fragment)
C:Species: Bombyx mori (silkworm)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C:Accession: S05913
R;Sporel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.

Query Match 23.1%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
|||
Db 6 FLL 8

RESULT 72
S05919
chorion class A protein L5 precursor - silkworm (fragment)
C:Species: Bombyx mori (silkworm)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C:Accession: S05919
R;Sporel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.
J. Mol. Biol. 209, 1-19, 1989
A:Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridization of Bombyx mori chorion DNA with Bombyx mori chorion DNA.
A:Reference number: S05913; MUID:90040707; PMID:2810362
A:Accession: S05919
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-17 <SPO>
A:Cross-references: EMBL:X15561; NID:g5786; PIDN:CAA33573.1; PID:g5787
A:Note: this sequence was submitted to the EMBL Data Library, Jun-1989
C:Genetics:
A:Map position: 2
C:Superfamily: chorion class A protein pc292

Query Match 23.1%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
|||
Db 6 FLL 8

RESULT 73
S05921
chorion class A protein L6 precursor - silkworm (fragment)
C:Species: Bombyx mori (silkworm)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C:Accession: S05921
R;Sporel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.
J. Mol. Biol. 209, 1-19, 1989
A:Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridization of Bombyx mori chorion DNA with Bombyx mori chorion DNA.
A:Reference number: S05913; MUID:90040707; PMID:2810362
A:Accession: S05921
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-17 <SPO>
A:Cross-references: EMBL:X15562; NID:g5791; PIDN:CAA33575.1; PID:g5792
A:Note: this sequence was submitted to the EMBL Data Library, Jun-1989
C:Genetics:
A:Map position: 2
C:Superfamily: chorion class A protein pc292

Query Match 23.1%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
|||
Db 6 FLL 8

RESULT 74

F58502

41k stone protein - unidentified bacterium (fragment)

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998

C;Accession: F58502

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: F58502

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <BIN>

A;Note: a secondary sequence SVFALNEQXM was also found

Query Match 23.1%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12
|||
Db 8 GPV 10

RESULT 75

S41207

F420-non-reducing-hydrogenase (EC 1.12.99.-) 51K chain - Methanobacterium thermoautotrop

C;Species: Methanobacterium thermoautotrophicum

A;Variety: strain Marburg

C;Date: 06-Feb-1995 #sequence_revision 17-Jul-1998 #text_change 07-May-1999

C;Accession: S41207

R;Setzke, E.; Hedderich, R.; Heiden, S.; Thauer, R.K.

Eur. J. Biochem. 220, 139-148, 1994

A;Title: H(2): heterodisulfide oxidoreductase complex from Methanobacterium thermoautot

A;Reference number: S41204; MUID:94164153; PMID:8119281

A;Accession: S41207

A;Molecule type: protein

A;Residues: 1-17 <SET>

A;Experimental source: strain Marburg

C;Complex: membrane-associated complex; holoenzyme is the hydrogen:heterodisulfide oxid

.-) and a F420-non-reducing-hydrogenase (EC 1.12.99.-) subcomplex; each of the subcomple

C;Function:

A;Description: reduction of coenzyme M-N-7-mercaptoheptanoylthreonine phosphate heterodi

ase (EC 1.12.99.2)

C;Keywords: membrane-associated complex; oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EPV 8
|||
Db 6 EPV 8

Search completed: November 25, 2003, 19:36:14

Job time : 9.9186 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 4.61047 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLXYQEPVLGPVR 13

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	30.8	12	1	TM2A_METWA
2	4	30.8	20	1	MAX6_BOMMX
3	4	30.8	20	1	MAX7_BOMMX
4	4	30.8	20	1	MAX8_BOMMX
5	3	23.1	9	1	FAR9_ASCSU
6	3	23.1	11	1	BPP3_BOTIN
7	3	23.1	13	1	CRBL_ICASP
8	3	23.1	13	1	VG16_BACSU
9	3	23.1	15	1	APF3_MALPA
10	3	23.1	15	1	FGF1_CANFA
11	3	23.1	15	1	LPL_TRETH
12	3	23.1	16	1	HBD_CLOPA
13	3	23.1	16	1	PA2_NAJSP
14	3	23.1	16	1	PGLT_PELAC
15	3	23.1	17	1	BOLA_MEGPE
16	3	23.1	17	1	BOL5_MEGPE
17	3	23.1	17	1	EPG_TREAO
18	3	23.1	17	1	MDH_ACIDE
19	3	23.1	18	1	PG6_PACGO
20	3	23.1	19	1	FLA3_SPLAU
21	3	23.1	19	1	OXLA_OPHHA
22	3	23.1	19	1	PCG7_PACGO
23	3	23.1	19	1	UKAI_HUMAN
24	3	23.1	19	1	UP25_UPEIN
25	3	23.1	19	1	UP27_UPEMJ
26	3	23.1	19	1	UP28_UPEMJ
27	3	23.1	20	1	AF2L_MALPA
28	3	23.1	20	1	BIP_PHAVU
29	3	23.1	20	1	CD4_SHEEP
30	3	23.1	20	1	FRE3_LITIN
31	2	15.4	4	1	FLRF_HIRME
32	2	15.4	4	1	FLRN_ATEL
33	2	15.4	6	1	ACPH_RABIT

ALIGNMENTS

RESULT 1


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QY      9 LGPV 12
Db      2 LGPV 5

RESULT 5
PAR9 ASCSU
ID FAR9 ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AP9.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 LGP 11
Db      2 LGP 4

RESULT 6
BPP3 BOTIN
ID BPP3 BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
PR: C37196; C37196
DR Hypotensive agent; Pyrrolidone carboxylic acid.
KW Hypotensive agent; PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

QY      9 LGPV 12
Db      2 LGPV 5

RESULT 7
CRBL ICASP
ID CRBL ICASP STANDARD; PRT; 13 AA.
AC P17237;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chemotactic peptide (i-CP).
OS Icaria sp. (Kopalidian wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Icaria.
OX NCBI_TaxID=7495;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (in) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1353 MW; 348DBC7AA30A3768 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 LGP 11
Db      5 LGP 7

RESULT 8
VG16 BACSU
ID VG16 BACSU STANDARD; PRT; 13 AA.
AC P80867;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vegetative protein 16 (VEG16) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RX STRAIN=168 / IS58;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-
RT regulation map for Bacillus subtilis.";
RL Electrophoresis 18:1451-1463(1997).
CC -!- CAUTION: Could not be found in the genome of B. subtilis 168.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1372 MW; 20FB27BDC9ECA2D7 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 EPV 8
Db      5 EPV 7

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DR InterPro; IPR002348; IL1_HBGF.
KW PROSITE; PS00247; HBGF_FGF; PARTIAL.
KW Growth factor; Mitogen; Angiogenesis; Heparin-binding.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1732 MW; 53CC9A3CADDADA1 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4
DB 7 LLY 9

RESULT 11
LPL_THETH
ID_LPL_THETH STANDARD; PRT; 15 AA.
AC F21234;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu leader peptide.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=88121725; PubMed=3323845;
RA Croft J.E., Love D.R., Bergquist P.L.;
RT "Expression of leucine genes from an extremely thermophilic bacterium
in Escherichia coli.";
RL Mol. Gen. Genet. 210:490-497(1987).
CC -!- FUNCTION: Involved in control of the biosynthesis of leucine.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X06604; CAA29823.1; -
KW Leucine biosynthesis; Leader peptide.
SQ SEQUENCE 15 AA; 1666 MW; C2F107A386D7620B CRC64;

Query Match 23.1%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
DB 13 GPV 15

RESULT 12
HBD_CLOPA
ID_HBD_CLOPA STANDARD; PRT; 16 AA.
AC P81343;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 38, Last annotation update)
DE 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) (Beta-
DE hydroxybutyryl-CoA dehydrogenase) (BHBD) (CP 26) (fragment).
GN HBD.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]

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RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -|- CATALYTIC ACTIVITY: (S)-3-hydroxybutanoyl-CoA + NADP(+) = 3-
acetoacetyl-CoA + NADPH.
CC -|- PATHWAY: BUTYRATE/BUTANOL-PRODUCING PATHWAY.
CC -|- SIMILARITY: BELONGS TO THE 3-HYDROXYACYL-COA DEHYDROGENASE FAMILY.
DR InterPro; IPR006180; 3HGDH.
DR PROSITE; PS00067; 3HGDH; PARTIAL.
KW Oxidoreductase; NADP; Fatty acid metabolism.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1570 MW; E3AD430D5C575785 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
Db 6 VLG 8

RESULT 13
PA2_NAJSP
ID PA2_NAJSP STANDARD; PRT; 16 AA.
AC Q10756;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)
OS (Muscarinic inhibitor) (Fragment).
OS Naja sputatrix (Malayan spitting cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=33626;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96195757; PubMed=8638927;
RA Miyoshi S.-I., Tu A.T.;
RT "Phospholipase A2 from Naja naja sputatrix venom is a muscarinic
acetylcholine receptor inhibitor.";
RL Arch. Biochem. Biophys. 328:17-25(1996).
CC -|- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
acyl groups in 3-sn-phosphoglycerides. Blocks neuromuscular
transmission at the postsynaptic site. Binds to the muscarinic
acetylcholine receptor.
CC -|- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a fatty acid anion.
CC -|- COFACTOR: Binds 1 calcium ion (By similarity).
CC -|- SUBUNIT: Monomer.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
SUBFAMILY.
CC PIR; S65520; S65520.
DR HSP; P00598; IPOA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; Phoslip; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Toxin; Neurotoxin;
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1969 MW; 9AC1F9834BBS585F0 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 3 LYQ 5
Db 2 LYQ 4

RESULT 14
PGTL_PELAC
ID PGTL_PELAC STANDARD; PRT; 16 AA.
AC P80563;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pyrogallol hydroxyltransferase large subunit (EC 1.97.1.2)
DE (transhydroxylase) (fragment).
OS Pelobacter acidigallii.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Pelobacteraceae; Pelobacter.
OX NCBI_TaxID=35816;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 2377 / Braunschweig;
RX MEDLINE=96215436; PubMed=8647079;
RA Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.;
RT "One molecule of molybdopterin guanine dinucleotide is associated
with each subunit of the heterodimeric Mo-Fe-S protein
transhydroxylase of Pelobacter acidigallii as determined by SDS/PAGE
and mass spectrometry.";
RL Eur. J. Biochem. 237:406-413(1996).
CC -|- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3-
trihydroxybenzene = 1,3,5-trihydroxybenzene + 1,2,3,5-
tetrahydroxybenzene.
CC -|- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).
CC -|- SUBUNIT: Heterodimer of a large and a small subunit.
DR PIR; S65430; S65430.
KW Oxidoreductase; Molybdenum; Iron-sulfur.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1620 MW; 56348D53A0AD6EE3 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
Db 13 GPV 15

RESULT 15
BOL4_MEGPE
ID BOL4_MEGPE STANDARD; PRT; 17 AA.
AC P07495;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin IV.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85105003; PubMed=2578459;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -|- FUNCTION: Mast cell degranulating peptide.
DR PIR; D22595; D22595.
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1873 MW; A34A43514BCDFB6 CRC64;
```

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Query Match      23.1%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VLG 10
      |||
Db      13 VLG 15

RESULT 16
BOL5 MEGPE
ID _BOL5 MEGPE STANDARD; PRT; 17 AA.
AC P07496;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin V.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
RT the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -|- FUNCTION: Mast cell degranulating peptide.
CC PIR: E22595; E22595.
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1731 MW; B076C091571606A5 CRC64;

Query Match      23.1%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VLG 10
      |||
Db      3 VLG 5

RESULT 17
EFG_THEAQ
ID _EFG_THEAQ STANDARD; PRT; 17 AA.
AC Q01697;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (Fragment).
GN FUSA OR FUS.
OS Thermus aquaticus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP 00276;
RX MEDLINE=92362620; PubMed=1499561;
RA Voss R.H., Hartmann R.K., Lippmann C., Jahn O.,
RA Erdmann V.;
RT "Sequence of the tufA gene encoding elongation factor EF-Tu from
RT Thermus aquaticus and overproduction of the protein in Escherichia
RT coli.";
RL Eur. J. Biochem. 207:839-846(1992).
CC -|- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

```

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CC EF-G/EF-2 SUBFAMILY.
CC -----
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DR EMBL: X66322; CAA46997.1; -.
DR HAMAP: MF_00054; -; 1.
DR InterPro: IPR000795; EFG_GTPbind.
DR PROSITE: PS00301; EFACTOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2054 MW; EA46E1EF05F86E1D CRC64;

Query Match      23.1%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YQE 6
      |||
Db      2 YQE 4

RESULT 18
MDH_ACIDE
ID _MDH_ACIDE STANDARD; PRT; 17 AA.
AC P80540;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
GN MDH.
OS Acidovorax delafieldii.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Acidovorax.
OX NCBI_TaxID=47920;
RN [1]
RP SEQUENCE
RC STRAIN=CCUG 12929;
RX MEDLINE=97334132; PubMed=9190829;
RA Charnock C.;
RT "Structural studies of malate dehydrogenases (MDHs): MDHs in
RT Brevundimonas species are the first reported MDHs in Proteobacteria
RT which resemble lactate dehydrogenases in primary structure.";
RL J. Bacteriol. 179:4086-4070(1997).
CC -|- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -|- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR InterPro: IPR001252; Mdh.
DR PROSITE: PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1662 MW; 110E8111A516909E CRC64;

Query Match      23.1%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 PVR 13
      |||
Db      4 PVR 6

RESULT 19
PCG6_PACGO
ID PCG6_PACGO STANDARD; PRT; 18 AA.
AC P82419;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE Ponericin G6.
OS Pachycondyla goeldii (Ponerine ant.).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST GRAM-POSITIVE BACTERIA AND
CC S.CEREVISIAE. HAS NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1818.15; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide; Amidation.
FT MOD RES 18 18
FT MOD RES 18 18
SQ SEQUENCE 18 AA; 1819 MW; 94876D83F60E8D3E CRC64;

Query Match 23.1%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
Db |||
5 VLG 7

RESULT 20
FLA3 SPIAU
ID FLA3 SPIAU STANDARD; PRT; 19 AA.
AC P21986;
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE Flagellar filament 32 kDa core protein (Minor) (Fragment).
OS Spirochaeta aurantia.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Spirochaeta.
OX NCBI_TaxID=147;
RN [1]
RP SEQUENCE.
RC STRAIN=M1;
RX MEDLINE=91123217; PubMed=1991729;
RA Parales J. Jr., Greenberg E.P.;
RT "N-terminal amino acid sequences and amino acid compositions of the
RT Spirochaeta aurantia flagellar filament polypeptides.";
RL J. Bacteriol. 173:1357-1359(1991).
CC -!- FUNCTION: COMPONENT OF THE CORE OF THE FLAGELLA.
CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF
CC REPEATING UNITS OF FLAA AROUND A CORE THAT CONTAINS ONE OR ALL OF
CC FIVE ANTIGENICALLY RELATED POLYPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
KW Flagella; Periplasmic.
FT NON TER 19 19
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2084 MW; 3D06277582B1A979 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
Db |||
15 VLG 17

RESULT 21
OXLA_OPHHA
ID OXLA_OPHHA STANDARD; PRT; 19 AA.

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AC P81383;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-1999 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-amino acid oxidase (EC 1.4.3.2) (LAO) (LAO) (Fragment).
OS Ophiophagus hannah (King cobra) (Naja hannah).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Ophiophagus.
OX NCBI_TaxID=8665;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94361525; PubMed=8080286;
RA Ponnudurai G., Chung M.C.M., Tan N.-H.;
RT "Purification and properties of the L-amino acid oxidase from Malaysian
RT pit viper (Calloselasma rhodostoma) venom.";
RL Arch. Biochem. Biophys. 313:373-378(1994).
RN [2]
RP SEQUENCE OF 1-15.
RC TISSUE=Venom;
RX MEDLINE=97449790; PubMed=9304806;
RA Ahn M.Y., Lee B.M., Kim Y.S.;
RT "Characterization and cytotoxicity of L-amino acid oxidase from the
RT venom of king cobra (Ophiophagus hannah).";
RL Int. J. Biochem. Cell Biol. 29:911-919(1997).
CC -!- FUNCTION: Has cytotoxic activity (By similarity).
CC -!- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid
CC + NH(3) + H(2)O(2).
CC -!- COFACTOR: FAD.
CC -!- SUBUNIT: Homodimer (Probable).
CC -!- PTM: Glycosylated.
CC -!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
CC -!- STRONG, TO MOUSE FIG-1.
KW Oxidoreductase; Flavoprotein; FAD; Glycoprotein; Toxin.
FT CONFLICT 1 1
FT NON TER 19 19
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2298 MW; DD911ASB414F1427 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QEP 7
Db |||
10 QEP 12

RESULT 22
PCG7_PACGO
ID PCG7_PACGO STANDARD; PRT; 19 AA.
AC P82420;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G7.
OS Pachycondyla goeldii (Ponerine ant.).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST GRAM-POSITIVE BACTERIA AND
CC S.CEREVISIAE. HAS NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.

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CC -!- MASS SPECTROMETRY: MW=1876.14; METHOD=MALDI.
 KW Antibiotic; Insect immunity; Fungicide
 SQ SEQUENCE 19 AA; 1876 MW; 4DA4876D83F6088D CRC64;

Query Match 23.1%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
 ||||
 Db 5 VLG 7

RESULT 23

UK1 HUMAN STANDARD; PRT; 19 AA.
 AC P31940;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of epidermal keratinocytes (Spot 1118) (Fragments).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 7.24, ITS MW IS: 23.5 kDa.
 DR Aarhus/Ghent-2DPAGE; 1118; IEF.
 FT NON TER 1 1
 FT UNSURE 6 6
 FT NON_CONS 6 7
 FT NON_CONS 12 13
 FT UNSURE 17 17
 FT NON TER 19 19
 SQ SEQUENCE 19 AA; 2087 MW; EF7515F79D50DE12 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QEP 7
 ||||
 Db 13 QEP 15

RESULT 24

UP25 UPEIN STANDARD; PRT; 19 AA.
 ID UP25 UPEIN
 AC P82031;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 2.5.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Rattery M.J., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;

RT "Novel uperin peptides from the dorsal glands of the Australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST M.LUTEUS,
 CC L.MESENTERIODES AND S.UBERIS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1940; METHOD=FAB.
 KW Amphibian defense peptide; Antibiotic.
 SQ SEQUENCE 19 AA; 1941 MW; 5E94C6C757B463D9 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
 ||||
 Db 9 VLG 11

RESULT 25

UP27 UPEMJ STANDARD; PRT; 19 AA.
 ID UP27 UPEMJ
 AC P82039;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 2.7.
 OS Uperoleia mjobergii (Australian toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104954;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "New antibiotic uperin peptides from the dorsal glands of the
 RT Australian toadlet Uperoleia mjobergii.";
 RL Aust. J. Chem. 49:1325-1331(1996).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1946; METHOD=FAB.
 KW Amphibian defense peptide.
 SQ SEQUENCE 19 AA; 1949 MW; 24E4F83A6BA35F21 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
 ||||
 Db 16 VLG 18

RESULT 26

UP28 UPEMJ STANDARD; PRT; 19 AA.
 ID UP28 UPEMJ
 AC P82040;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 2.8.
 OS Uperoleia mjobergii (Australian toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104954;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "New antibiotic uperin peptides from the dorsal glands of the

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RT  Australian toadlet Uperoleia mjobergii.;
RL  Aust. J. Chem. 49:1325-1331(1996).
CC  -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC  S.EPIDERMIS AND S.UBERIS.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC  -!- MASS SPECTROMETRY: MW=1978; METHOD=FAB.
KW  Amphibian defense peptide.
SQ  SEQUENCE 19 AA; 1979 MW; 48524822C8A340F9 CRC64;

Query Match      23.1%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 VLG 10
DB  16 VLG 18

RESULT 27
AF2L_MALPA
ID  AF2L_MALPA STANDARD; PRT; 20 AA.
AC  P83143;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Antifungal protein 2, large subunit (CW-2) (Fragment).
OS  Malva parviflora (Little mallow) (Cheeseweed).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX  NCBI_TaxID=145753;
RN  [1]
RP  SEQUENCE, AND FUNCTION.
RC  TISSUE=Seed;
RX  MEDLINE=20568734; PubMed=11118343;
RA  Wang X., Bunkers G.J.;
RT  "Potent heterologous antifungal proteins from cheeseweed (Malva
RT  parviflora).";
RL  Biochem. Biophys. Res. Commun. 279:669-673(2000).
CC  -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC  not F.graminearum.
CC  -!- SUBUNIT: Heterodimer of a large and a small subunit.
CC  -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC  concentration.
DR  GO; GO:0003799; F:antifungal peptide activity; IDA.
KW  Fungicide; Antibiotic.
FT  NON TER 20 20
SQ  SEQUENCE 20 AA; 2603 MW; 6E766A5E342036DA CRC64;

Query Match      23.1%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 YQE 6
DB  8 YQE 10

RESULT 28
BIP_PHAVU
ID  BIP_PHAVU STANDARD; PRT; 20 AA.
AC  P80089;
DT  01-DEC-1992 (Rel. 24, Created)
DT  01-DEC-1992 (Rel. 24, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Luminal binding protein (78 kDa glucose-regulated protein homolog)
DE  (GRP 78) (Fragment).
OS  Phaseolus vulgaris (Kidney bean) (French bean).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX  NCBI_TaxID=3885;

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RN  [1]
RP  SEQUENCE.
RC  STRAIN=cv. Greensleeves; TISSUE=Cotyledon;
RX  MEDLINE=94221064; PubMed=1344885;
RA  D'Amico L., Valsasina B., Daminati M.G., Fabbri M.S., Nitti G.,
RA  Bollini R., Ceriotti A., Vitale A.;
RT  "Bean homologs of the mammalian glucose-regulated proteins: induction
RT  by tunicamycin and interaction with newly synthesized seed storage
RT  proteins in the endoplasmic reticulum.";
RL  Plant J. 2:443-455(1992).
CC  -!- FUNCTION: PROBABLY PLAYS A ROLE IN FACILITATING THE ASSEMBLY OF
CC  MULTIMERIC PROTEIN COMPLEXES INSIDE THE ER.
CC  -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC  -!- INDUCTION: By tunicamycin.
CC  -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR  InterPro; IPR001023; Hsp70.
DR  PROSITE; PS00297; HSP70_1; PARTIAL.
DR  PROSITE; PS00329; HSP70_2; PARTIAL.
DR  PROSITE; PS01036; HSP70_3; PARTIAL.
KW  ATP-binding; Endoplasmic reticulum.
FT  UNSURE 4 4
FT  UNSURE 18 18 OR T.
FT  NON TER 20 20
SQ  SEQUENCE 20 AA; 2147 MW; 809D43AF21A21476 CRC64;

Query Match      23.1%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 VLG 10
DB  6 VLG 8

RESULT 29
CD4_SHEEP
ID  CD4_SHEEP STANDARD; PRT; 20 AA.
AC  P05542;
DT  01-NOV-1988 (Rel. 09, Created)
DT  01-NOV-1988 (Rel. 09, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)
DE  (Fragment).
GN  CD4.
OS  Ovis aries (Sheep).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Caprinae; Ovis.
OX  NCBI_TaxID=9940;
RN  [1]
RP  SEQUENCE.
RC  MEDLINE=86166694; PubMed=3082751;
RA  Classon B.J., Tsagaratos J., Kirszbaum L., Maddox J., McKay C.R.,
RA  Brandon M., McKenzie I.F.C., Walker I.D.;
RT  "The L3T4 antigen in mouse and the sheep equivalent are
RT  immunoglobulin-like.";
RL  Immunogenetics 23:129-132(1986).
CC  -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC  RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
CC  -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
DR  PIR; B47642; B47642.
DR  GO; GO:0042101; C:T-cell receptor complex; ISS.
DR  GO; GO:0015026; F:coreceptor activity; ISS.
DR  GO; GO:0042289; F:MHC class II protein binding activity; ISS.
DR  GO; GO:0006955; P:immune response; ISS.
DR  GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR  GO; GO:0030217; P:T-cell differentiation; ISS.
DR  GO; GO:0045058; P:T-cell selection; ISS.
DR  GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
KW  Immunoglobulin domain; T-cell; Immune response.
FT  NON TER 20 20
SQ  SEQUENCE 20 AA; 1928 MW; 421F09570FEA97EE CRC64;

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Query Match      23.1%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VLG 10
      ||||
Db      4 VLG 6

RESULT 30
FREN_LITIN
ID_FREN_LITIN STANDARD; PRT; 20 AA.
AC P56249;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Frenatin 3.
OS Litoria infrafrenata (Giant tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=61195;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion; PubMed=9225251;
RX MEDLINE=97368637;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of
the giant tree frog Litoria infrafrenata.";
RL J. pept. Sci. 2:117-124(1996).
CC -!- FUNCTION: Wide spectrum antimicrobial peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
glands.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 20 AA; 1956 MW; 7E4ABE30EA17B20C CRC64;

Query Match      23.1%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VLG 10
      ||||
Db      5 VLG 7

RESULT 31
FLRF_HIRME
ID_FLRF_HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FLRamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RC SPECIES=H. medicinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=H. trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRPamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 582 MW; 69D40729A000000000 CRC64;

Query Match      15.4%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FL 2
      ||
Db      1 FL 2

RESULT 32
FLRN_ANTEL
ID_FLRN_ANTEL STANDARD; PRT; 4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actinillidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuizen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid R.K., Nockner H.-P., Staley A.L.;
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 549 MW; 64540729A000000000 CRC64;

Query Match      15.4%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FL 2
      ||
Db      1 FL 2

RESULT 33
ACPH_RABIT
ID_ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;

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RX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wold F.;
RT "N-Terminal sequence analysis of N alpha-acetylated proteins after
RL Anal. Biochem. 199;45-50(1991).
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR EIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro; IPR002471; Prol endopep ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD RES 1 1 ACETYLATION.
FT NON-TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VL 9
Db 5 VL 6

RESULT 34
ALL3_CARMA STANDARD; PRT; 7 AA.
ID ALL3_CARMA
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinostatin 3.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]_
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 7 AA; 796 MW; 672879DCB476B70 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EP 7
Db 1 EP 2

RESULT 35
E105_LITRU STANDARD; PRT; 7 AA.
ID E105_LITRU
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 5.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 7 7
FT NON-TER 7 7
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EP 7
Db 3 EP 4

RESULT 36
FAR1_HELTI STANDARD; PRT; 7 AA.
ID FAR1_HELTI
AC P41871;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide GDPFLRP-amide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
CC THE KIDNEY, MANTLE AND SKIN.
CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
FT NON-TER 7 7
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FL 2
Db 4 FL 5

RESULT 37
FAR1_MACRS STANDARD; PRT; 7 AA.
ID FAR1_MACRS
AC P83274;
DT 28-FEB-2003 (Rel. 41, Created)

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Db 3 LL 4

RESULT 41

MNP1_LEPDE
 ID MNP1_LEPDE STANDARD; PRT; 7 AA.
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Myotropic neuropeptide 1 (Led-MNP-1).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=95380343; PubMed=7651886;
 RA Spitaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of
 RT a novel myotropic neuropeptide in the Colorado potato beetle,
 RT Leptinotarsa decemlineata.";
 RL Peptides 16:365-374(1995).
 CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC -!- OVIDUCT.
 KW Neuropeptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 GP 11
 DB 4 GP 5

RESULT 42

PPH2_LYCES
 ID PPH2_LYCES STANDARD; PRT; 7 AA.
 AC P83379;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
 RC GLYCOSYLATION.
 RX STRAIN=cv. Moneymaker; TISSUE=Seed;
 RX MEDLINE=22361242; PubMed=12473124;
 RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
 RT "Purification and characterization of two secreted purple acid
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
 RT esculentum) cell cultures.";
 RL Eur. J. Biochem. 269:6278-6286(2002).
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2O) = an
 CC alcohol + phosphate.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: Glycosylated.
 CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of
 CC purple acid phosphatase.
 KW Hydrolase; Glycoprotein.

FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FL 2
 DB 1 FL 2

RESULT 43

UN06_PINPS
 ID UN06_PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 25 KDa.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 LY 4
 DB 1 LY 2

RESULT 44

AL15_CARMA
 ID AL15_CARMA STANDARD; PRT; 8 AA.
 AC P81818;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinus maenas (Common shore crab).
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

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KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 AMIDATION
SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 2 GP 3

RESULT 45
ALL6_CARMA
ID ALL6_CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RN SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 2 GP 3

RESULT 46
ALL5_CALVO
ID ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RN SEQUENCE.
RC TISSUE=;
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RN CHARACTERIZATION, AND HYDROXYLATION.

RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; E47393; E47393.
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD_RES 3 HYDROXYLATION (20%).
FT MOD_RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 1 GP 2

RESULT 47
ALL6_CVDPO
ID ALL6_CVDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RN SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LY 4
DB 3 LY 4

RESULT 48
ALL8_CARMA
ID ALL8_CARMA STANDARD; PRT; 8 AA.
AC P81811;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas 8.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

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OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 795 MW; 922879CDCB47687D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
 ||
 Db 2 GP 3

RESULT 49
 ALL9_CARMA STANDARD; PRT; 8 AA.
 ID ALL9_CARMA
 AC P81812;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 9.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 781 MW; 7C2879CDCB476878 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
 ||
 Db 2 GP 3

RESULT 50
 B44K_PORGI STANDARD; PRT; 8 AA.
 ID B44K_PORGI
 AC P81886;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 44 kDa immunogenic protein (Fragment).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).

OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VPB 3492;
 RX MEDLINE=20198497; PubMed=10731616;
 RA Norris J.M., Love D.N.;
 RT "Serum antibody responses of cats to soluble whole cell antigens of
 RT feline Porphyromonas gingivalis.";
 RL Vet. Microbiol. 73:37-49 (2000).
 CC -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
 KW Antigen.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQ 5
 ||
 Db 3 YQ 4

RESULT 51
 CADI_ENTFA STANDARD; PRT; 8 AA.
 ID CADI_ENTFA
 AC P13268;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CADI.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85051889; PubMed=6437872;
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B., Suzuki A.;
 RT "Isolation and structure of the bacterial sex pheromone, CADI, that
 RT induces plasmid transfer in Streptococcus faecalis.";
 RL FEBS Lett. 178:97-100 (1984).
 CC -!- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PAD1.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VL 9
 ||
 Db 5 VL 6

RESULT 52
 CLP_THICU STANDARD; PRT; 8 AA.
 ID CLP_THICU
 AC P80488;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Chemolithotroph-specific protein (Fragment).
 OS Thiobacillus cuprinus.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Thiomonas.
 OX NCBI_TaxID=36860;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 5494;

RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.
 CC -!- MISCELLANEOUS; FOUND SPECIFICALLY IN CELLS CULTURED
 CC CHEMOLITHOTROPHICALLY.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 785 MW; 91497B06DDC2D76D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PV 8
 DB 2 PV 3

RESULT 53
 ID CON2_CONPU STANDARD; PRT; 8 AA.
 AC P58785;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leu-contryphan-P.
 OS Conus purpurascens (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OC NCBI_TaxID=41690;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC STRAIN=Clipperton Island, TISSUE=Venom;
 RX MEDLINE=9938839; PubMed=10461743;
 RA Jacobsen R.B., Jlmenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
 RA Olivera B.M.;
 RT "A novel D-leucine-containing Conus peptide: diverse conformational
 RT dynamics in the contryphan family.";
 RL J. Pept. Res. 54:93-99(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
 KW Toxin; Hydroxylation; D-amino acid.
 FT DISULFID 2 4 8
 FT MOD_RES 4 4 D-LEUCINE.
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LL 3
 DB 4 LL 5

RESULT 54
 ID CPD1_ENTFA STANDARD; PRT; 8 AA.
 AC P13269;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CPD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OC NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85040388; PubMed=6436978;
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B.;
 RT "Isolation and structure of bacterial sex pheromone, CPD1.";

RL Science 226:849-850(1984).
 CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC BACTERIOCIN PLASMID PPDI.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2
 DB 1 FL 2

RESULT 55
 ID FAR1_PANRE STANDARD; PRT; 8 AA.
 AC P41872;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuropeptide PF1 (SDPNFLRP-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OC NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93027659; PubMed=1408999;
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
 RA Garrison R.D., Williams J.F., Friedman A.R.;
 RT "Two FMRamide-like peptides from the free-living nematode
 RT Panagrellus redivivus.";
 RL Peptides 13:209-214(1992).
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
 CC CAUDALLY TO THE BASE OF THE PHARYNX.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2
 DB 5 FL 6

RESULT 56
 ID FAR1_PENMO STANDARD; PRT; 8 AA.
 AC P83316;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FUP1 (GDRNFLRP-amide).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OC NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupuem J., Krungkarn C., Longyant S.,
 RA Chaisithangkura P., Sithigorngul W., Pitsom A.;
 RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk

RT of the giant tiger prawn Penaeus monodon";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.

CC Neuropeptide; Amidation.
 KW MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2
 ||
 5 FL 6
 Db

RESULT 57

FAR2_HOMAM
 ID FAR2_MACRS STANDARD; PRT; 8 AA.

AC P83275;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLP2 (ADKNFLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 CC Palaemonoidea; Palaemonidae; Macrobrachium.
 OS NCBI_TaxID=79674;
 RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RA Sithigorngul P.; Sarathongkum W., Jaidechoey S., Longyant S.,
 RA Sithigorngul W.;
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn Macrobrachium rosenbergii.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -!- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
 CC GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C433AAD CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2
 ||
 5 FL 6
 Db

RESULT 58

FAR3_HOMAM
 ID FAR3_MACRS STANDARD; PRT; 8 AA.

AC P41486;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide 3 (FLI 3) (F2).
 OS Homarus americanus (American lobster).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 CC Nephropoidea; Nephropidae; Homarus.
 OS NCBI_TaxID=6706;
 RN [1]

RP SEQUENCE.

RC TISSUE=Pericardial organs;

CC Ascarididae; Ascaris.

OS Ascarididae; Ascaris.

CC Ascarididae; Ascaris.

OS Ascarididae; Ascaris.

CC Ascarididae; Ascaris.

OS Ascarididae; Ascaris.

RX MEDLINE=88116164; PubMed=3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT "Purification and characterization of FMRFamide-like immunoreactive
 RT substances from the lobster nervous system: isolation and sequence
 RT analysis of two closely related peptides.";
 RL J. Comp. Neurol. 266:16-26(1987).
 CC -!- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 MM
 CC POTASSIUM IN THE PRESENCE OF CALCIUM.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2
 ||
 5 FL 6
 Db

RESULT 59

FAR4_HOMAM

ID FAR4_HOMAM STANDARD; PRT; 8 AA.

AC P41487;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide 4 (FLI 4) (F1).
 OS Homarus americanus (American lobster).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 CC Nephropoidea; Nephropidae; Homarus.
 OS NCBI_TaxID=6706;
 RN [1]

RP SEQUENCE.

RC TISSUE=Pericardial organs;

RX MEDLINE=88116164; PubMed=3429714;

RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;

RT "Purification and characterization of FMRFamide-like immunoreactive

RT substances from the lobster nervous system: isolation and sequence

RT analysis of two closely related peptides.";

RL J. Comp. Neurol. 266:16-26(1987).

CC -!- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC

CC NEUROMUSCULAR JUNCTIONS.

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD RES 8 8 AMIDATION.

SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2
 ||
 5 FL 6
 Db

RESULT 60

FAR7_ASCSU

ID FAR7_ASCSU STANDARD; PRT; 8 AA.

AC P43171;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFamide-like neuropeptide AF7.

OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).

CC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;

CC Ascarididae; Ascaris.

OS Ascarididae; Ascaris.

CC Ascarididae; Ascaris.

OS Ascarididae; Ascaris.

CC Ascarididae; Ascaris.

OS Ascarididae; Ascaris.

CC Ascarididae; Ascaris.

OS Ascarididae; Ascaris.

CC Ascarididae; Ascaris.

OS Ascarididae; Ascaris.

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OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel PMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC NEUROPEPTIDE; Amidation.
KW Neuropeptide; Amidation.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 2 GP 3

RESULT 61
NPB_BOVIN
ID NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -|- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2
DB 1 FL 2

RESULT 62
RS7_MYCIT
ID RS7_MYCIT STANDARD; PRT; 8 AA.
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S7 (Fragment).
GN RPSG..
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93197130; PubMed=8451173;
RA Nait J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
RT Mycobacterium intracellulare.";
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -|- FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the head
CC domain of the 30S subunit. Is located at the subunit interface
CC close to the decoding center, probably blocks exit of the E-site
CC rRNA (by similarity).
CC -|- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
CC and S11 (by similarity).
CC -|- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L08171; AAR25376.1; -.
DR PIR; S35538; S35538.
DR HAMAP; MF_00480; -.
DR InterPro; IPR000235; Ribosomal_S7.
DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribosomal protein; rRNA-binding; rRNA-binding; tRNA-binding.
FT INIT MET 0 0 BY SIMILARITY.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 4 GP 5

RESULT 63
UC26_MAIZE
ID UC26_MAIZE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Fernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.0 ITS MW IS: 57.2 kDa.
CC Maize-2DPAGE; P80632; COLEOPTILE.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;

```

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EP 7
DB 2 EP 3

RESULT 64

UPAL MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
CC NON TER 8
FT SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;
SQ

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EP 7
DB 3 EP 4

RESULT 65

UPAL RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Fleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
CC NON TER 8
FT SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;
SQ

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QE 6
DB 1 QE 2

RESULT 66

UPAL HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tiesot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.9, ITS MW IS: 65 kDa.
CC SWISS-2DPAGE; P30087; HUMAN.
DR NON TER 1
FT UNSURE 8
FT NON TER 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;
SQ

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QE 6
DB 2 QE 3

RESULT 67

VGLG HSV2B STANDARD; PRT; 8 AA.
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
2: GH, GB, GC, GD, GI, AND GE.
CC -1- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
HSV-1.
CC NON TER 8
FT SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;
SQ

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 6 GP 7

RESULT 68

BS43_SERPL
ID -B943 SERPL STANDARD; PRT; 9 AA.
AC P81375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RX MEDLINE=2293561; PubMed=12406768;
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenbergh I.,
RA Van Beeunen J., Thonart P.;
RT "Characterization of serracin P, a phase-tail-like bacteriocin, and
its activity against *Erwinia amylovora*, the fire blight pathogen.";
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium
E. amylovora.
DR InterPro: IPR006498; Tail tube.
DR Pfam: PF04985; Phage_tube; 1.
KW Antibiotic; Bacteriocin.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1095 MW; 1E66D412C871E1FB CRC64;

Query Match 15.4%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VL 9
Db 8 VL 9

RESULT 69
ID -BUK CLOPA STANDARD; PRT; 9 AA.
AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 36) (Fragment).
GN BUK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from *Clostridium pasteurianum* W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
phosphate to butyrate (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the acetate kinase family.
DR HAMAP; MF_00542; -; 1.
DR InterPro: IPR000890; Acetate kin.
DR PROSITE; PS01075; ACETATE_KINASE_1; PARTIAL.
DR PROSITE; PS01076; ACETATE_KINASE_2; PARTIAL.
KW Transferase; Kinase.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 15.4%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LL 3
Db 4 LL 5

RESULT 70
ID -FAR2 PANRE STANDARD; PRT; 9 AA.
AC P41873;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide PP2 (SADPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RA Garrison R.D., Williams J.F., Friedman A.R.;
RT "Two FMRFamide-like peptides from the free-living nematode
Panagrellus redivivus.";
RL Peptides 13:209-214(1992).
CC -!- FUNCTION: MYOACTIVE.
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
CAUDALLY TO THE BASE OF THE PHARYNX.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 15.4%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FL 2
Db 6 FL 7

RESULT 71
ID -FAR3 MACRS STANDARD; PRT; 9 AA.
AC P83276;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP3 (NYDKNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Rumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigorngul P., Sarathongkum W., Jaidechoy S., Longyant S.,
RA Sithigorngul W.;
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
freshwater prawn *Macrobrachium rosenbergii*.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -!- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
DR GO:0007218; P-neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.

```

FT  MOD RES      9      9      AMIDATION.
SQ  SEQUENCE 9 AA; 1216 MW; 18220729C443ABB CRC64;

Query Match      15.4%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 FL 2
    ||
Db  6 FL 7

RESULT 72
FAR5_PANRE
ID  FAR5_PANRE      STANDARD;      PRT;      9 AA.
AC  P82661,
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  FMRFamide-like neuropeptide PFS (AMRNALVRF-amide).
OS  Panagrellus redivivus.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC  Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX  NCBI_TaxID=6233;
[1]
RN  SEQUENCE, FUNCTION, AND AMIDATION.
RA  Moffet C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA  Maule A.G.;
RT  "Isolation, characterization and pharmacology of FMRFamide-related
RL  peptides (FaRPs) from free-living nematode, Panagrellus redivivus.";
RL  Submitted (JUL-2000) to the SWISS-PROT data bank.
CC  -!- FUNCTION: MYOACTIVE.
CC  -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC  FAMILY.
KW  Neuropeptide; Amidation.
FT  MOD RES      9      9      AMIDATION.
SQ  SEQUENCE 9 AA; 1077 MW; A0D112C72DD45406 CRC64;

Query Match      15.4%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  12 VR 13
    ||
Db  7 VR 8

RESULT 73
FAR6_MACRS
ID  FAR6_MACRS      STANDARD;      PRT;      9 AA.
AC  P83279,
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  FMRFamide-like neuropeptide FLP6 (DGRNFLRF-amide).
OS  Macrobrachium rosenbergii (Giant fresh water prawn).
OC  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC  Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC  Palaemonoidea; Palaemonidae; Macrobrachium.
OX  NCBI_TaxID=79674;
[1]
RN  SEQUENCE, AND MASS SPECTROMETRY.
RC  TISSUE=Eyestalk;
RX  MEDLINE=21107394; PubMed=11179812;
RA  Sithigorngul P., Saraihongkum W., Longyant S., Panchan N.,
RA  Sithigorngul W., Petsom A.;
RT  "Three more novel FMRFamide-like neuropeptide sequences from the
RT  eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL  Peptides 22:191-197(2001).
CC  -!- MASS SPECTROMETRY: MW=1080.7; METHOD=WALDI.
CC  -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC  FAMILY.
KW  Neuropeptide; Amidation.
FT  MOD RES      9      9      AMIDATION.
SQ  SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;

Query Match      15.4%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 FL 2
    ||
Db  6 FL 7

RESULT 75
FAR6_CALSI
ID  FAR6_CALSI      STANDARD;      PRT;      9 AA.
AC  P38495;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  01-NOV-1995 (Rel. 32, Last annotation update)
DE  FMRFamide-like neuropeptide.
OS  Callinectes sapidus (Blue crab).
OC  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC  Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC  Eubrachyura; Portunodea; Portunidae; Callinectes.
OX  NCBI_TaxID=6763;
[1]
RN  SEQUENCE.
RP  MEDLINE=92270479; PubMed=1815216;
RX  Krajniak K.G.;
RA  "The identification and structure-activity relations of a
RT  cardioactive FMRFamide-related peptide from the blue crab Callinectes
RT  sapidus.";
RL  Peptides 12:1295-1302(1991).

```

CC -!- FUNCTION: CARDIOACTIVE PEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;
Query Match 15.4%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FL 2
Db 6 FL 7

Search completed: November 25, 2003, 19:28:27
Job time : 5.68189 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 24.4128 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-32
Perfect score: 13
Sequence: 1 FLLYQEPVLGPVR 13

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0
Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL_23.*

- 1: sp.arched.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organella.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.virus.*
- 13: sp.vertibrate.*
- 14: sp.unclassified.*
- 15: sp.rvirus.*
- 16: sp.bacteriap.*
- 17: sp.archae.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	30.8	16	12 Q9WMC6	Q9WMC6 sigma virus
2	4	30.8	17	10 Q9S8K1	Q9S8K1 solanum tub
3	4	30.8	18	4 Q9UCL4	Q9UCL4 homo sapien
4	4	30.8	20	4 Q96A79	Q96A79 homo sapien
5	3	23.1	7	8 Q9S182	Q9S182 gnatholebia
6	3	23.1	8	2 Q93SP2	Q93SP2 pseudomonas
7	3	23.1	8	2 Q9R4M3	Q9R4M3 enterococcu
8	3	23.1	8	8 Q94VCL	Q94VCL varanus rud
9	3	23.1	8	8 Q8HR64	Q8HR64 clivia caul
10	3	23.1	8	10 Q8L802	Q8L802 zea mays (m
11	3	23.1	8	11 Q82598	Q82598 rattus norv
12	3	23.1	9	2 Q8R7H9	Q8R7H9 haemophilus
13	3	23.1	9	2 P83157	P83157 anabaena sp
14	3	23.1	14	9 Q9UCN5	Q9UCN5 homo sapien
15	3	23.1	10	2 Q47091	Q47091 escherichia
16	3	23.1	10	5 Q95NT8	Q95NT8 musca domes

Q9tru6 bos taurus	10	6	Q9TRU6
Q63389 rattus norv	10	11	Q63389
Q9115 mus musculu	10	11	Q9115
Q9198 tt virus. o	10	12	Q91IG8
Q902V8 paitacus e	10	13	Q902V8
Q75595 human immun	10	15	Q75595
Q9tqb3 homo sapien	11	7	Q9TQB3
Q96829 psophocarpu	11	10	Q9S829
Q9umg9 homo sapien	12	4	Q9UMQ9
Q91v15 homo sapien	12	4	Q91V15
Q9xnr6 pyiaetella l	12	8	Q9XNR6
Q925V7 mus musculu	12	11	Q925V7
Q90213 xenopus lae	12	13	Q902L3
Q50117 mycobacteri	13	2	Q50117
Q53693 streptomyce	13	2	Q53693
Q49230 mycoplasma	13	2	Q49230
Q9rfj7 actinobacill	13	2	Q9RFJ7
Q75905 homo sapien	13	4	Q75905
Q14461 homo sapien	13	4	Q14461
Q99188 rivulus cau	13	8	Q99188
Q94re2 leptomonas	13	8	Q94RE2
Q88176 mus musculu	13	11	Q88176
Q9pab5 duck hepati	13	12	Q9PAB5
P82064 limnodynast	13	13	P82064
Q9r5p6 legionella	14	2	Q9R5P6
Q9uhm5 homo sapien	14	4	Q9UHM5
Q9umf6 hordeum mur	14	8	Q9UMF6
Q8v1h7 hepatitis b	14	12	Q8V1H7
Q9jp39 pseudomonas	15	2	Q9JP39
Q9r598 micrococcu	15	2	Q9R598
Q9ucc2 homo sapien	15	4	Q9UCC2
Q9trn9 sus scrofa	15	6	Q9TRN9
Q9th04 grus amERIC	15	8	Q9TH04
P92818 paralichthy	15	8	P92818
Q9xlj8 grus leucog	15	8	Q9XLJ8
Q9th03 grus paradi	15	8	Q9TH03
Q9sap4 solanum tub	15	10	Q9SAP4
P82431 nicotiana t	15	10	P82431
Q9qv34 rattus sp.	15	11	Q9QV34
Q44610 buchnera ap	16	2	Q44610
Q9r4x4 pseudomonas	16	2	Q9R4X4
P82597 bacillus sp	16	4	P82597
Q9npq7 homo sapien	16	4	Q9NPQ7
Q9tw22 macrobodella	16	5	Q9TW22
Q62810 equus cabal	16	6	Q62810
Q9tr97 oryctolagus	16	6	Q9TR97
P92070 euhadra her	16	8	P92070
Q9t2g6 solanum tub	16	8	Q9T2G6
Q8cis2 mus musculu	16	11	Q8CIS2
Q55091 shigella so	17	2	Q55091
Q9eup4 thermus the	17	2	Q9EUP4
Q9r560 bacillus su	17	2	Q9R560
Q00074 aspergillus	17	3	Q00074
Q9ujh1 homo sapien	17	4	Q9UJH1
Q9upk4 homo sapien	17	4	Q9UPK4
Q9ucl9 homo sapien	17	4	Q9UCL9
Q9uc43 homo sapien	17	4	Q9UC43
Q17205 bombyx mori	17	5	Q17205
Q26832 trypanosoma	17	5	Q26832
Q9tvv3 bombyx mori	17	5	Q9TVV3
Q9tvx7 bombyx mori	17	5	Q9TVX7
Q17203 bombyx mori	17	5	Q17203
Q9try8 sus sp. ins	17	6	Q9TRY8
Q9quj4 mus sp. mep	17	11	Q9QUJ4
Q9quw6 rattus sp.	17	11	Q9QUW6
Q9qz24 mus musculu	17	11	Q9QZ24
Q9pru8 gallus gall	17	13	Q9PRU8
Q9uc87 homo sapien	18	4	Q9UC87
Q9uc81 homo sapien	18	4	Q9UC81
Q9um83 homo sapien	18	4	Q9UM83
Q9uj81 homo sapien	18	4	Q9UJ81
Q9ucf4 homo sapien	18	4	Q9UCF4
Q9ucr5 homo sapien	18	4	Q9UCR5

O8ned1 homo sapien
O4334 homo sapien
Q9trg2 oryctolagus
Q9tr57 sus scrofa
Q8m0a0 tockus leuc
Q8vbm8 mus musculu
Q61840 mus musculu
Q90912 gallus gall
Q87587 chimpanzee
Q87589 chimpanzee
Q87593 chimpanzee

ALIGNMENTS

RESULT 1

Q9WMG6
ID Q9WMG6 PRELIMINARY; PRT; 16 AA.
AC Q9WMG6;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE 2 protein (Fragment).
GN 2.
OS Sigma virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; unclassified Rhabdoviridae.
OX NCBI_TaxID=11301;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212481; PubMed=8384742;
RA Teninges D., Bras F., Dezelee S.;
RT "Genome organization of the sigma rhabdovirus: six genes and a gene overlap".
RL Virology 193:1018-1023(1993).
DR EMBL; S57847; AAD40699.1; -.
FT NON TER 1
SQ SEQUENCE 16 AA; 1904 MW; F96DBC468601967E CRC64;

Query Match 30.8%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EPVL 9
Db 10 EPVL 13

RESULT 2

Q9S8K1
ID Q9S8K1 PRELIMINARY; PRT; 17 AA.
AC Q9S8K1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE 20 kDa knittz-type proteinase inhibitor (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RX MEDLINE=95093035; PubMed=8000008;
RA Mitsuori C., Yamagishi K., Fujino K., Kikuta Y.;
RT "Detection of immunologically related Kunitz and Bowman-Birk
RT proteinase inhibitors expressed during potato tuber development".;
RL Plant Mol. Biol. 26:961-969(1994).
SQ SEQUENCE 17 AA; 1872 MW; 44F34F5775B0F832 CRC64;

Query Match 30.8%; Score 4; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PVLG 10
Db 7 PVLG 10

RESULT 3

Q9UCL4
ID Q9UCL4 PRELIMINARY; PRT; 18 AA.
AC Q9UCL4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Insulin-like growth factor binding protein 30 kDa form (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93091816; PubMed=1726837;
RA Roghani M., Segovia B., Whitechurch O., Binoux M.;
RT "Purification from human cerebrospinal fluid of insulin-like growth
RT factor binding proteins (IGFBPs). Isolation of IGFBP-2, an altered form
RT of IGFBP-3 and a new IGFBP species".;
RL Growth Regul. 1:125-130(1991).
SQ SEQUENCE 18 AA; 1689 MW; 10F5516240C6298B CRC64;

Query Match 30.8%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 7 LGPV 10

RESULT 4

Q96A79
ID Q96A79 PRELIMINARY; PRT; 20 AA.
AC Q96A79;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Connective tissue growth factor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Blom I.B., van Dijk A.J., de Weger R.A., Tilanus M.G.J.,
RA Goldschmeding R.;
RT "Identification of human CCN2 (connective tissue growth factor)
RT promoter polymorphisms".;
RL J. Clin. Pathol. 54:192-196(2001).
DR EMBL; AF316366; AAK60505.1; -.
DR EMBL; AF316367; AAK60506.1; -.
DR EMBL; AF316368; AAK60507.1; -.
FT NON TER 20
SQ SEQUENCE 20 AA; 2050 MW; 0110FF079D4516B6 CRC64;

Query Match 30.8%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPCR 13
Db 7 GPCR 10

RESULT 5

O99182
 ID Q99182 PRELIMINARY; PRT; 7 AA.
 AC Q99182;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cytochrome oxidase I (Fragment).
 GN COI
 OS Gnatholebias zonatus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
 OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
 NCBI_TaxID=135316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20072928; PubMed=10603257;
 RX Murphy W.J., Thomson J.E., Collier G.E.;
 RT "Phylogeny of the Neotropical killifish family Rivulidae
 RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
 RT sequences.";
 RL Mol. Phylogenet. Evol. 13:289-301 (1999).
 DR EMBL; AF002591; AAD01074.1; --
 KW Mitochondrion.
 FT NON TER
 SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;

 Query Match 23.1%; Score 3; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 3 LYQ 5
 Db 2 LYQ 4

 RESULT 6
 Q93SP2
 ID Q93SP2 PRELIMINARY; PRT; 8 AA.
 AC Q93SP2;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Quaternary ammonium compound-resistance protein QacEdelta1
 DE (Fragment).
 GN QACEDELTA1.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=YM704; TRANSPOSON=class I integron;
 RC Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
 RA "VIM-2 metallo-beta-lactamase gene-containing integron in a
 RT Pseudomonas aeruginosa clinical isolate.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY029772; AAK50441.1; --
 FT NON TER
 SQ SEQUENCE 8 AA; 920 MW; FE2729C732C87336 CRC64;

 Query Match 23.1%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 FLL 3
 Db 6 FLL 8

 RESULT 7
 Q9R4M3
 ID Q9R4M3 PRELIMINARY; PRT; 8 AA.
 AC Q9R4M3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE COBI=ACTERIAL sex pheromone.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=95290767; PubMed=7772836;
 RX Nakayama J., Abe Y., Ono Y., Isogai A., Suzuki A.;
 RA "Isolation and structure of the Enterococcus faecalis sex pheromone,
 RT COBI, that induces conjugal transfer of the hemolysin/bacteriocin
 RT plasmids, pOBI and pYII.";
 RL Biosci Biotechnol. Biochem. 59:703-705 (1995).
 SQ SEQUENCE 8 AA; 741 MW; 83D87732C732CDC2 CRC64;

 Query Match 23.1%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 8 VLG 10
 Db 5 VLG 7

 RESULT 8
 Q94VCI
 ID Q94VCI PRELIMINARY; PRT; 8 AA.
 AC Q94VCI;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Varanus rudicollis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 NCBI_TaxID=169851;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0 (2001).
 DR EMBL; AF407521; AAL10116.1; --
 KW Mitochondrion.
 FT NON TER
 SQ SEQUENCE 8 AA; 1053 MW; FE2729D5A36411A6 CRC64;

 Query Match 23.1%; Score 3; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 FLL 3
 Db 6 FLL 8

 RESULT 9
 Q8HR64
 ID Q8HR64 PRELIMINARY; PRT; 8 AA.
 AC Q8HR64;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Rps16 protein (Fragment).
 GN RPS16.
 OS Clivia caulescens.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OX Clivia
NCBI_TaxID=152470;
RN [1]
RP SEQUENCE FROM N.A.
RA Conrad F., Reeves G., Rourke J.P.;
RT "Phylogenetic relationships of the recently discovered species Clivia
RT mirabilis.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ519544; CAD59437.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 909 MW; 9FA87729C732C9 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
Db 4 FLL 6

RESULT 10
Q8L802 PRELIMINARY; PRT; 8 AA.
AC Q8L802
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Pat (Fragment).
DE PAT.
GN Zea mays (Maize).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Ronning S.B., Berdal K.G., Vaithilingom M.M., Holst-Jensen A.;
RT "Transformation event-specific quantitative real-time PCR for
RT genetically modified Bt11 maize (Zea mays) and estimation of the
RT impact of exogenous DNA on the limit of quantification.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123624; AA089275.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 909 MW; 6046C1B2D77412D7 CRC64;

Query Match 23.1%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13
Db 1 PVR 3

RESULT 11
P82598 PRELIMINARY; PRT; 8 AA.
AC P82598
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 3kDa non-arginase growth inhibitory factor (NAGIF) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RA Sprague-Dawley; Tissue=Liver;
RC STRAIN=Sprague-Dawley; Tissue=Liver;
RX MEDLINE=20198203; PubMed=10731662;

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RA Kim K.-Y., Choi I., Kim S.-S.;
RT "Purification and characterization of a novel inhibitor of the
RT proliferation of hepatic stellate cells.";
RL J. Biochem. 127;23-27(2000).
CC -!- FUNCTION: MAY ACT AS A NEGATIVE EFFECTOR IN THE REGULATION OF THE
CC HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE
CC ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.
CC -!- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG
CC PROTEIN.
FT NON TER
SQ SEQUENCE 8 AA; 914 MW; 80A3676802D76B1D CRC64;

Query Match 23.1%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPV 8
Db 2 EPV 4

RESULT 12
Q9R7H9 PRELIMINARY; PRT; 9 AA.
AC Q9R7H9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lipoprotein (Fragment).
GN NLPD.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98083063; PubMed=9422600;
RA Martin K., Morlin G., Smith A., Nordyke A., Eisenstark A., Golomb M.;
RT "The tryptophanase gene cluster of Haemophilus influenzae type b:
RT evidence for horizontal gene transfer.";
RL J. Bacteriol. 180;107-118(1998).
DR EMBL; AF003252; AAB96582.1; -.
FT NON TER
SQ SEQUENCE 9 AA; 1152 MW; 35A017673B4412D7 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13
Db 2 PVR 4

RESULT 13
P83157 PRELIMINARY; PRT; 9 AA.
AC P83157
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

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CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR InterPro; IPR001189; SODismutase.
 DR PROSITE; PS0088; SOD MN; PARTIAL.
 KW Oxidoreductase; Iron; Metal-binding.
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QEP 7
 Db 4 QEP 6

RESULT 14

ID Q9UCN5 PRELIMINARY; PRT; 9 AA.
 AC Q9UCN5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE Cell-surface heparin/HEPARANSULFATE-binding protein peptide 2
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92291065; PubMed=1601862;
 RA Raboudi N., Julian J., Rohde L.H., Carson D.D.;
 RT "Identification of cell-surface heparin/heparan sulfate-binding
 RT proteins of a human uterine epithelial cell line (RL95).";
 RL J. Biol. Chem. 267:11930-11939(1992).
 SQ SEQUENCE 9 AA; 1008 MW; CBS6D0544732C732 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
 Db 1 PVL 3

RESULT 15

ID Q47091 PRELIMINARY; PRT; 10 AA.
 AC Q47091;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Colicin E1 (Fragment).
 OS Escherichia coli.
 OG Plasmid ColE1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86094231; PubMed=3936034;
 RA Waleh N.S.; Johnson P.H.;
 RT "Structural and functional organization of the colicin E1 operon.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:8389-8393(1985).
 DR EMBL; M12543; AAA23065.1; -;
 KW Plasmid.
 FT NON TER 1 1
 SQ SEQUENCE 10 AA; 1085 MW; 88F00B32CB144041 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
 Db 7 VLG 9

RESULT 16

ID Q95NT8 PRELIMINARY; PRT; 10 AA.
 AC Q95NT8;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Cytochrome P450 (Fragment).
 GN CYP6D3.
 OS Musca domestica (House fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
 OC Muscidae; Musca.
 OX NCBI_TaxID=7370;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LPR;
 RA Kasai S., Scott J.G.;
 RT "5' flanking sequence of CYP6D3.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS;
 RA Kasai S., Scott J.G.;
 RT "Cytochrome P450 CYP6D3 5' flanking sequence.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF283258; AAK59543.1; -;
 DR EMBL; AF283259; AAK69544.1; -;
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1190 MW; 550408A0572729C7 CRC64;

Query Match 23.1%; Score 3; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
 Db 4 FLL 6

RESULT 17

ID Q9TRU6 PRELIMINARY; PRT; 10 AA.
 AC Q9TRU6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE GAP-3, GTPase-activating protein (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92112868; PubMed=1309786;
 RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
 RA Burgess A.W.;
 RT "The purification of a Rap1 GTPase-activating protein from bovine
 RT brain cytosol.";
 RL J. Biol. Chem. 267:1546-1553(1992).
 FT NON TER 1 1
 SQ SEQUENCE 10 AA; 1149 MW; 59370A51A72321A7 CRC64;

Query Match 23.1%; Score 3; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
 DB 1 FLL 3

RESULT 18
 Q63389 ID Q63389 PRELIMINARY; PRT; 10 AA.
 AC Q63389;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Ornithine decarboxylase (ODC).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=89255378; PubMed=2722815;
 RA Wen L., Huang J.K., Blackshear P.J.;
 RT "Rat ornithine decarboxylase gene. Nucleotide sequence, potential
 RT regulatory elements, and comparison to the mouse gene.";
 RL J. Biol. Chem. 264:9016-9021(1989).
 DR EMBL; J04791; AAA66163.1; -;
 SQ SEQUENCE 10 AA; 1074 MW; 30F6EE69D415BDC7 CRC64;

Query Match 23.1%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
 DB 8 PVL 10

RESULT 19
 Q9JLI5 ID Q9JLI5 PRELIMINARY; PRT; 10 AA.
 AC Q9JLI5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Melanocortin type 1 receptor MCL1R (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=20090876; PubMed=106230832;
 RA Adachi S., Morii E., Kim D.-k., Ogihara H., Jippo T., Ito A., Lee Y.M.,
 RA Kitamura Y.;
 RT "Involvement of mi-transcription factor in expression of alpha-
 RT melanocyte-stimulating hormone receptor in cultured mast cells of
 RT mice.";
 RL J. Immunol. 164:855-860(2000).
 DR EMBL; AF176016; AAF37323.1; -;
 KW Receptor.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1148 MW; 95B58A26C76B06C1 CRC64;

Query Match 23.1%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QEP 7
 DB 4 QEP 6

RESULT 20
 Q9JIG8 ID Q9JIG8 PRELIMINARY; PRT; 10 AA.
 AC Q9JIG8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE ORF2.
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ITV-SC232;
 RX MEDLINE=20251008; PubMed=10790123;
 RA Niel C., Saback F.L., Lampe E.;
 RT "Coinfection with Multiple TT Virus Strains Belonging to Different
 RT Genotypes Is a Common Event in Brazilian Healthy Adults.";
 RL J. Clin. Microbiol. 38:1926-1930(2000).
 DR EMBL; AP216453; AAF66889.1; -;
 SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD771B5B9CB CRC64;

Query Match 23.1%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13
 DB 7 PVR 9

RESULT 21
 Q90ZV8 ID Q90ZV8 PRELIMINARY; PRT; 10 AA.
 AC Q90ZV8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Adenylate kinase (Fragment).
 OS Psittacus erithacus (grey parrot).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae; Psittacus.
 NCBI_TaxID=57247;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shapiro L.H.; Dumbacher J.P.;
 RT "Adenylate kinase intron 5: a new nuclear locus for avian
 RT systematics.";
 RL Auk 118:248-255(2001).
 DR EMBL; AF307895; AAK43534.1; -;
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1099 MW; 22847A272731B777 CRC64;

Query Match 23.1%; Score 3; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4
 DB 7 LLY 9

RESULT 22
 Q75595 ID Q75595 PRELIMINARY; PRT; 10 AA.
 AC Q75595;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=T12B;
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RT "The Tat and C2-V3 Envelope Genes in the Molecular Epidemiology of
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U57303; AAB17863.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1182 MW; 22252E34176AB2D7 CRC64;

Query Match      23.1%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 EPV 8
Db      |||
        2 EPV 4

RESULT 23
Q9TOB3
ID Q9TOB3 PRELIMINARY; PRT; 11 AA.
AC Q9TOB3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class I related protein 1 (Fragment).
GN MR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98451457; PubMed=9780177;
RA Riegert P., Wanner V., Bahram S.;
RT "Genomics, isoforms, expression, and phylogeny of the MHC class I-
related MR1 gene.";
RT J. Immunol. 161:4066-4077(1998).
DR EMBL; AF039526; AAD02172.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1235 MW; 5E71A31E29CDD697 CRC64;

Query Match      23.1%; Score 3; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLL 3
Db      |||
        7 FLL 9

RESULT 24
Q9S8Z9
ID Q9S8Z9 PRELIMINARY; PRT; 11 AA.
AC Q9S8Z9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE W1 peptide (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

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OC Psophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytochemistry 31:731-735(1992).
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1120 MW; 8391BABCDD7772D1 CRC64;

Query Match      23.1%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PVL 9
Db      |||
        7 PVL 9

RESULT 25
Q9UMQ9
ID Q9UMQ9 PRELIMINARY; PRT; 12 AA.
AC Q9UMQ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
GN FBP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20237676; PubMed=10773464;
RA Tillmann H., Stein S., Liehr T., Eschrich K.;
RT "Structure and chromosomal localization of the human and mouse muscle
fructose-1,6-bisphosphatase genes.";
RL Gene 247:241-253(2000).
DR EMBL; AJ238490; CAB53366.1; -.
KW Hydroxylase.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1432 MW; 28E901A093072338 CRC64;

Query Match      23.1%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLY 4
Db      |||
        9 LLY 11

RESULT 26
Q8IVIS
ID Q8IVIS PRELIMINARY; PRT; 12 AA.
AC Q8IVIS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pro-alpha-1 collagen type 1 (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83064528; PubMed=6183642;
RA Chu M.L., Myers J.C., Bernard M.P., Ding J.F., Ramirez F.;
RT "Cloning and characterization of five overlapping cDNAs specific for

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RT the human pro alpha 1(I) collagen chain.;"
 RL Nucleic Acids Res. 10:5925-5934 (1982).
 DR EMBL: J00113; AAN86574.1; --
 KW Collagen.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1330 MW; 85A00329C66862CA CRC64;

Query Match 23.1%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
 Db 7 GPV 9

RESULT 27

Q9XNR6 PRELIMINARY; PRT; 12 AA.
 ID Q9XNR6;
 AC Q9XNR6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE NADH:ubiquinone oxidoreductase subunit 3 (Fragment).
 GN NAD3.
 OS Pylaiella littoralis.
 OG Mitochondrion.
 OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
 OC Acinetosporaceae; Pylaiella.
 OC NCBI_TaxID=2885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=toscoff.
 RX MEDLINE=99346148; PubMed=10415341;
 RA Oudot M.P., Kloareg B., Loiseaux-de Goer S.;
 RT "The Mitochondrial Pylaiella littoralis nad11 gene contains only the
 RT N-terminal P68-binding domain.";
 RL Gene 235:131-137 (1999).
 DR EMBL; AF110139; AAD44051.1; --
 KW Mitochondrion; Ubiquinone.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1501 MW; 49750746424B5B13 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
 Db 2 FLL 4

RESULT 28

Q925V7 PRELIMINARY; PRT; 12 AA.
 ID Q925V7;
 AC Q925V7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Alpha 1 type I collagen (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rippe R.A., Umezawa A., Kimball J.P., Breindl M., Brenner D.A.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50767; AAA96053.1; --
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1296 MW; 98E20329C668705A CRC64;

Query Match 23.1%; Score 3; DB 11; Length 12;

Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
 Db 7 GPV 9

RESULT 29

Q90ZL3 PRELIMINARY; PRT; 12 AA.
 ID Q90ZL3;
 AC Q90ZL3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Casein kinase 2 alpha subunit (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilhelm V., Neckelman G., Allende C.C., Allende J.B.;
 RT "The Genomic Structure of Two Protein Kinase CK2 alpha Genes of
 RT Xenopus laevis and Features of the Putative Promoter Region.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY032954; AAK50341.1; --
 KW Kinase.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1320 MW; D005098DFD15A772 CRC64;

Query Match 23.1%; Score 3; DB 13; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
 Db 3 GPV 5

RESULT 30

Q50117 PRELIMINARY; PRT; 13 AA.
 ID Q50117;
 AC Q50117;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE U650w.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Robison K.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U15184; AAA63055.1; --
 SQ SEQUENCE 13 AA; 1503 MW; CAABF1429DED5412 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 BPV 8
 Db 4 BPV 6

RESULT 31

Q53693 PRELIMINARY; PRT; 13 AA.
 AC Q53693;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Leader peptide.
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CU-18;
 RX MEDLINE=96105213; PubMed=8529876;
 RA De Rossi E., Leva R., Gusbetti L., Manachini P.L., Riccardi G.;
 RT "Cloning, sequencing and expression of the ilvNC gene cluster from
 Streptomyces avermitilis.";
 RL Gene 166:127-132(1995).
 DR EMBL; L39268; AAA93097.1; -;
 SQ SEQUENCE 13 AA; 1499 MW; 5E080E40FD4E32C7 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
 |||
 Db 7 VLG 9

RESULT 32

Q49230 PRELIMINARY; PRT; 13 AA.
 AC Q49230;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical 1.6 kDa protein (Fragment).
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G-37;
 RA Peterson S.N.;
 RT "Characterization and analysis of the Mycoplasma genitalium genome.";
 RL Thesis (1992), University of North Carolina Medical School, USA.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G-37;
 RX MEDLINE=94075230; PubMed=8253680;
 RA Peterson S.N., Hu P.C., Bott K.F., Hutchison C.A. III.;
 RT "A survey of the Mycoplasma genitalium genome by using random
 sequencing.";
 RL J. Bacteriol. 175:7918-7930(1993).
 DR EMBL; U01781; AAD10602.1; -;
 KW Hypothetical protein.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1642 MW; EC726B2670F6D2C1 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
 |||
 Db 8 FLL 10

RESULT 33

Q9RFJ7 PRELIMINARY; PRT; 13 AA.
 AC Q9RFJ7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ApXI (Fragment)
 OS Actinobacillus lignieresii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Actinobacillus.
 OX NCBI_TaxID=720;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC49236;
 RX MEDLINE=20293481; PubMed=10931859;
 RA Schaller A., Kuhnert P., de la Puente-Redondo V.A., Nicolet J.,
 RA Frey J.;
 RT "ApX toxins in Pasteurellaceae species from animals.";
 RL Vet. Microbiol. 74:365-376(2000).
 DR EMBL; AF188870; AAF23115.1; -;
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1466 MW; 076D88D59020C974 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
 |||
 Db 10 VLG 12

RESULT 34

O75905 PRELIMINARY; PRT; 13 AA.
 AC O75905; Q9HAQ9;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Prosaposin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98426155; PubMed=9751800;
 RA Sun Y., Jin P., Witte D.P., Grabowski G.A.;
 RT "Isolation and characterization of the human prosaposin promoter.";
 RL Gene 218:37-47(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sun Y., Jin P., Grabowski G.A.;
 RT "Isolation and characterization of the human prosaposin promoter.";
 RL Gene 0:0-0(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21205763; PubMed=11309366;
 RA Hukova H., Cervenkova M., Ledvinov J., Tochackova M., Hrebicek M.,
 RA Poupetova H., Befekadu A., Berna L., Paton B.C., Harzer K., Boeoeer A.,
 RA Smid F., Elleder M.;
 RT "A novel mutation in the coding region of the prosaposin gene leads to
 a complete deficiency of prosaposin and saposins, and is associated
 with a complex sphingolipidosis dominated by lactosylceramide
 accumulation.";
 RL Hum. Mol. Genet. 10:927-940(2001).
 DR EMBL; AF057307; AAC64921.2; -;
 DR EMBL; AF307850; AAG31635.1; -;
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1383 MW; 57585B6C1784D727 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
Db 5 FLL 7

RESULT 35
Q14461 PRELIMINARY; PRT; 13 AA.
AC Q14461; Q14842;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Glycophorin B (Fragment).
GN GYFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90264417; PubMed=1971625;
RA Rearden A., Phan H., Dubnicoff T., Kudo S., Fukuda M.;
RT "Identification of the crossing-over point of a hybrid gene encoding
human glycoporphin variant Sta. Similarity to the crossing-over point in
haptoglobin-related genes.";
RL J. Biol. Chem. 265:9259-9263 (1990).
RN [2]
RP SEQUENCE OF 1-9 FROM N.A.
RA Carttron J.P.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBDJ databases.
RN [3]
RP SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=90005483; PubMed=2792104;
RA Vignal A., Rahuel C., El-Malliki B., London J., Le Vankim C.,
RA Blanchard C.D.;
RT "Molecular analysis of glycoporphin A and B gene structure and
expression in homozygous Miltenberger class V (M1. V) human
erythrocytes.";
RL Eur. J. Biochem. 184:337-344 (1989).
DR EMBL; M33505; AAA53152.1; -.
DR EMBL; X15824; CAA33822.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1565 MW; 466944F750D145B7 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 5
Db 11 LYQ 13

RESULT 36
Q09188 PRELIMINARY; PRT; 13 AA.
AC Q09188;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN COI.
OS Rutilus caudomarginatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulidae; Rivulus.
CX NCBI_TaxID=60318;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=20072928; PubMed=10603257;
RA Murphy W.J., Thomerson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
(Cyprinodontiformes, Aplocheilidae) inferred from mitochondrial DNA
sequences.";
RL Mol. Phylogenet. Evol. 13:289-301 (1999).
DR EMBL; AF002597; AACU1080.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 13 AA; 1705 MW; 404DF35AEFFE79C7 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 5
Db 2 LYQ 4

RESULT 37
Q04RE2 PRELIMINARY; PRT; 13 AA.
AC Q04RE2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ATPase (Fragment).
GN A6.
OS Leptomonas seymouri.
OG Mitochondrion.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leptomonas.
CX NCBI_TaxID=5684;
RN [1]
RP SEQUENCE FROM N.A.
RA Merzlyak E.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBDJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kolesnikov A.A.;
RT "Cyb and A6 gene transcribed and edited in polycistron.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AJ313532; CAC67493.1; -.
KW Mitochondrion.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1626 MW; 471B78F48BDCCB7 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4
Db 10 LLY 12

RESULT 38
O08176 PRELIMINARY; PRT; 13 AA.
ID O08176;
AC O08176;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Balb-c; TISSUE=Liver;

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RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RL of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncaml.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 23.1%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
DB 5 PVL 7

RESULT 39
Q9PXB5
ID Q9PXB5 PRELIMINARY; PRT; 13 AA.
AC Q9PXB5
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE 170 kDa DHBV pre-S region binding protein (Fragment).
OS Duck hepatitis B virus (DHBV).
OC Viruses; Retroviruses; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=12639;
RN [1]
RP SEQUENCE.
RX MEDLINE=96013813; PubMed=7474130;
RA Tong S., Li J., Wands J.R.;
RT "Interaction between duck hepatitis B virus and a 170-kilodalton
RT cellular protein is mediated through a neutralizing epitope of the pre-
RT S region and occurs during viral infection.";
RL J. Virol. 69:7106-7112(1995).
SQ SEQUENCE 13 AA; 1397 MW; DC47BFE014BCD772 CRC64;

Query Match 23.1%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
DB 7 PVL 9

RESULT 40
P82064
ID P82064 PRELIMINARY; PRT; 13 AA.
AC P82064
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE FLETCHERIN.
OS Limnodynastes fletcheri (Barking marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
OX NCBI_TaxID=39403;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW -!- MASS SPECTROMETRY: MW=1197; METHOD=FAB.
Amphibian skin.
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SQ SEQUENCE 13 AA; 1197 MW; 56B5BB1FAEA7C723 CRC64;

Query Match 23.1%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
DB 2 GPV 4

RESULT 41
Q9R5P6
ID Q9R5P6 PRELIMINARY; PRT; 14 AA.
AC Q9R5P6
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Major outer membrane protein 31 kDa subunit, MOMP 31 kDa subunit
DE (Fragment).
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE.
RX MEDLINE=92121130; PubMed=1310095;
RA Hofman P.S., Seyer J.H., Butler C.A.;
RT "Molecular characterization of the 28- and 31-kilodalton subunits of
RT the Legionella pneumophila major outer membrane protein.";
RL J. Bacteriol. 174:908-913(1992).
FT NON TER 1
FT NON TER 14
SQ SEQUENCE 14 AA; 1490 MW; 3541B0FB1AF5F48 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
DB 1 GPV 3

RESULT 42
Q9UHM5
ID Q9UHM5 PRELIMINARY; PRT; 14 AA.
AC Q9UHM5
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Islet cell autoantigen ICA69 (Fragment).
GN ICA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Friday R.P., Trucco M., Pietropaolo M.;
RT "Refined genomic organization of the diabetes autoantigen ICA69 gene
RT locus.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF147807; AAF20021.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1656 MW; 1AEB6ACD19E2F9CB CRC64;

Query Match 23.1%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 5
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Db          6 LYQ 8

RESULT 43
Q9MRP6
ID Q9MRP6 PRELIMINARY; PRT; 14 AA.
AC Q9MRP6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE PSI 9 kDa protein (Fragment).
GN PSAC.
OS
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=97361;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;
RT "Conservation of the start codon by editing in ndhD-encoded
RT transcribed is not restricted to dicotyledonous plants.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ278355; CAB96127.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1589 MW; 8F14E36A13B7D911 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
Db 2 LGP 4

RESULT 44
Q8V1H7
ID Q8V1H7 PRELIMINARY; PRT; 14 AA.
AC Q8V1H7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Truncated HbsAg.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FH10;
RA Wen Y.M., Liu F., Ma Z.M.;
RT "Structural and functional analysis of hepatitis B virus genomes in
RT fulminant hepatitis B patients.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461362; AAL66336.1; -.
SQ SEQUENCE 14 AA; 1427 MW; 2F487846CB391E28 CRC64;

Query Match 23.1%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
Db 9 LGP 11

RESULT 45
Q9JP39
ID Q9JP39 PRELIMINARY; PRT; 15 AA.
AC Q9JP39;

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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE HrpK (Fragment).
GN HRPK.
OS Pseudomonas syringae (pv. syringae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=321;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=61;
RX MEDLINE=97348579; PubMed=9204563;
RA Alfano J.R., Kim H.S., Delaney T.P., Collmer A.;
RT "Evidence that the Pseudomonas syringae pv. syringae hrp-linked hrpA
RT gene encodes an Avr-like protein that acts in an hrp-dependent manner
RT within tobacco cells.";
RL Mol. Plant Microbe Interact. 10:580-588(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=61;
RX MEDLINE=20243785; PubMed=10781092;
RA Alfano J.R., Charkowski A.O., Deng W.L., Badel J.L.,
RA Petnicki-Ocwieja T., van Dijk K., Collmer A.;
RT "The Pseudomonas syringae Hrp pathogenicity island has a tripartite
RT mosaic structure composed of a cluster of type III secretion genes
RT bounded by exchangeable effector and conserved effector loci that
RT contribute to parasitic fitness and pathogenicity in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4856-4861(2000).
DR EMBL; AF232003; AAF71482.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1696 MW; C0E7FAC1E44EAB20 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
Db 4 PVL 6

RESULT 46
Q9RS98
ID Q9RS98 PRELIMINARY; PRT; 15 AA.
AC Q9RS98;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE DNA topoisomerase I (Fragment).
OS Micrococcus luteus (Micrococcus lysodeikticus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Micrococcaceae; Micrococcus.
OX NCBI_TaxID=1270;
RN [1]
RP SEQUENCE.
RX MEDLINE=93249439; PubMed=8387285;
RA Anderluzzi D., Pedrini A.M.;
RT "Structural similarities between M. luteus and E. coli DNA
RT topoisomerase I.";
RL Biochem. Biophys. Res. Commun. 192:657-664(1993).
SQ SEQUENCE 15 AA; 1508 MW; D36D28F43AA6E2F9 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
Db 5 LGP 7

RESULT 47

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Q9UCC2
ID Q9UCC2 PRELIMINARY; PRT; 15 AA.
AC Q9UCC2;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE 35 kDa heparin-RELEASABLE protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94059921; PubMed=8241100;
RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the
RT cytokines midkine and pleiotrophin, in human postheparin plasma.";
RL Arterioscler. Thromb. 13:1798-1805(1993).
SQ SEQUENCE 15 AA; 1454 MW; 0585FEF4FE8F6265 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
DB 4 GPV 6

RESULT 48
QSTRN9
ID Q9TRN9 PRELIMINARY; PRT; 15 AA.
AC Q9TRN9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE LOW MR zona pellucida binding protein (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92378826; PubMed=1510840;
RA Parry R.V., Barker P.J., Jones R.;
RT "Characterization of low Mr zona pellucida binding proteins from boar
RT spermatozoa and seminal plasma.";
RL Mol. Reprod. Dev. 33:1108-1115(1992).
SQ SEQUENCE 15 AA; 1574 MW; C8C0FAB43F233D6C CRC64;

Query Match 23.1%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPV 8
DB 1 EPV 3

RESULT 49
Q9TH04
ID Q9TH04 PRELIMINARY; PRT; 15 AA.
AC Q9TH04;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
GN ND6.
OS Grus americana (whooping crane).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.
OX NCBI_TaxID=9117;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LMS B3394;
RA Glenn T.C., Stephan W., Braun M.J.;
RT "Effects of a Population Bottleneck on Whooping Crane Mitochondrial
RT DNA Variation.";
RL Conserv. Biol. 0:0-0(1999).
DR EMBL; AF112373; AAD23994.1; -.
KW Mitochondrion.
FT NON TER 15
SQ SEQUENCE 15 AA; 1759 MW; A7F711A65B9F934F CRC64;

Query Match 23.1%; Score 3; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
DB 13 VLG 15

RESULT 50
P92818
ID P92818 PRELIMINARY; PRT; 15 AA.
AC P92818;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NADH dehydrogenase subunit-4L (Fragment).
OS Paralichthys olivaceus (Flounder).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Saitoh K.;
RT "Characterization of cloned mitochondrial fragments from the Japanese
RT flounder.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB000674; BAA20924.1; -.
KW Mitochondrion.
FT NON TER 15
SQ SEQUENCE 15 AA; 1613 MW; D1BAA2018C95FE80 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
DB 12 FLL 14

RESULT 51
Q9XLJ8
ID Q9XLJ8 PRELIMINARY; PRT; 15 AA.
AC Q9XLJ8;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
GN ND6.
OS Grus leucogeranus (Siberian crane).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.
OX NCBI_TaxID=40819;
RN [1]
RP SEQUENCE FROM N.A.

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RA Glenn T.C., Stephan W., Braun M.J.;
 RT "Effects of a Population Bottleneck on Whooping Crane Mitochondrial
 DNA Variation."
 RL Conserv. Biol. 0:0-0(1999).
 DR EMBL; AF112371; AAD23992.1; --
 KW Mitochondrion.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1807 MW; A7FFB3A65B8A734F CRC64;

Query Match 23.1%; Score 3; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
 Db 13 VLG 15

RESULT 52

Q9TH03
 ID Q9TH03 PRELIMINARY; PRT; 15 AA.
 AC Q9TH03;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE NADH dehydrogenase subunit 6 (Fragment).
 GN N06.
 OS Grus paradisea (Blue crane).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.
 OX NCBI_TaxID=40825;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Glenn T.C., Stephan W., Braun M.J.;
 RT "Effects of a Population Bottleneck on Whooping Crane Mitochondrial
 DNA Variation."
 RL Conserv. Biol. 0:0-0(1999).
 DR EMBL; AF112372; AAD23993.1; --
 KW Mitochondrion.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1807 MW; A7FFB3A65B8A734F CRC64;

Query Match 23.1%; Score 3; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
 Db 13 VLG 15

RESULT 53

Q9SAP4
 ID Q9SAP4 PRELIMINARY; PRT; 15 AA.
 AC Q9SAP4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Serine proteinase inhibitor (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Irish Cobbler;
 RA Yanagishi K., Kikuta Y.;
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X70376; CAA49837.1; --
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1667 MW; 8093D41B4CA0D1EC CRC64;

Query Match 23.1%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
 Db 9 FLL 11

RESULT 54

P82431
 ID P82431 PRELIMINARY; PRT; 15 AA.
 AC P82431;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE 100 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 tobacco culture."
 RL Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1694 MW; 5F3B8D2E48187626 CRC64;

Query Match 23.1%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EPV 8
 Db 1 EPV 3

RESULT 55

Q9QV34
 ID Q9QV34 PRELIMINARY; PRT; 15 AA.
 AC Q9QV34;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE CHOLIC acid transport protein P50 (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94183413; PubMed=8136027;
 RA Hoffmann A., Mullner S., Ziegler K., Fasold H.;
 RT "Purification and partial sequence of proteins involved in the cholic
 acid transport into rat liver hepatocytes."
 RL J. Protein Chem. 12:765-769(1993).
 SQ SEQUENCE 15 AA; 1597 MW; D719DFB7C75AC0B CRC64;

Query Match 23.1%; Score 3; DB 11; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVL 9
 Db 11

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Db          3 PVL 5

RESULT 56
Q44610
ID Q44610 PRELIMINARY; PRT; 16 AA.
AC Q44610;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Shikimate dehydrogenase (Fragment).
GN AROB.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
ON NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95212914; PubMed=7535281;
RA Roubaksh D., Baumann P.;
RT "Characterization of a putative 23S-5S rRNA operon of Buchnera
RT aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
RT gene.";
RL Gene 155:107-112(1995).
DR EMBL; U10499; AAA79128.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1891 MW; 72A8175598D30DF1 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPV 8
Db 13 EPV 15

RESULT 57
Q9R4X4
ID Q9R4X4 PRELIMINARY; PRT; 16 AA.
AC Q9R4X4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2000 (TrEMBLrel. 13, Last sequence update)
DE Exotoxin A (Fragment).
DE Pseudomonas aeruginosa.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Bacteroidetes; Pseudomonas.
ON NCBI_TaxID=287;
RN [1]
RP SEQUENCE.
RX MEDLINE=94356232; PubMed=8075811;
RA Wolz C., Lehmann R., Vasil M.L., Bischoff R., Doring G.;
RT "A new extracellular protein of Pseudomonas aeruginosa PA103 regulated
RT by regA.";
RL Microbiology 140:1755-1761(1994).
SQ SEQUENCE 16 AA; 1628 MW; D6C94C87B6823274 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
Db 13 LGP 15

RESULT 58
P82597
ID P82597 PRELIMINARY; PRT; 16 AA.
AC P82597;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

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DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Thermotable monoacylglycerol lipase (MGLP) (24 kDa) (EC 3.1.1.23)
DE (Fragment).
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxID=1409;
RN [1]
RP SEQUENCE.
RX STRAIN=H-257;
RX MEDLINE=20198254; PubMed=10731713;
RA Imamura S., Kitaura S.;
RT "Purification and characterization of a monoacylglycerol lipase from
RT the moderately thermophilic Bacillus sp. H-257.";
RL J. Biochem. 127:419-425(2000).
CC -|- FUNCTION: HYDROLYSES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY
CC OCCURRING WITH 1-MONOLAURYLGLYCEROL.
CC -|- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY
CC INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.
CC -|- SUBUNIT: MONOMER.
CC -|- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM
CC TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.
CC -|- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS
CC OTHER BACTERIAL LIPASES.
KW Hydrolase.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
Db 5 PVL 7

RESULT 59
Q9NPQ7
ID Q9NPQ7 PRELIMINARY; PRT; 16 AA.
AC Q9NPQ7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AK001912 hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
RA Lehrach H., Poustka A., Lundeberg J.;
RT "The European IMAGE consortium for integrated Molecular analysis of
RT human gene transcripts.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL389982; CAB97537.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1484 MW; 97C92837C881A371 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
Db 14 GPV 16

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RESULT 60

Q9TWN2 ID Q9TWN2 PRELIMINARY; PRT; 16 AA.
 AC Q9TWN2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Sialidase L (Fragment).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Aynchobdellida; Hirudiniiformes; Hirudinidae; Macrobdella.
 OX NCBI_TaxID=6405;
 RN [1]
 RP MEDLINE=94308136; PubMed=8034634;
 RX Chou M.Y., Li S.C., Kiso M., Hasegawa A., Li Y.T.;
 RA "Purification and characterization of sialidase L, a NeuAc alpha 2--
 RT >3Gal-specific sialidase."; Indels 0; Gaps 0;
 RL J. Biol. Chem. 269:11821-11826(1994).
 SQ SEQUENCE 16 AA; 1910 MW; 0822879C79EC6EE0 CRC64;

Query Match 23.1%; Score 3; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LYQ 5
 Db 7 LYQ 9

RESULT 61

O62810 ID O62810 PRELIMINARY; PRT; 16 AA.
 AC O62810;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 13, Last annotation update)
 DE Pregnancy-associated glycoprotein (Fragment).
 GN PAG.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Green J.A., Xie S., Szafranska B., Gan X., Newman A.G., McDowell K.,
 RA Roberts R.M.;
 RT "Identification of a new aspartic proteinase expressed by the outer
 RT chorionic cell layer of the equine placenta."
 RL Biol. Reprod. 60:1069-1077(1999).
 DR EMBL; AF061198; AAC15768.1; -;
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1830 MW; 733B85DC7AAC213F CRC64;

Query Match 23.1%; Score 3; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLQ 10
 Db 6 VLQ 8

RESULT 62

Q9TR97 ID Q9TR97 PRELIMINARY; PRT; 16 AA.
 AC Q9TR97;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Lactate transporter (Fragment).
 OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=95071287; PubMed=7980443;
 RA Poole R.C., Halestrap A.P.;
 RT "N-terminal protein sequence analysis of the rabbit erythrocyte
 RT lactate transporter suggests identity with the cloned monocarboxylate
 RT transport protein MCT1."
 RL Biochem. J. 303:755-759(1994).
 SQ SEQUENCE 16 AA; 1438 MW; 2AB33D7BAEAFB0D CRC64;

Query Match 23.1%; Score 3; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12
 Db 6 GPV 8

RESULT 63

P92070 ID P92070 PRELIMINARY; PRT; 16 AA.
 AC P92070;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NADH dehydrogenase subunit 6 (Fragment).
 OS Euhadra herklotsi.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Helicoidea; Bradybaenidae; Euhadra.
 OX NCBI_TaxID=58912;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hepatopancreas;
 RA Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
 RA Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
 RA Watanabe K., Thomas R.H.;
 RT "Evolution of pulmonate gastropod mitochondrial genomes: comparisons
 RT of complete gene organization of Euhadra, Cepaea and Albinaria and
 RT implications of unusual tRNA secondary structures."
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z71694; CAA96364.1; -;
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 16 AA; 1836 MW; 258908495BFBCAE CRC64;

Query Match 23.1%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
 Db 10 FLL 12

RESULT 64

Q9TQ06 ID Q9TQ06 PRELIMINARY; PRT; 16 AA.
 AC Q9TQ06;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Cytochrome-C reductase 11 kDa subunit (EC 1.10.2.2) (Fragment).
 OS Solanum tuberosum (Potato).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;


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RN SEQUENCE.
RP MEDLINE=94198758; PubMed=7764624;
RA Braun H.P., Kruft V., Schmitz U.K.;
RL Planta 193:99-106(1994).
SQ SEQUENCE 16 AA; 1904 MW; AFC237AE7549E2B5 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
DB 8 VLG 10

RESULT 65
Q8CIS2 PRELIMINARY; PRT; 16 AA.
AC Q8CIS2;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Plasminogen (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RX PubMed=12149246;
RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
RA Parner R.J., Miles L.A.;
RT "Localization of Regulatory Elements Mediating Constitutive and
RT Cytokine-stimulated plasminogen Gene Expression.";
RL J. Biol. Chem. 277:38579-38588(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RA Garcia Bannach F., Fowler B.J., Gutierrez A., Bugge T.H., Degen J.L.,
RA Parner R.J., Miles L.A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY134430; AAN15805.1; -.
FT NON TER 16
SQ SEQUENCE 16 AA; 1922 MW; 647558FC6EDB15CC CRC64;

Query Match 23.1%; Score 3; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
DB 10 FLL 12

RESULT 66
Q5091 PRELIMINARY; PRT; 17 AA.
AC Q5091;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Beta-lactamase (Fragment).
GN AMPC.
OS Shigella sonnei.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=624;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=OS10;
RX MEDLINE=84170267; PubMed=6369321;

RA Olsson O., Bergstrom S., Lindberg F.P., Normark S.;
RT "ampC beta-lactamase hyperproduction in Escherichia coli: Natural
RT ampicillin resistance generated by horizontal chromosomal DNA transfer
RT from Shigella.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:7556-7560(1983).
DR EMBL; K01234; AAA26514.1; -.
DR InterPro; IPR001586; Beta_lactamase_C.
DR PROSITE; PS00336; BETA_LACTAMASE_C_1.
FT NON TER 17
SQ SEQUENCE 17 AA; 1756 MW; 7FAC3A40A4809623 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
DB 15 VLG 17

RESULT 67
Q9EUP4 PRELIMINARY; PRT; 17 AA.
AC Q9EUP4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Cell division associated protein (Fragment).
GN DIVIVA.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN-KT8;
RA Spada S., Gibert Y., Pembroke J.T., Wall J.G.;
RT "Cloning and characterisation of the ylmB homologue of Thermus
RT thermophilus.";
RL DNA Seq. 11:5007-5014(2001).
DR EMBL; AJ297409; CAC21427.1; -.
FT NON TER 17
SQ SEQUENCE 17 AA; 2084 MW; 0C642E1D509D87E3 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQE 6
DB 10 YQE 12

RESULT 68
Q9R560 PRELIMINARY; PRT; 17 AA.
AC Q9R560;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Menaguiol oxidase (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]_
RP SEQUENCE.
RX MEDLINE=93356600; PubMed=8394685;
RA Lemma E., Schagger H., Kroger A.;
RT "The menaguiol oxidase of Bacillus subtilis W23.";
RL Arch. Microbiol. 159:574-578(1993).
SQ SEQUENCE 17 AA; 1750 MW; 87A251230A5831C3 CRC64;

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Query Match		23.1%; Score 3; DB 2; Length 17;
Best Local Similarity		100.0%; Pred. No. 1.3e+04;
Matches		3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 GPV 12	
Db	11 GPV 13	
	11 GPV 13	
RESULT 69		
Q00074	PRELIMINARY; PRT; 17 AA.	
ID	Q00074	
AC	Q00074;	
DT	01-NOV-1996 (TrEMBLrel. 01, Created)	
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	
DE	Extracellular acid protease (Fragment).	
GN	PEPA.	
OS	Aspergillus niger.	
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;	
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.	
OX	NCBI_TaxID=5061;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=N400;	
RX	MEDLINE=95163121; PubMed=7532112;	
RA	Jarai G., Buxton F.;	
RT	"Nitrogen, carbon, and pH regulation of extracellular acidic proteases	
RT	of Aspergillus niger.";	
RL	Curr. Genet. 26:238-244(1994).	
DR	EMBL: U03507; AAC48920.1; --	
DR	MEROPS; A01.016; --	
KW	Protease.	
FT	NON TER	
SQ	SEQUENCE 17 AA; 1694 MW; FF01D0BEC9FEAE0B CRC64;	
Query Match		
Best Local Similarity		
Matches		
QY		
Db		
RESULT 70		
Q9UJH1	PRELIMINARY; PRT; 17 AA.	
ID	Q9UJH1	
AC	Q9UJH1;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	DJ436M11.2 (Retinosis (X-linked, juvenile) 1 (XLRSL1))	
DE	(Fragment).	
GN	RS1.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Grafham D.;	
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; Z94056; CAB40073.1; --	
FT	NON TER	
SQ	SEQUENCE 17 AA; 2029 MW; 8100E1B78C52C7FB CRC64;	
Query Match		
Best Local Similarity		
Matches		
QY		
Db		
RESULT 71		
Q9UPK4	PRELIMINARY; PRT; 17 AA.	
ID	Q9UPK4	
AC	Q9UPK4;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last annotation update)	
DE	UCRY HUMAN (Fragment).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Lamerdin J.B., McCready P.M., Skowronski E., Adamson A.W.,	
RA	Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,	
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,	
RA	Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,	
RA	Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,	
RA	Coeffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,	
RA	Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,	
RA	Kobayashi A., Olsen A.S., Carrano A.V.;	
RT	"Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a	
RT	serine protease gene cluster.";	
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AC005321; AAC27374.1; --	
FT	NON TER	
SQ	SEQUENCE 17 AA; 2166 MW; B73A34E7EDB2DE5D CRC64;	
Query Match		
Best Local Similarity		
Matches		
QY		
Db		
RESULT 72		
Q9UCL9	PRELIMINARY; PRT; 17 AA.	
ID	Q9UCL9	
AC	Q9UCL9;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)	
DE	Proteoglycan 80 kDa polypeptide (Fragment).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE	
RX	MEDLINE=93054750; PubMed=1429726;	
RA	Perides G., Rahemulla F., Lane W.S., Asher R.A., Bignami A.;	
RT	"Isolation of a large aggregating proteoglycan from human brain.";	
RL	J. Biol. Chem. 267:23883-23887(1992).	
SQ	SEQUENCE 17 AA; 1771 MW; 1BDA8561B2F71614 CRC64;	
Query Match		
Best Local Similarity		
Matches		
QY		
Db		
RESULT 73		
Q9UC43	PRELIMINARY; PRT; 17 AA.	
ID	Q9UC43	

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AC Q9UC43;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Interferon-alpha-induced protein (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=96132854; PubMed=8557639;
RA Rich S.A.; Bose M.; Tempest P.; Rudofsky U.H.;
RT "Purification, microsequencing, and immunolocalization of p36, a new
RT interferon-alpha-induced protein that is associated with human lupus
RT inclusions."
RL J. Biol. Chem. 271:1118-1126(1996).
SQ SEQUENCE 17 AA; 2027 MW; 762BE7300049ACEC CRC64;

Query Match      23.1%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
DB 8 PVL 10

RESULT 74
Q17205
ID Q17205 PRELIMINARY; PRT; 17 AA.
AC Q17205;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE A.L6 protein (Fragment).
GN A.L6.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=703;
RX MEDLINE=90040707; PubMed=2810362;
RA Spoerel N.A.; Nguyen H.T.; Riekhush T.H.; Kafatos F.C.;
RT "Gene Evolution and Regulation in the Chorion Complex of Bombyx mori:
RT Hybridization and Sequence Analysis of Multiple Developmentally Middle
RT A/B Chorion Gene Pairs."
RL J. Mol. Biol. 209:1-19(1989).
DR EMBL; X15562; CAA33575.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1877 MW; 577145043395539D CRC64;

Query Match      23.1%; Score 3; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
DB 6 FLL 8

RESULT 75
Q26832
ID Q26832 PRELIMINARY; PRT; 17 AA.
AC Q26832;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Iatad 1.2) variant surface glycoprotein ELC gene (Fragment).
OS Trypanosoma brucei.

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OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278091; PubMed=2942540;
RA Brown K.H.; Brentano S.T.; Donelson J.E.;
RT "Mung bean nuclease cleaves preferentially at the boundaries of
RT variant surface glycoprotein gene transpositions in trypanosome DNA."
RL J. Biol. Chem. 261:10352-10358(1986).
DR EMBL; M14020; AAA30305.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 1973 MW; 9E00FBD261B8FFBF CRC64;

Query Match      23.1%; Score 3; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
DB 14 FLL 16

Search completed: November 25, 2003, 19:34:14
Job time : 25.4128 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 33.1802 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLLYQEPVLGPVR 13

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq 13Jun03.*

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	13	22	Colostrinin derive
2	13	100.0	13	22	Colostrinin peptid
3	13	100.0	13	22	Colostrinin peptid
4	13	100.0	13	22	Ewe colostrinin pe
5	13	100.0	13	23	Colostrinin consti
6	13	100.0	13	23	Colostrinin consti
7	13	100.0	13	23	Neural cell regula
8	9	69.2	15	23	Antiviral composi
9	9	69.2	16	23	Antiviral composi

10	8	61.5	12	23	AAU83299	Antiviral composi
11	8	61.5	13	23	AAU83302	Antiviral composi
12	8	61.5	13	23	AAU83305	Antiviral composi
13	8	61.5	14	23	AAU83316	Antiviral composi
14	7	53.8	7	22	AAE07190	Colostrinin peptid
15	7	53.8	8	22	AAE07200	Modified colostrin
16	7	53.8	8	23	AAU83286	Antiviral composi
17	7	53.8	13	23	AAU83309	Antiviral composi
18	7	53.8	16	23	AAU83336	Antiviral composi
19	7	53.8	17	15	AAE58340	Hypotensive polyde
20	7	53.8	19	15	AAE58341	Hypotensive polyde
21	7	53.8	19	20	AAE17233	Casein antimicrobi
22	6	46.2	7	22	AAE72273	Colostrinin derive
23	6	46.2	7	22	AAE72526	Colostrinin peptid
24	6	46.2	7	22	AAE72558	Colostrinin peptid
25	6	46.2	7	22	AAE59337	Ewe colostrinin pe
26	6	46.2	7	23	AAE20255	Colostrinin consti
27	6	46.2	7	23	AAE51062	Colostrinin consti
28	6	46.2	7	23	AAO14604	Neural cell regula
29	6	46.2	9	22	AAE59356	Ewe colostrinin pe
30	6	46.2	11	23	AAU83297	Antiviral composi
31	6	46.2	12	23	AAU83300	Antiviral composi
32	6	46.2	14	23	AAU83325	Antiviral composi
33	6	46.2	19	23	AAU83341	Antiviral composi
34	5	38.5	9	23	AAU83290	Antiviral composi
35	5	38.5	13	18	AAW43973	Human myelin oligo
36	5	38.5	13	23	AAU83314	Antiviral composi
37	5	38.5	14	23	AAU83320	Antiviral composi
38	5	38.5	15	18	AAW37539	Human myelin oligo
39	5	38.5	15	23	AAU99584	Human zinc finger
40	5	38.5	15	23	AAU83332	Antiviral composi
41	5	38.5	16	23	AAU83339	Antiviral composi
42	5	38.5	18	20	AAE33019	Human serine prote
43	5	38.5	20	16	AAE80294	Trehalose releasin
44	5	38.5	20	16	AAE80296	Trehalose releasin
45	5	38.5	20	18	AAW37541	Human myelin oligo
46	4	30.8	5	14	AAE65510	Endothelin antagon
47	4	30.8	6	19	AAW75347	Hexapeptide #2 bin
48	4	30.8	6	19	AAW75279	Hexapeptide #2 bin
49	4	30.8	6	22	AAU08616	Human olfactory re
50	4	30.8	6	22	AAE63026	Amino acid sequenc
51	4	30.8	6	22	AAE63034	Amino acid sequenc
52	4	30.8	6	22	AAE63043	Amino acid sequenc
53	4	30.8	6	22	AAE63065	Amino acid sequenc
54	4	30.8	6	22	AAE63106	Amino acid sequenc
55	4	30.8	6	22	AAE63108	Amino acid sequenc
56	4	30.8	6	22	AAE87132	Human TANGO 393 cy
57	4	30.8	6	22	AAE87133	Mouse TANGO 393 cy
58	4	30.8	6	23	AAO18910	Human butyrylcholi
59	4	30.8	6	24	ABU67261	Olfactory receptor
60	4	30.8	6	24	ABU58261	Peptide binding to
61	4	30.8	6	24	ABU58271	Peptide binding to
62	4	30.8	6	24	ABU58273	Peptide binding to
63	4	30.8	6	24	ABU58291	Poliovirus-binding
64	4	30.8	6	24	ABU58293	Poliovirus-binding
65	4	30.8	6	24	ABU58312	Peptide binding to
66	4	30.8	7	17	AAW04280	Milk derived non-a
67	4	30.8	7	18	AAW30407	HRE-1 affinity pep
68	4	30.8	7	23	ABG60365	Selective targetin
69	4	30.8	7	23	ABG34932	Human bone marrow
70	4	30.8	7	24	ABJ19880	Human bone marrow
71	4	30.8	7	24	ABJ19880	Human bone marrow
72	4	30.8	8	15	AAE58333	Hypotensive polyde
73	4	30.8	8	17	AAE84066	Retinal pigment ep
74	4	30.8	8	22	ABP13191	HIV A02 super moti
75	4	30.8	8	22	ABP14660	HIV A03 super moti
76	4	30.8	8	22	ABP19350	HIV B62 super moti
77	4	30.8	8	22	ABP21575	HIV A03 motif pol
78	4	30.8	8	22	ABP23480	HIV A11 motif pol
79	4	30.8	8	23	AAW49592	Human beta-defensi
80	4	30.8	8	24	ABJ20035	MHC binding peptid
81	4	30.8	8	24	ABJ20044	MHC binding peptid
82	4	30.8	9	15	AAE38067	Hepatitis B virus-

83 4 30.8 9 15 AAY38223 HIV-derived HLA-bi
 84 4 30.8 9 15 AAY38224 HIV-derived HLA-bi
 85 4 30.8 9 15 AAR73798 Antigen fragment 1
 86 4 30.8 9 15 AAR62873 Metal binding CDR3
 87 4 30.8 9 17 AAR98049 Pseudostralin E,
 88 4 30.8 9 19 AAW67187 aPL immunoreactive
 89 4 30.8 9 19 AAW67194 aPL immunoreactive
 90 4 30.8 9 19 AAW67198 aPL immunoreactive
 91 4 30.8 9 19 AAW54412 MHC Class I peptid
 92 4 30.8 9 20 AAY53442 HIV-1 RT protein (I
 93 4 30.8 9 20 AAY53442 Immunogenic peptid
 94 4 30.8 9 20 AAY45635 Immunogenic peptid
 95 4 30.8 9 20 AAY45793 Immunogenic peptid
 96 4 30.8 9 20 AAY45794 Immunogenic peptid
 97 4 30.8 9 20 AAY45795 Immunogenic peptid
 98 4 30.8 9 20 AAY46637 Immunogenic peptid
 99 4 30.8 9 20 AAY46638 Immunogenic peptid
 100 4 30.8 9 20 AAY40291 Amino acid sequenc

ALIGNMENTS

RESULT 1
 AAB72277 standard; peptide; 13 AA.
 AC AAB72277;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Colostrinin derived cytokine inducing peptide SEQ ID 32.
 XX
 KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX
 OS Synthetic.
 XX
 PN WO200111937-A2.
 XX
 XX 22-FEB-2001.
 PD
 XX 17-AUG-2000; 2000WO-US22818.
 PF
 XX 17-AUG-1999; 99US-0149311.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 PI WPI; 2001-202804/20.
 DR
 XX Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX SQ Sequence 13 AA;
 Query Match 100.0%; Score 13; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLLYQEPVLGPVR 13
 Db 1 FLLYQEPVLGPVR 13
 |||||
 RESULT 2
 AAB72530 standard; Peptide; 13 AA.
 ID AAB72530
 XX
 AC AAB72530;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #31.
 KW Dermatalogical; oxidative stress regulator; colostrinin.
 XX
 OS Unidentified.
 XX
 PN WO200112650-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22665.
 PR 17-AUG-1999; 99US-0149310.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX WPI; 2001-218342/22.
 DR
 XX Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX
 PS Claim 6; Page 26; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.
 XX
 XX SQ Sequence 13 AA;
 Query Match 100.0%; Score 13; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLLYQEPVLGPVR 13
 Db 1 FLLYQEPVLGPVR 13
 |||||
 RESULT 3
 AAB72562 standard; Peptide; 13 AA.
 ID AAB72562
 XX
 AC AAB72562;
 XX
 DT 09-MAY-2001 (first entry)
 XX

DE Colostrinin peptide #31.
XX
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
OS Unidentified.
XX
XX WO200112651-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22774.
XX
XX 17-AUG-1999; 99US-0149633.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Boldogh I;
XX
XX WPI; 2001-226545/23.
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX
XX Claim 6; Page 22; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX Sequence 13 AA;
SQ
Query Match 100.0%; Score 13; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQEPVLGPVR 13
Db 1 FLLYQEPVLGPVR 13
RESULT 4
AAB59338
ID AAB59338 standard; Peptide; 13 AA.
XX
XX AAB59338;
XX
XX 21-MAR-2001 (first entry)
XX
XX Ewe colostrinin peptide fragment C-13.
DE
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX Ovis sp.
XX
XX WO200075173-A2.
XX
XX 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-GB02128.
XX
XX 02-JUN-1999; 99GB-0012852.
XX
XX (REGE-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA;
XX
XX WPI; 2001-071058/08.
XX
XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
XX
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques.
XX
XX Sequence 13 AA;
SQ
Query Match 100.0%; Score 13; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQEPVLGPVR 13
Db 1 FLLYQEPVLGPVR 13
RESULT 5
AAB20259
ID AAB20259 standard; peptide; 13 AA.
XX
XX AAE20259;
XX
XX 18-JUN-2002 (first entry)
XX
XX Colostrinin constituent peptide #31.
DE
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnuary.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 13
FT /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 26; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 13 AA;

Query Match 100.0%; Score 13; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQEPVLGPVR 13
 |||||

Db 1 FLLYQEPVLGPVR 13
 |||||

RESULT 6

AA051065
 ID AA051065 standard; Peptide; 13 AA.

XX
 AC AA051065;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide (casein amino acids 203-214).

XX Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Modified-site 13

FT /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 203-214. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

SQ Sequence 13 AA;

Query Match 100.0%; Score 13; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQEPVLGPVR 13
 |||||

Db 1 FLLYQEPVLGPVR 13
 |||||

RESULT 7

AA014608
 ID AA014608 standard; peptide; 13 AA.

XX
 AC AA014608;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 31.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 13

FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

PS Claim 7; Page 22; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in

```
CC the method of the invention.
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 13; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQEPVLGPVR 13
DB 1 FLLYQEPVLGPVR 13
RESULT 8
AAU83327
ID AAU83327 standard; Peptide; 15 AA.
XX
AC AAU83327;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #45.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
PN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
PF 17-JAN-2001; 2001US-0764017.
XX
PR 22-OCT-1996; 96US-0735236.
XX
PR 25-JUN-1999; 99US-0344095.
XX
PA (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI Friedland B, Hirschman SZ, Taraporewala IB;
XX
DR WPI; 2002-163727/21.
XX
PT New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
PS Disclosure; Page 8; 37pp; English.
XX
CC The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
SQ Sequence 16 AA;
Query Match 69.2%; Score 9; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQEPVL 9
DB 8 FLLYQEPVL 16
RESULT 10
AAU83299
ID AAU83299 standard; Peptide; 12 AA.
XX
AC AAU83299;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #17.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
PN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
```

```
CC the method of the invention.
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 13; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQEPVLGPVR 13
DB 1 FLLYQEPVLGPVR 13
RESULT 8
AAU83327
ID AAU83327 standard; Peptide; 15 AA.
XX
AC AAU83327;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #45.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
PN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
PF 17-JAN-2001; 2001US-0764017.
XX
PR 22-OCT-1996; 96US-0735236.
XX
PR 25-JUN-1999; 99US-0344095.
XX
PA (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI Friedland B, Hirschman SZ, Taraporewala IB;
XX
DR WPI; 2002-163727/21.
XX
PT New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
PS Disclosure; Page 8; 37pp; English.
XX
CC The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
SQ Sequence 15 AA;
Query Match 69.2%; Score 9; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQEPVL 9
DB 7 FLLYQEPVL 15
RESULT 9
AAU83335
ID AAU83335 standard; Peptide; 16 AA.
XX
```


PF 17-JAN-2001; 2001US-0764017.
 XX 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX (ADVI-) ADVANCED VIRAL RES CORP.
 XX Friedland B, Hirschman SZ, Taraporewala IB;
 XX WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 12 AA;
 Query Match 61.5%; Score 8; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLLYQEPV 8
 Db 5 FLLYQEPV 12
 |||||
 RESULT 11
 AAU83302
 ID AAU83302 standard; Peptide; 13 AA.
 XX
 AC AAU83302;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #20.
 XX
 DE Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 XX (ADVI-) ADVANCED VIRAL RES CORP.
 XX Friedland B, Hirschman SZ, Taraporewala IB;
 XX WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 7; 37pp; English.

CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 13 AA;
 Query Match 61.5%; Score 8; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLYQEPV 8
 Db 6 FLLYQEPV 13
 |||||
 RESULT 12
 AAU83305
 ID AAU83305 standard; Peptide; 13 AA.
 XX
 AC AAU83305;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #23.
 XX
 DE Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 XX (ADVI-) ADVANCED VIRAL RES CORP.
 XX Friedland B, Hirschman SZ, Taraporewala IB;
 XX WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 13 AA;
 Query Match 61.5%; Score 8; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYQEPV 8
 Db 6 FLYQEPV 13

RESULT 13
 AAU83316
 ID AAU83316 standard; Peptide; 14 AA.
 XX AC AAU83316;
 XX DT 23-APR-2002 (first entry)
 XX DE Antiviral composition peptide-A, fragment #34.
 XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX OS Synthetic.
 XX PN US2002004579-A1.
 XX PD 10-JAN-2002.
 XX PF 17-JAN-2001; 2001US-0764017.
 XX PR 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX PT New peptides compositions, useful for treating viral infections and
 XX PT stimulating the immune system -
 XX PS Disclosure; Page 8; 37pp; English.
 XX CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

XX SQ Sequence 14 AA;
 Query Match 61.5%; Score 8; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYQEPV 8
 Db 7 FLYQEPV 14

RESULT 14
 AAU83316
 ID AAU83316 standard; Peptide; 14 AA.
 XX AC AAU83316;
 XX DT 06-NOV-2001 (first entry)
 XX DE Colostrinin peptide 6.
 XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral.
 XX Unidentified.
 XX WO200155199-A1.
 XX PN 02-AUG-2001.
 XX PD 26-JAN-2001; 2001WO-GB00329.
 XX PF 26-JAN-2000; 2000GB-0001825.
 XX PR (REGE-) REGEN THERAPEUTICS PLC.
 XX PA Georgiades JA;
 XX PI WPI; 2001-488775/53.
 XX DR Peptide useful as an inter alia in the treatment of e.g. disorders of
 XX PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX PS Claim 1; Page 15; 40pp; English.
 XX CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is colostrinin peptide 6 related to the invention.
 CC Colostrinin peptide 6 corresponds to position 204-210 of beta-caesin.

XX SQ Sequence 7 AA;
 Query Match 53.8%; Score 7; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQEPV 8
 Db 1 LLYQEPV 7

RESULT 15
 AAU83316
 ID AAU83316 standard; peptide; 8 AA.
 XX AC AAU83316;
 XX DT 06-NOV-2001 (first entry)
 XX DE Modified colostrinin cyclic peptide #6.
 XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;

KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.
 XX
 XX Synthetic.
 OS
 XX
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Val found at the C-terminal end"
 XX
 XX WO200155199-A1.
 PN
 XX
 XX 02-AUG-2001.
 PD
 XX
 XX 26-JAN-2001; 2001WO-GB00329.
 PF
 XX 26-JAN-2000; 2000GB-0001825.
 PR
 XX (REG-) REGEN THERAPEUTICS PLC.
 XX
 XX Georgiades JA;
 PI
 XX WPI; 2001-488775/53.
 DR
 XX
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX
 XX Example 2; Page 9; 40pp; English.
 PS
 XX The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is modified colostrinin cyclic peptide #6 related to
 CC the invention.
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 53.8%; Score 7; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 LLYQEPV 8
 Db 2 LLYQEPV 8
 |||||
 |||||
 RESULT 16
 AAU83286
 ID AAU83286 standard; Peptide; 8 AA.
 XX
 XX AAU83286;
 AC
 XX 23-APR-2002 (first entry)
 DT
 Query Match 53.8%; Score 7; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 LLYQEPV 8
 Db 2 LLYQEPV 8
 |||||
 |||||
 RESULT 17
 AAU83309
 ID AAU83309 standard; Peptide; 13 AA.
 XX
 XX AAU83309;
 AC
 XX 23-APR-2002 (first entry)
 DT
 XX
 XX Antiviral composition peptide-A, fragment #27.
 DE
 XX Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 XX Synthetic.
 OS
 XX
 XX US2002004579-A1.
 PN
 XX 10-JAN-2002.
 PD
 XX 17-JAN-2001; 2001US-0764017.
 PF
 XX 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 XX (ADVI-) ADVANCED VIRAL RES CORP.
 PA
 XX Friedland B, Hirschman SZ, Taraporewala IB;
 PI
 XX WPI; 2002-163727/21.
 DR
 XX
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 PT
 XX Disclosure; Page 7; 37pp; English.
 PS
 XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 53.8%; Score 7; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FLLYQEP 7
 Db 2 FLLYQEP 8
 |||||
 |||||

XX Antiviral composition peptide-A, fragment #4.
 DE
 XX Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 XX Synthetic.
 OS
 XX US2002004579-A1.
 PN
 XX 10-JAN-2002.
 PD
 XX 17-JAN-2001; 2001US-0764017.
 PF
 XX 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 XX (ADVI-) ADVANCED VIRAL RES CORP.
 PA
 XX Friedland B, Hirschman SZ, Taraporewala IB;
 PI
 XX WPI; 2002-163727/21.
 DR
 XX
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 PT
 XX Disclosure; Page 7; 37pp; English.
 PS
 XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 53.8%; Score 7; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FLLYQEP 7
 Db 2 FLLYQEP 8
 |||||
 |||||
 RESULT 17
 AAU83309
 ID AAU83309 standard; Peptide; 13 AA.
 XX
 XX AAU83309;
 AC
 XX 23-APR-2002 (first entry)
 DT
 XX
 XX Antiviral composition peptide-A, fragment #27.
 DE
 XX Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 XX Synthetic.
 OS
 XX US2002004579-A1.
 PN
 XX 10-JAN-2002.
 PD
 XX 17-JAN-2001; 2001US-0764017.
 PF
 XX 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX

XX 22-SEP-1994 (first entry)
 XX Hypotensive polypeptide.
 XX Hypotensive; antioxidative; calcium absorption; salt; food;
 KW pharmaceuticals; physiologically active agents.
 XX Lactobacillus helveticus.
 XX JP06041191-A.
 XX 15-FEB-1994.
 XX 03-MAR-1993; 93JP-0043047.
 XX 04-MAR-1992; 92JP-0047340.
 XX (CALV) CALPIS SHOKUHIN KOGYO KK.
 XX WPI; 1994-089332/11.
 XX New polypeptide - used in physiologically active agents having
 PT e.g. hypotensive antioxidative and calcium absorption promoting
 PT activity
 XX Claim 1-2; Page 10; 10pp; Japanese.
 XX Sequences (AAB5819-341) are used in conjunction with
 CC physiologically active agents showing a property such as
 CC hypotensive activity, calcium absorption promoting activity and
 CC antioxidative activity. The peptides are non-toxic and can be
 CC used in physiologically active agents.
 XX Sequence 19 AA;
 SQ Query Match 53.8%; Score 7; DB 15; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PVLGPVR 13
 DB 6 PVLGPVR 12
 RESULT 21
 AAY17233
 ID AAY17233 standard; peptide; 19 AA.
 AC AAY17233;
 XX 09-AUG-1999 (first entry)
 DE Casein antimicrobial peptide.
 XX Antimicrobial peptide; casein; dental caries; periodontal disease;
 KW antiplaque agent.
 XX Bos sp.
 XX WO9926971-Al.
 PN 03-JUN-1999.
 XX 24-NOV-1998; 98WO-AU00972.
 XX 24-NOV-1997; 97AU-0000514.
 XX (UYME) UNIV MELBOURNE.
 PA (VICT-) VICTORIAN DAIRY IND AUTHORITY.
 XX Dashper SG, Malkoski M, O'Brien-Simpson NM, Reynolds EC;
 PI Talbo GH;

XX WPI; 1999-357812/30.
 XX Antimicrobial peptides, useful for prevention and treatment of
 PT periodontal disease
 XX Claim 1; Page 43; 57pp; English.
 XX Sequences AAY17229-245 represent non-glycosylated antimicrobial peptides
 CC that are derived from casein. The peptides are useful in antimicrobial
 CC compositions for treating or preventing dental caries or periodontal
 CC disease. The new peptides are clinically efficacious, safe and natural
 CC antiplaque agents, unlike prior art agents which have undesirable side-
 CC effects, negligible intra-oral activity, or an incompatibility with
 CC toothpaste formulations.
 XX Sequence 19 AA;
 SQ Query Match 53.8%; Score 7; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PVLGPVR 13
 DB 13 PVLGPVR 19
 RESULT 22
 AAB72273
 ID AAB72273 standard; peptide; 7 AA.
 XX AAB72273;
 AC AAB72273;
 XX 14-MAY-2001 (first entry)
 DT Colostrin derived cytokine inducing peptide SEQ ID 28.
 DE Colostrin; immune response; cytokine; blood cell proliferation;
 XX central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX Synthetic.
 XX OS WO200111937-A2.
 PN 22-FEB-2001.
 XX 17-AUG-2000; 2000WO-US22818.
 XX 17-AUG-1999; 99US-0149311.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 PI WPI; 2001-202804/20.
 DR Inducing a cytokine and modulating an immune response, useful for
 XX treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrin as an immunological
 PT regulator -
 XX Claim 1; Page 34; 50pp; English.
 PS Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
XX acquired immunological deficiencies.

SQ Sequence 7 AA;
Query Match 46.2%; Score 6; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLYQE 6
Db 2 FLLYQE 7

RESULT 23
AAB72526
ID AAB72526 standard; Peptide; 7 AA.
XX AC AAB72526;
XX DT 09-MAY-2001 (first entry)
XX DE Colostrinin peptide #27.
XX KW Dermatological; oxidative stress regulator; colostrinin.
XX OS Unidentified.
XX PN WO200112650-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US222665.
XX PR 17-AUG-1999; 99US-0149310.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2001-218342/22.
XX PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX Claim 6; Page 26; 48pp; English.

CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidizing species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 7 AA;
Query Match 46.2%; Score 6; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLYQE 6
Db 2 FLLYQE 7

RESULT 24
AAB72558
ID AAB72558 standard; Peptide; 7 AA.
XX

AC AAB72558;
XX 09-MAY-2001 (first entry)
DT Colostrinin peptide #27.
DE Neuroprotective; neural cell differentiation regulator; colostrinin;
XX colostrum.
XX Unidentified.
XX PN WO200112651-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US22774.
XX PR 17-AUG-1999; 99US-0149633.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Boldogh I;
XX WPI; 2001-226545/23.
XX PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX Claim 6; Page 22; 35pp; English.

XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.

XX SQ Sequence 7 AA;
Query Match 46.2%; Score 6; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLYQE 6
Db 2 FLLYQE 7

RESULT 25
AAB59337
ID AAB59337 standard; Peptide; 7 AA.
XX AC AAB59337;
XX DT 21-MAR-2001 (first entry)
XX DE Ewe colostrinin peptide fragment C-12.
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.
XX PN WO200075173-A2.
XX PD 14-DEC-2000.
XX PF 02-JUN-2000; 2000WO-GB02128.
XX PR 02-JUN-1999; 99GB-0012852.
XX PA (REGE-) REGEN THERAPEUTICS PLC.
XX PI Georgiades JA;

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XX WPI; 2001-071058/08.
XX
XX Peptides having an N-terminal amino acid sequence isolated from
XX colostrin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
XX
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
XX Sequence 7 AA;
XX
XX Query Match 46.2%; Score 6; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FLLYQE 6
XX | | | | |
XX Db 2 FLLYQE 7
XX
XX RESULT 26
XX AAEE20255
XX ID AAEE20255 standard; peptide; 7 AA.
XX AC AAEE20255;
XX
XX 18-JUN-2002 (first entry)
XX
XX Colostrin constituent peptide #27.
XX
XX Blood cell regulator; colostrin; constituent peptide; oxidative stress;
XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX transplantation; implantation; dermatological; vulnery.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Modified-site 7
XX /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Stanton GU, Hughes TK, Boldogh I;
XX
XX WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
XX patient comprises a blood cell regulator selected from colostrin, its
XX constituent peptide and/or analog -
XX
XX Claim 6; Page 26; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
XX regulator selected from colostrin, its constituent peptide and/or

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analogue. The invention is used for modulating the oxidative stress level in a cell e.g. mammalian or human cell present in a cell culture, tissue, organ, or organism; or for treating oxidative damage to the skin of a patient e.g. animal or human; to modulate oxidative stress during/after a premature birth or normal birth, preventing/delaying aging in a patient, enhancing wound healing, and the reduction of side effects of cosmetic procedures. The method changes the level of an oxidizing species in the cell, such as decreases or prevents increase in the level of damage to a biomolecule of the patient selected from DNA, protein and/or lipid, compared to the same conditions when the oxidative stress regulator is not present. The modulation of oxidative stress results in enhanced repair, regeneration, and replacement of cells, tissues and organs (e.g. kidney, liver, pancreas, skin, and the other internal and external organs), as well as enhanced preservation of such organs for transplantation, implantation, or scientific research. The present sequence is a colostrinin constituent peptide.

XX
SQ Sequence 7 AA;

Query Match 46.2%; Score 6; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 FLLYQE 6
|||
DB 2 FLLYQE 7

RESULT 27
AAM51062
ID AAM51062 standard; Peptide; 7 AA.
XX
AC AAM51062;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostrinin constituent peptide (casein amino acids 202-208).
XX
KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 7
FT notes "optional C-terminal amidation"
XX
PN W0200213849-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22775.
XX
PR 17-AUG-2000; 2000WO-US22775.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGG-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2002-269150/31.
XX
PT Modulation of blood cell proliferation in a patient involves use of
PT blood cell regulator selected from colostrinin, its constituent peptide
PT and/or analogue -
XX
XX Claim 1; Page 34; 54pp; English.
XX
XX The present sequence is that of a colostrinin constituent peptide
XX that is used as an immunological regulator and as a blood cell
XX regulator in claimed methods of the invention. It is classified
XX as having a beta-casein homologue precursor, and corresponds to
XX casein amino acids 202-208. Methods are claimed for: inducing a

CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the
 CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.
 XX
 SQ Sequence 7 AA;
 Query Match 46.2%; Score 6; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLLYQE 6
 |||||
 Db 2 FLLYQE 7
 |||||
 RESULT 28
 AAO14604
 ID AAO14604 standard; peptide; 7 AA.
 XX
 AC AAO14604;
 XX
 DT 27-MAY-2002 (first entry)
 XX
 DE Neural cell regulatory colostrinin peptide 27.
 XX
 XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 7 /note= "Optional C-terminal amide"
 FT
 XX WO200213851-A1.
 PN
 XX
 PD 21-FEB-2002.
 XX
 XX 17-AUG-2000; 2000WO-US22777.
 XX
 PR 17-AUG-2000; 2000WO-US22777.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I, Stanton JG, Hughes TK;
 PI
 XX WPI; 2002-269152/31.
 DR
 XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -
 XX
 XX Claim 7; Page 22; 37pp; English.
 PS
 XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.
 XX
 SQ Sequence 7 AA;
 Query Match 46.2%; Score 6; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLLYQE 6
 |||||
 Db 2 FLLYQE 7
 |||||
 RESULT 29
 AAB59356
 ID AAB59356 standard; Peptide; 9 AA.
 XX
 AC AAB59356;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrinin peptide fragment derived sequence #16.
 XX
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-GB02128.
 XX
 PR 02-JUN-1999; 99GB-0012852.
 XX
 XX (REGG-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-071058/08.
 DR
 XX Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 XX Claim 8; Page 27; 63pp; English.
 PS
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 9 AA;
 Query Match 46.2%; Score 6; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLLYQE 6
 |||||
 Db 4 FLLYQE 9
 |||||

XX Disclosure; Page 8; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified

CC peptide sequence. The composition comprises nucleotide-peptide comprising

CC a peptide linked through a serine residue and diphosphodiester to a

CC nucleotide; or peptides with about 31 amino acid residues capable of

CC stimulating production of interleukin-8 in cultured cells; or peptides

CC with about 31 amino acid residues capable of stimulating production of

CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful

CC for treating viral infections and stimulating the immune system.

CC AAU83282-AAU83401 represent peptides used in the composition of the

CC invention.

XX Sequence 14 AA;

SQ

Query Match 46.2%; Score 6; DB 23; Length 14;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQE 6

Db 9 FLLYQE 14

RESULT 33

AAU83341

ID AAU83341 standard; Peptide; 19 AA.

AC AAU83341;

DT 23-APR-2002 (first entry)

XX Antiviral composition peptide-A, fragment #59.

XX Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.

XX Synthetic.

OS

XX US2002004579-A1.

PN 10-JAN-2002.

PD

XX 17-JAN-2001; 2001US-0764017.

PF

XX 22-OCT-1996; 96US-0735236.

PR

XX 25-JUN-1999; 99US-0344095.

PR

XX (ADVI-) ADVANCED VIRAL RES CORP.

PA

XX Friedland B, Hirschman SZ, Taraporewala IB;

PI

XX WPI; 2002-163727/21.

DR

XX New peptides compositions, useful for treating viral infections and

PT stimulating the immune system -

XX

XX Disclosure; Page 8; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified

CC peptide sequence. The composition comprises nucleotide-peptide comprising

CC a peptide linked through a serine residue and diphosphodiester to a

CC nucleotide; or peptides with about 31 amino acid residues capable of

CC stimulating production of interleukin-8 in cultured cells; or peptides

CC with about 31 amino acid residues capable of stimulating production of

CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful

CC for treating viral infections and stimulating the immune system.

CC AAU83282-AAU83401 represent peptides used in the composition of the

CC invention.

XX Sequence 19 AA;

SQ

Query Match 46.2%; Score 6; DB 23; Length 19;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQE 6

Db 14 FLLYQE 19

RESULT 34

AAU83290

ID AAU83290 standard; Peptide; 9 AA.

XX AAU83290;

AC

XX 23-APR-2002 (first entry)

DT

XX Antiviral composition peptide-A, fragment #8.

DE

XX Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.

KW

XX Synthetic.

OS

XX US2002004579-A1.

PN 10-JAN-2002.

PD

XX 17-JAN-2001; 2001US-0764017.

PF

XX 22-OCT-1996; 96US-0735236.

PR

XX 25-JUN-1999; 99US-0344095.

PR

XX (ADVI-) ADVANCED VIRAL RES CORP.

PA

XX Friedland B, Hirschman SZ, Taraporewala IB;

PI

XX WPI; 2002-163727/21.

DR

XX New peptides compositions, useful for treating viral infections and

PT stimulating the immune system -

XX

XX Disclosure; Page 7; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified

CC peptide sequence. The composition comprises nucleotide-peptide comprising

CC a peptide linked through a serine residue and diphosphodiester to a

CC nucleotide; or peptides with about 31 amino acid residues capable of

CC stimulating production of interleukin-8 in cultured cells; or peptides

CC with about 31 amino acid residues capable of stimulating production of

CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful

CC for treating viral infections and stimulating the immune system.

CC AAU83282-AAU83401 represent peptides used in the composition of the

CC invention.

XX Sequence 9 AA;

SQ

Query Match 38.5%; Score 5; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQ 5

Db 5 FLLYQ 9

RESULT 35

AAU43973

ID AAU43973 standard; peptide; 13 AA.

XX AAU43973;

AC

XX 22-APR-1998 (first entry)

DT

XX DE Human myelin oligodendrocyte glycoprotein peptide MOG 181-193.
XX KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
XX KW autoimmune response; MBP; myelin basic protein; demyelinating.
XX OS Homo sapiens.
XX PN WO9735879-A1.
XX PD 02-OCT-1997.
XX PF 01-MAY-1996; 96WO-US06072.
XX PR 28-MAR-1996; 96US-0623406.
XX PA (IMMU-) IMMUNOLOGIC PHARM CORP.
XX PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;
XX WPI; 1997-489564/45.
XX PT Human myelin oligodendrocyte glyco-protein peptide - useful to treat
XX PT multiple sclerosis in mammal by down-regulating auto-immune response
XX PS Disclosure; Fig 2; 108pp; English.
XX CC The present sequence represents a novel peptide of human myelin
XX CC oligodendrocyte glycoprotein (MOG). The peptides of human MOG and
XX CC MBP (myelin basic protein) can be used to treat multiple sclerosis
XX CC in a mammal by down-regulating an autoimmune response in the mammal.
XX CC They can also be used to diagnose and treat other demyelinating
XX CC autoimmune diseases in humans, or to prepare antibodies for the
XX CC detection or diagnosis of autoimmune diseases.
XX SQ Sequence 13 AA;
Query Match 38.5%; Score 5; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PVLGP 11
Db 8 PVLGP 12
RESULT 36
AAU83314
ID AAU83314 standard; Peptide; 13 AA.
AC AAU83314;
XX DT 23-APR-2002 (first entry)
XX DE Antiviral composition peptide-A, fragment #32.
XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
XX KW monocyte chemotactic protein 1; immune system.
XX OS Synthetic.
XX PN US2002004579-A1.
XX PD 10-JAN-2002.
XX PF 17-JAN-2001; 2001US-0764017.
XX PR 22-OCT-1996; 96US-0735236.
XX PR 25-JUN-1999; 99US-0344095.
XX PA (ADVI-) ADVANCED VIRAL RES CORP.
XX PI Friedland B, Hirschman SZ, Taraporewala IB;
XX WPI; 2002-163727/21.
XX PT New peptides compositions, useful for treating viral infections and
XX PT stimulating the immune system -
XX PS Disclosure; Page 8; 37pp; English.
XX CC The invention relates to a new peptide composition comprising a specified
XX CC peptide sequence. The composition comprises nucleotide-peptide comprising
XX CC a peptide linked through a serine residue and diphosphodiester to a
XX CC nucleotide; or peptides with about 31 amino acid residues capable of
XX CC stimulating production of interleukin-8 in cultured cells; or peptides
XX CC with about 31 amino acid residues capable of stimulating production of
XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX CC for treating viral infections and stimulating the immune system.
XX CC AAU83282-AAU83401 represent peptides used in the composition of the
XX CC invention.

XX DR WPI; 2002-163727/21.
XX PT New peptides compositions, useful for treating viral infections and
XX PT stimulating the immune system -
XX PS Disclosure; Page 8; 37pp; English.
XX CC The invention relates to a new peptide composition comprising a specified
XX CC peptide sequence. The composition comprises nucleotide-peptide comprising
XX CC a peptide linked through a serine residue and diphosphodiester to a
XX CC nucleotide; or peptides with about 31 amino acid residues capable of
XX CC stimulating production of interleukin-8 in cultured cells; or peptides
XX CC with about 31 amino acid residues capable of stimulating production of
XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX CC for treating viral infections and stimulating the immune system.
XX CC AAU83282-AAU83401 represent peptides used in the composition of the
XX CC invention.

SQ Sequence 13 AA;
Query Match 38.5%; Score 5; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQ 5
Db 9 FLLYQ 13
RESULT 37
AAU83320
ID AAU83320 standard; Peptide; 14 AA.
XX AC AAU83320;
XX DT 23-APR-2002 (first entry)
XX DE Antiviral composition peptide-A, fragment #38.
XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
XX KW monocyte chemotactic protein 1; immune system.
XX OS Synthetic.
XX PN US2002004579-A1.
XX PD 10-JAN-2002.
XX PF 17-JAN-2001; 2001US-0764017.
XX PR 22-OCT-1996; 96US-0735236.
XX PR 25-JUN-1999; 99US-0344095.
XX PA (ADVI-) ADVANCED VIRAL RES CORP.
XX PI Friedland B, Hirschman SZ, Taraporewala IB;
XX WPI; 2002-163727/21.
XX PT New peptides compositions, useful for treating viral infections and
XX PT stimulating the immune system -
XX PS Disclosure; Page 8; 37pp; English.
XX CC The invention relates to a new peptide composition comprising a specified
XX CC peptide sequence. The composition comprises nucleotide-peptide comprising
XX CC a peptide linked through a serine residue and diphosphodiester to a
XX CC nucleotide; or peptides with about 31 amino acid residues capable of
XX CC stimulating production of interleukin-8 in cultured cells; or peptides
XX CC with about 31 amino acid residues capable of stimulating production of
XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX CC for treating viral infections and stimulating the immune system.

```

CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
SQ Sequence 14 AA;
Query Match 38.5%; Score 5; DB 23; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
QY 1 FLLYQ 5
Db 10 FLLYQ 14
|||||

RESULT 38
AAW37539
ID AAW37539 standard; peptide; 15 AA.
XX
AC AAW37539;
XX
DT 22-APR-1998 (first entry)
XX
DE Human myelin oligodendrocyte glycoprotein peptide MOG 181-195.
XX
KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
KW autoimmune response; MBP; myelin basic protein; demyelinating.
XX
OS Homo sapiens.
XX
PN WO9735879-A1.
XX
PD 02-OCT-1997.
XX
PF 01-MAY-1996; 96WO-US06072.
XX
PR 28-MAR-1996; 96US-0623406.
XX
PA (IMMU-) IMMULOGIC PHARM CORP.
XX
PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;
XX
DR WPI; 1997-489564/45.
XX
PT Human myelin oligodendrocyte glyco-protein peptide - useful to treat
PT multiple sclerosis in mammal by down-regulating auto-immune response
XX
PS Claim 1; Page 12; 108pp; English.
XX
CC The present sequence represents a novel peptide of human myelin
CC oligodendrocyte glycoprotein (MOG). The peptide of human MOG and
CC MBP (myelin basic protein) can be used to treat multiple sclerosis
CC in a mammal by down-regulating an autoimmune response in the mammal.
CC They can also be used to diagnose and treat other demyelinating
CC autoimmune diseases in humans, or to prepare antibodies for the
CC detection or diagnosis of autoimmune diseases.
XX
SQ Sequence 15 AA;
Query Match 38.5%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
QY 7 PVLGP 11
Db 7 PVLGP 11
|||||

RESULT 39
AAU99584
ID AAU99584 standard; peptide; 15 AA.
XX
AC AAU99584;
XX

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```

DT 21-OCT-2002 (first entry)
XX
DE Human zinc finger protein NY-REN-21 antigen 52.03, N-terminus.
XX
KW Human; zinc finger protein NY-REN-21 antigen 52.03; tumour;
KW embryonic development deformity; diabetes; menstrual disorder;
KW peptic ulcer; arrhythmia; anaemia; epilepsy.
XX
OS Homo sapiens.
XX
PN CN1341657-A.
XX
PD 27-MAR-2002.
XX
PF 07-SEP-2000; 2000CN-0125079.
XX
PR 07-SEP-2000; 2000CN-0125079.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-520725/56.
XX
PT Novel zinc finger protein NY-REN-21 antigen 52.03 -
XX
PS Example 6; Page 21 (disclosure); 35pp; Chinese.
XX
CC The present invention relates to the isolation of human zinc finger
CC protein NY-REN-21 antigen 52.03, and the polynucleotide encoding it.
CC Also described is the process for preparing the protein by DNA
CC recombination and the application of the polypeptide and
CC polynucleotide in treating various diseases such as embryonic
CC development deformities, tumours, diabetes, menstrual disorders,
CC peptic ulcers, arrhythmia, anaemia and epilepsy. The present sequence
CC representing the N-terminal peptide of human zinc finger protein
CC NY-REN-21 antigen 52.03 is used in an enzyme-linked immunosorbent
CC assay (ELISA) in the examples of the present invention.
XX
SQ Sequence 15 AA;
Query Match 38.5%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
QY 7 PVLGP 11
Db 10 PVLGP 14
|||||

RESULT 40
AAU83332
ID AAU83332 standard; Peptide; 15 AA.
XX
AC AAU83332;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #50.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
PN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
PF 17-JAN-2001; 2001US-0764017.
XX
PR 22-OCT-1996; 96US-0735236.
PR 25-JUN-1999; 99US-0344095.

```


Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11
DB 6 PVLGP 10

RESULT 43
AAR80294
ID AAR80294 standard; Protein; 20 AA.
XX AC
XX AAR80294;
DT 19-JAN-1996 (first entry)
XX
DE Trehalose releasing enzyme N-terminal fragment.
XX
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriosyltrehalose; alpha-maltotetrasyltrehalose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
XX
OS Arthrobacter sp. Q36.
XX
XX EP671470-A2.
XX PN
XX
XX
DT 19-JAN-1996 (first entry)
XX
DE Trehalose releasing enzyme N-terminal fragment.
XX
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriosyltrehalose; alpha-maltotetrasyltrehalose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
XX
OS Arthrobacter sp. Q36.
XX
XX EP671470-A2.
XX PN
XX
XX
DT 13-SEP-1995.
XX
DE
PF 07-MAR-1995; 95EP-0301474.
XX
XX 07-MAR-1994; 94JP-0059840.
PR 07-MAR-1994; 94JP-0059834.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
XX
XX WPI; 1995-312772/41.
DR
XX
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
PT from a non-reducing saccharide having a trehalose structure as an
PT end unit.
XX
PS Example 4; Page 25; 45pp; English.
XX
CC The trehalose releasing enzyme can be used for the preparation of
CC trehalose with high yields and efficiency from non-reducing
CC saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriosyltrehalose, alpha-maltotetrasyltrehalose and
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
CC This is the N-terminal sequence of the enzyme.
XX
SQ Sequence 20 AA;

Query Match 38.5%; Score 5; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11
DB 11 PVLGP 15

RESULT 44
AAR80296
ID AAR80296 standard; Protein; 20 AA.
XX AC
XX AAR80296;
XX

DT 19-JAN-1996 (first entry)
XX
DE Trehalose releasing enzyme internal fragment.
XX
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriosyltrehalose; alpha-maltotetrasyltrehalose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
XX
OS Arthrobacter sp. Q36.
XX
XX EP671470-A2.
XX PN
XX
XX
DT 13-SEP-1995.
XX
DE
PF 07-MAR-1995; 95EP-0301474.
XX
XX 07-MAR-1994; 94JP-0059840.
PR 07-MAR-1994; 94JP-0059834.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
XX
XX WPI; 1995-312772/41.
DR
XX
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
PT from a non-reducing saccharide having a trehalose structure as an
PT end unit.
XX
PS Example 4; Page 26; 45pp; English.
XX
CC The trehalose releasing enzyme can be used for the preparation of
CC trehalose with high yields and efficiency from non-reducing
CC saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriosyltrehalose, alpha-maltotetrasyltrehalose and
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
CC This is an internal sequence of the enzyme.
XX
SQ Sequence 20 AA;

Query Match 38.5%; Score 5; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11
DB 1 PVLGP 5

RESULT 45
AAW37541
ID AAW37541 standard; peptide; 20 AA.
XX
XX AAW37541;
XX
XX
DT 22-APR-1998 (first entry)
XX
XX
DE Human myelin oligodendrocyte glycoprotein peptide MOG 181-200.
XX
XX Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
KW autoimmune response; MBP; myelin basic protein; demyelinating.
XX
XX Homo sapiens.
OS
XX
XX WO9735879-A1.
FN
XX
PD 02-OCT-1997.
XX
XX
XX 01-MAY-1996; 96WO-US06072.

XX 28-MAR-1996; 96US-0623406.
 XX (IMMU-) IMMULOGIC PHARM CORP.
 XX Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;
 XX WPI; 1997-489564/45.
 XX Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 PT multiple sclerosis in mammal by down-regulating auto-immune response
 XX
 XX Claim 1; Page 12; 108pp; English.
 XX The present sequence represents a novel peptide of human myelin
 CC oligodendrocyte glycoprotein (MOG). The peptide of human MOG and
 CC MBP (myelin basic protein) can be used to treat multiple sclerosis
 CC in a mammal by down-regulating an autoimmune response in the mammal.
 CC They can also be used to diagnose and treat other demyelinating
 CC autoimmune diseases in humans, or to prepare antibodies for the
 CC detection or diagnosis of autoimmune diseases.
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 38.5%; Score 5; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 PVLGP 11
 Db 7 PVLGP 11
 RESULT 46
 AAR65510
 ID AAR65510 standard; peptide; 5 AA.
 XX
 AC AAR65510;
 XX
 DT 15-DEC-1994 (first entry)
 XX
 DE Endothelin antagonist cyclic pentapeptide.
 XX
 KW Endothelin; antagonist; hyperlipidaemia; hyperlipaemia; hypolipaemic.
 XX cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-Trp"
 FT Misc-difference 2 /note= "D-Glu"
 FT Misc-difference 4 /note= "D-Val"
 FT Modified-site 1.5
 FT /note= "Leu(5) is condensed onto D-Trp(1) to form
 FT a cyclic pentapeptide"
 XX
 XX JP05194254-A.
 XX
 PD 03-AUG-1993.
 XX
 PF 22-JAN-1992; 92JP-0031540.
 XX
 PR 22-JAN-1992; 92JP-0031540.
 XX
 PA (BANY) BANYU PHARM CO LTD.
 XX
 DR WPI; 1993-278210/35.
 XX
 XX Anti-hyperlipidaemic agent contg. endothelin antagonist - pref.
 PT cyclic penta:peptide

XX Disclosure; Page 8; 31pp; Japanese.
 PS
 XX
 CC A therapeutic drug for treating hyperlipidaemia is claimed, which
 CC contains an endothelin antagonist as active component. The endothelin
 CC antagonist is a peptide of the type disclosed in EP-460679 or is a
 CC specified cyclic pentapeptide described by a highly generic formula.
 CC The present sequence is a specific example of the generic
 CC cyclic pentapeptide.
 XX
 SQ Sequence 5 AA;
 Query Match 30.8%; Score 4; DB 14; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 EPVL 9
 Db 2 EPVL 5
 RESULT 47
 AAW75347
 ID AAW75347 standard; peptide; 6 AA.
 XX
 AC AAW75347;
 XX
 DT 02-FEB-1999 (first entry)
 XX
 DE Hexapeptide #2 binds anti-Ad5 fibre head MAb 7A2.7.
 XX
 KW Cellular receptor; virus; immobilisation; monoclonal antibody; fibre;
 KW viral surface protein; hexapeptide expression library; adenovirus;
 KW major histocompatibility complex; MHC; fibronectin; gene therapy;
 KW genetic disease; acquired immune deficiency syndrome; AIDS; cancer.
 XX
 OS Synthetic.
 XX
 FN FR2758821-A1.
 XX
 PD 31-JUL-1998.
 XX
 PF 30-JAN-1997; 97FR-0001005.
 XX
 PR 30-JAN-1997; 97FR-0001005.
 PR
 PR 09-SEP-1997; 97FR-0011166.
 XX
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Boulanger P, Hong SS, Karayan L;
 XX WPI; 1998-416458/36.
 XX
 XX Use of peptide(s) for facilitating or modulating attachment of
 FT adenovirus to cells - useful for, e.g. treating or preventing
 FT infection and improving uptake of gene therapy vectors
 XX
 XX Example 2; Fig 1; 48pp; French.
 PS
 XX The invention relates to methods for selecting and identifying a
 CC cellular receptor for a virus, by immobilising, on a support, a
 CC monoclonal antibody targeted to a viral surface protein that determines
 CC attachment of the virus to the receptor. The immobilised antibody is
 CC incubated with a hexapeptide expression library and peptides bound to the
 CC immobilised antibody are eluted by competitive binding with recombinant
 CC fragments of the viral surface protein. In a reverse method, the viral
 CC surface protein is immobilised and incubated with the peptide library. In
 CC this case, the bound peptides are eluted by competitive binding with the
 CC monoclonal antibody. The hexapeptides AAW75346-W75360 represent
 CC peptides isolated by biopanning the library with the immobilised
 CC monoclonal antibody (MAb) 7A2.7 and eluted using an adenovirus type 5
 CC fibre head protein (AAW75335).
 CC The methods are used to identify peptides from MHC Class I and/or

CC type III fibronectin proteins that allow or facilitate attachment by
 CC adenovirus (Ad) to host cells and/or entry into the cells, and to
 CC identify ligands that modulate Ad infection mediated by these peptides,
 CC e.g. to treat or prevent Ad infections or to facilitate infection by Ad
 CC gene therapy vectors used to treat genetic diseases, acquired immune
 CC deficiency syndrome or cancer.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 6 AA;
 SQ Query Match 30.8%; Score 4; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 LGPV 12
 Db ||||
 1 LGPV 4

RESULT 48
 AAW75279
 ID AAW75279 standard; peptide; 6 AA.
 XX AC AAW75279;
 XX DT 25-MAR-2003 (updated)
 DT 02-FEB-1999 (first entry)
 XX DE Hexapeptide #2 binds anti-Ad5 fibre head MAb 7A2.7.
 XX KW Cellular receptor; virus; immobilisation; monoclonal antibody; fibre;
 KW viral surface protein; hexapeptide expression library; adenovirus;
 KW major histocompatibility complex; MHC; fibronectin; gene therapy;
 KW genetic disease; acquired immune deficiency syndrome; AIDS; cancer.
 XX OS Synthetic.
 XX PN FR2758885-A1.
 XX PD 31-JUL-1998.
 XX PF 10-JUL-1997; 97FR-0008796.
 XX PR 30-JAN-1997; 97FR-0001005.
 PR 10-JUL-1997; 97FR-0008796.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Boulanger P, Hong SS, Karayan L;
 XX WPI; 1998-416493/36.
 XX DR Selection and identification of cellular receptors for viruses -
 PT used to control attachment and entry of adenovirus into cells, e.g.
 PT for treating infection or in gene therapy
 XX Example 2; Fig 1; 43pp; French.
 XX The invention relates to methods for selecting and identifying a
 CC cellular receptor for a virus, by immobilising, on a support, a
 CC monoclonal antibody targeted to a viral surface protein that determines
 CC attachment of the virus to the receptor. The immobilised antibody is
 CC incubated with a hexapeptide expression library and peptides bound to the
 CC immobilised antibody are eluted by competitive binding with recombinant
 CC fragments of the viral surface protein. In a reverse method, the viral
 CC surface protein is immobilised and incubated with the peptide library. In
 CC this case, the bound peptides are eluted by competitive binding with the
 CC monoclonal antibody. The hexapeptides AAW75278-W75292 represent
 CC peptides isolated by biopanning the library with the immobilised
 CC monoclonal antibody (MAb) 7A2.7 and eluted using an adenovirus type 5
 CC fibre head protein (AAW75267).
 CC The methods are used to identify peptides from MHC Class I and/or
 CC type III fibronectin proteins that allow or facilitate attachment by
 CC adenovirus (Ad) to host cells and/or entry into the cells, and to

CC identify ligands that modulate Ad infection mediated by these peptides,
 CC e.g. to treat or prevent Ad infections or to facilitate infection by Ad
 CC gene therapy vectors used to treat genetic diseases, acquired immune
 CC deficiency syndrome or cancer.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 6 AA;
 SQ Query Match 30.8%; Score 4; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 LGPV 12
 Db ||||
 1 LGPV 4

RESULT 49
 AAU08616
 ID AAU08616 standard; Peptide; 6 AA.
 XX AC AAU08616;
 XX DT 18-DEC-2001 (first entry)
 DT Human olfactory receptor PCR primer design motif #1.
 DE Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 KW food additive; cosmetic; fragrance; pharmaceutical additive.
 XX OS Homo sapiens.
 XX PN WO200168805-A2.
 XX PD 20-SEP-2001.
 XX PF 13-MAR-2001; 2001WO-US07771.
 XX PR 13-MAR-2000; 2000US-0188914.
 PR 24-MAR-2000; 2000US-0192033.
 PR 12-APR-2000; 2000US-0198474.
 PR 24-APR-2000; 2000US-0199335.
 PR 26-MAY-2000; 2000US-0207702.
 PR 23-JUN-2000; 2000US-0213849.
 PR 16-AUG-2000; 2000US-0226534.
 PR 07-SEP-2000; 2000US-0230732.
 PR 07-FEB-2001; 2001US-0268862.
 XX PA (SENO-) SENOMYX INC.
 XX PI Zozulya S;
 XX WPI; 2001-570867/64.
 XX PT Nucleic acids encoding human olfactory G protein-coupled receptors,
 PT useful for screening for compounds involved in olfactory sensation,
 PT where the compounds can be used in the food, pharmaceutical and
 PT cosmetic industries to customise odours -
 PT Disclosure; Page 42; 319pp; English.
 XX The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence is a human olfactory receptor
 CC protein motif end used to design PCR primers against the first
 CC transmembrane domain.


```

XX SQ Sequence 6 AA;
XX
XX Query Match 30.8%; Score 4; DB 22; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 FLLY 4
DB 2 FLLY 5
XX
XX RESULT 50
XX AAG63026
XX ID AAG63026 standard; peptide; 6 AA.
XX AC AAG63026;
XX XX
XX DT 01-OCT-2001 (first entry)
XX XX
XX DE Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.
XX KW Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;
XX KW virus binding domain.
XX OS Unidentified.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue"
XX XX
XX PN WO200140265-A2.
XX XX
XX PD 07-JUN-2001.
XX XX
XX PF 01-DEC-2000; 2000WO-US42515.
XX XX
XX PR 02-DEC-1999; 99US-0453115.
XX XX
XX PA (VITE-) VI TECHNOLOGIES INC.
XX XX
XX PI Hammond DJ;
XX XX
XX DR WPI; 2001-475677/51.
XX XX
XX PT Identifying ligands that interact with a target by Quick Assay for
XX PT Selecting Affinity Resins, involves differentiating specific or
XX PT non-specific false positive interactions from target-specific
XX PT interactions -
XX XX
XX PS Claim 4; Page 27; 39pp; English.
XX XX
XX CC The present sequence represents a Hepatitis A virus (HAV)-binding
XX CC domain. It was identified using the method of the invention. The method
XX CC identifies ligands that interact with a target by Quick Assay for
XX CC Selecting Affinity Resins. The method comprise differentiating false
XX CC positive interactions (either specific or non-specific) from
XX CC target-specific interaction, by distinguishing non-specific binding of
XX CC ligands to agents in the screening solution from specific binding
XX CC between a ligand and target. The method is useful for identifying
XX CC ligands that interact with the target, and for multiple screenings of
XX CC the same surface-immobilized library for a number of different ligands.
XX XX
XX SQ Sequence 6 AA;
XX
XX Query Match 30.8%; Score 4; DB 22; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 FLLY 4
DB 1 FLLY 4
XX
XX RESULT 52
XX AAG63043
XX ID AAG63043 standard; peptide; 6 AA.
XX XX
XX AC AAG63043;
XX XX
XX DT 01-OCT-2001 (first entry)
XX XX
XX DE Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.
XX KW Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;
XX KW virus binding domain.
XX OS Unidentified.
XX XX

```

XX WO200140265-A2.
 XX
 XX 07-JUN-2001.
 XX
 XX 01-DEC-2000; 2000WO-US42515.
 XX
 XX 02-DEC-1999; 99US-0453115.
 XX
 XX (VITE-) VI TECHNOLOGIES INC.
 XX
 XX Hammond DJ;
 XX
 XX WPI; 2001-475677/51.
 XX
 XX Identifying ligands that interact with a target by Quick Assay for
 PT Selecting Affinity Resins, involves differentiating specific or
 PT non-specific false positive interactions from target-specific
 PT interactions -
 XX
 XX Claim 4; Page 27; 39pp; English.
 XX
 XX The present sequence represents a Hepatitis A virus (HAV)-binding
 CC domain. It was identified using the method of the invention. The method
 CC identifies ligands that interact with a target by Quick Assay for
 CC Selecting Affinity Resins. The method comprise differentiating false
 CC positive interactions (either specific or non-specific) from
 CC target-specific interaction, by distinguishing non-specific binding of
 CC ligands to agents in the screening solution from specific binding
 CC between a ligand and target. The method is useful for identifying
 CC ligands that interact with the target, and for multiple screenings of
 CC ligands that interact with the target, and for multiple screenings of
 CC the same surface-immobilized library for a number of different ligands.
 XX
 XX Sequence 6 AA;
 SQ

Query Match 30.8%; Score 4; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLLY 4
 DB 1 FLLY 4
 RESULT 53
 AAG63065
 ID AAG63065 standard; peptide; 6 AA.
 XX
 XX AAG63065;
 XX
 XX 01-OCT-2001 (first entry)
 DE Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.
 XX
 XX Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;
 KW virus binding domain.
 KW
 XX Unidentified.
 OS
 XX WO200140265-A2.
 PN
 XX 07-JUN-2001.
 PD
 XX
 XX 01-DEC-2000; 2000WO-US42515.
 PF
 XX 02-DEC-1999; 99US-0453115.
 PR
 XX (VITE-) VI TECHNOLOGIES INC.
 PA
 XX Hammond DJ;
 PI
 XX WPI; 2001-475677/51.
 DR
 XX

PT Identifying ligands that interact with a target by Quick Assay for
 PT Selecting Affinity Resins, involves differentiating specific or
 PT non-specific false positive interactions from target-specific
 PT interactions -
 XX
 XX Claim 10; Page 28; 39pp; English.
 XX
 XX The present sequence represents a Hepatitis A virus (HAV)-binding
 CC domain. It was identified using the method of the invention. The method
 CC identifies ligands that interact with a target by Quick Assay for
 CC Selecting Affinity Resins. The method comprise differentiating false
 CC positive interactions (either specific or non-specific) from
 CC target-specific interaction, by distinguishing non-specific binding of
 CC ligands to agents in the screening solution from specific binding
 CC between a ligand and target. The method is useful for identifying
 CC ligands that interact with the target, and for multiple screenings of
 CC the same surface-immobilized library for a number of different ligands.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 30.8%; Score 4; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLLY 4
 DB 1 FLLY 4
 RESULT 54
 AAG63106
 ID AAG63106 standard; peptide; 6 AA.
 XX
 XX AAG63106;
 XX
 XX 01-OCT-2001 (first entry)
 DT
 XX Amino acid sequence of a Poliovirus-binding domain.
 DE
 XX Poliovirus; Quick Assay for Selecting Affinity Resins;
 KW virus binding domain.
 KW
 XX Unidentified.
 OS
 XX WO200140265-A2.
 PN
 XX 07-JUN-2001.
 PD
 XX
 XX 01-DEC-2000; 2000WO-US42515.
 PF
 XX 02-DEC-1999; 99US-0453115.
 PR
 XX (VITE-) VI TECHNOLOGIES INC.
 PA
 XX Hammond DJ;
 PI
 XX WPI; 2001-475677/51.
 DR
 XX
 XX Identifying ligands that interact with a target by Quick Assay for
 PT Selecting Affinity Resins, involves differentiating specific or
 PT non-specific false positive interactions from target-specific
 PT interactions -
 XX
 XX Claim 30; Page 30; 39pp; English.
 XX
 XX The present sequence represents a Poliovirus-binding domain. It was
 CC identified using the method of the invention. The method identifies
 CC ligands that interact with a target by Quick Assay for Selecting Affinity
 CC Resins. The method comprise differentiating false positive interactions
 CC (either specific or non-specific) from target-specific interaction, by
 CC distinguishing non-specific binding of ligands to agents in the
 CC screening solution from specific binding between a ligand and target.
 CC The method is useful for identifying ligands that interact with the

CC target, and for multiple screenings of the same surface-immobilized
CC library for a number of different ligands.

XX SQ Sequence 6 AA;

Query Match 30.8%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLY 4
Db 1 FLLY 4

RESULT 55
AAG63108
ID AAG63108 standard; peptide; 6 AA.

XX AC AAG63108;

XX DT 01-OCT-2001 (first entry)

XX DE Amino acid sequence of a Poliovirus-binding domain.

XX KW Poliovirus; Quick Assay for Selecting Affinity Resins;
XX virus binding domain.

XX OS Unidentified.

XX PN WO200140265-A2.

XX PD 07-JUN-2001.

XX PF 01-DEC-2000; 2000WO-US42515.

XX PR 02-DEC-1999; 99US-0453115.

XX PA (VITE-) VI TECHNOLOGIES INC.

XX PI Hammond DU;

XX DR WPI; 2001-475677/51.

XX PT Identifying ligands that interact with a target by Quick Assay for
PT Selecting Affinity Resins, involves differentiating specific or
PT non-specific false positive interactions from target-specific
PT interactions -

XX PS Claim 30; Page 30; 39pp; English.

XX CC The present sequence represents a Poliovirus-binding domain. It was
CC identified using the method of the invention. The method identifies
CC ligands that interact with a target by Quick Assay for Selecting Affinity
CC Resins. The method comprise differentiating false positive interactions
CC (either specific or non-specific) from target-specific interaction, by
CC distinguishing non-specific binding of ligands to agents in the
CC screening solution from specific binding between a ligand and target.
CC The method is useful for identifying ligands that interact with the
CC target, and for multiple screenings of the same surface-immobilized
CC library for a number of different ligands.

XX SQ Sequence 6 AA;

Query Match 30.8%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLY 4
Db 1 FLLY 4

RESULT 56

AAB87132
ID AAB87132 standard; peptide; 6 AA.

XX AC AAB87132;

XX DT 04-MAY-2001 (first entry)

XX DE Human TANGO 393 cytoplasmic domain, SEQ ID NO:134.

XX KW Secreted protein; transmembrane protein; TANGO; human; drug screening;
XX activity modulator; expression modulator; cancer; immunological disorder;
XX cytostatic; immunomodulatory; gene therapy.

XX OS Homo sapiens.

XX PN WO200109162-A2.

XX PD 08-FEB-2001.

XX PF 31-JUL-2000; 2000WO-US20935.

XX PR 30-JUL-1999; 99US-0365164.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Fraser CC, Sharp JD, Kirst SJ, Barnes TM, Wrighton N, Myers PS;
XX Pan Y;

XX DR WPI; 2001-138647/14.

XX CC Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful
XX for the prevention, diagnosis and treatment of, e.g. cancers and immune
XX disorders -

XX PS Disclosure; Page 279; 332pp; English.

XX CC The invention relates to novel secreted/transmembrane proteins, and
XX nucleic acids encoding them. The novel proteins are designated TANGO 339,
XX TANGO 353, TANGO 358, TANGO 365, TANGO 368, TANGO 369, TANGO 383, TANGO
XX 393, TANGO 402, MANGO 346, and MANGO 349 and are of human origin, and a
XX murine TANGO 393 is also included within the scope of the invention. The
XX invention also encompasses fragments and variants of the proteins of the
XX invention, and nucleic acids encoding them. The invention additionally
XX relates to host cells comprising a nucleic acid of the invention; methods
XX for the production of a protein of the invention; an antibody specific
XX for a protein of the invention; methods for detecting a protein or
XX nucleic acid of the invention; and methods of identifying agents which
XX bind to or modulate the activity of a protein of the invention. The novel
XX secreted proteins, nucleic acids encoding them, and antibodies against
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression or activity of the secreted
XX proteins. The secreted proteins of the invention may also be used to
XX identify modulators of expression or activity, which may be useful in
XX the treatment of disorders associated with the proteins of the
XX invention e.g., cancers and immunological disorders. The present
XX sequence represents a fragment of a human TANGO protein of the
XX invention.

XX SQ Sequence 6 AA;

Query Match 30.8%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLGP 11
Db 2 VLGP 5

RESULT 57
AAB87133
ID AAB87133 standard; peptide; 6 AA.
XX

AC AAB87133;
XX
XX DT (first entry)
XX
XX DE Mouse TANGO 393 cytoplasmic domain, SEQ ID NO:135.
XX
XX KW Secreted protein; transmembrane protein; TANGO; human; drug screening;
KW activity modulator; expression modulator; cancer; immunological disorder;
KW cytostatic; immunomodulatory; gene therapy.
XX
XX OS Mus musculus.
XX
XX PN WO200109162-A2.
XX
XX PD 08-FEB-2001.
XX
XX PF 31-JUL-2000; 2000WO-US20935.
XX
XX PR 30-JUL-1999; 99US-0365164.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Fraser CC, Sharp JD, Kirst SJ, Barnes TM, Wrighton N, Myers PS;
PI Pan Y;
XX
XX DR WPI; 2001-138647/14.
XX
XX PT Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful
PT for the prevention, diagnosis and treatment of, e.g. cancers and immune
PT disorders -
XX
XX PS Disclosure; Page 279; 332pp; English.
XX
XX CC The invention relates to novel secreted/transmembrane proteins, and
CC nucleic acids encoding them. The novel proteins are designated TANGO 339,
CC TANGO 353, TANGO 358, TANGO 365, TANGO 369, TANGO 383, TANGO
CC 393, TANGO 402, MANGO 346 and MANGO 349 and are of human origin, and a
CC murine TANGO 393 is also included within the scope of the invention. The
CC invention also encompasses fragments and variants of the proteins of the
CC invention, and nucleic acids encoding them. The invention additionally
CC relates to host cells comprising a nucleic acid of the invention; methods
CC for the production of a protein of the invention; an antibody specific
CC for a protein of the invention; methods for detecting a protein or
CC nucleic acid of the invention; and methods of identifying agents which
CC bind to or modulate the activity of a protein of the invention. The novel
CC secreted proteins, nucleic acids encoding them, and antibodies against
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression or activity of the secreted
CC proteins. The secreted proteins of the invention may also be used to
CC identify modulators of expression or activity, which may be useful in
CC the treatment of disorders associated with the proteins of the
CC invention e.g., cancers and immunological disorders. The present
CC sequence represents a fragment of a human TANGO protein of the
XX invention.
XX
XX SQ Sequence 6 AA;
Query Match 30.8%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VLGP 11
Db 2 VLGP 5
|||
|||
RESULT 58
AAO18910
ID AAO18910 standard; Peptide; 6 AA.
XX
XX AC AAO18910;
XX
XX DT 02-DEC-2002 (first entry)

XX Human butyrylcholinesterase variant peptide fragment #5.
XX DE
XX KW Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
KW cocaine addiction; antiaddictive; antidote.
XX
XX OS Homo sapiens.
XX
XX PN WO200264796-A2.
XX
XX PD 22-AUG-2002.
XX
XX PF 21-DEC-2001; 2001WO-US50450.
XX
XX PR 26-DEC-2000; 2000US-0748739.
XX
XX PR 20-DEC-2001; 2001US-0032233.
XX
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX (UYNE-) UNIV NEBRASKA MEDICAL CENT.
XX
XX PI Lockridge O, Watkins JD, Pancook JD;
XX WPI; 2002-636633/68.
XX
XX DR New human butyrylcholinesterase variant polypeptides, useful for
XX treating cocaine-induced conditions -
XX PT
XX PS Disclosure; Fig 8; 150pp; English.
XX
XX CC The present invention relates to mutants of human butyrylcholinesterase.
XX CC The enzymes have an increased cocaine hydrolysis activity and can be used
XX CC for treating a cocaine-induced condition. The present sequence is a
XX CC protein shown in the exemplification of the invention.
XX
XX SQ Sequence 6 AA;
Query Match 30.8%; Score 4; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLY 4
Db 3 FLLY 6
|||
|||
RESULT 59
ABU67261
ID ABU67261 standard; Peptide; 6 AA.
XX
XX AC ABU67261;
XX
XX DT 28-MAY-2003 (first entry)
XX
XX DE Olfactory receptor ligand binding region I peptide.
XX
XX KW Olfactory receptor; odourant; ligand-binding region;
KW olfactory neuron; olfactory epithelium; 7 transmembrane receptor;
XX olfactory response.
XX
XX OS Mammalia.
XX
XX PN US6492143-B1.
XX
XX PD 10-DEC-2002.
XX
XX PF 17-DEC-1999; 99US-0465901.
XX
XX PR 17-DEC-1998; 98US-112605P.
XX
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX
XX PI Reed RR, Yau K, Krautwurst D;

DR WPI; 2003-327314/31.
 XX Novel amplification primer sequence pair for amplifying nucleic acid
 PT encoding an olfactory receptor ligand-binding region -
 XX
 XX Disclosure; Column 14; 46pp; English.
 PS
 CC The invention relates to an amplification primer sequence pair for
 CC amplifying a nucleic acid encoding an olfactory receptor ligand-binding
 CC region, comprising a primers appearing as ACA04888 and ACA04889.
 CC Also included is a kit for amplifying olfactory receptor sequences
 CC comprising the primers. The primers are useful for generating a nucleic
 CC acid sequence that encodes a ligand-binding region of an olfactory
 CC receptor. The amplified nucleic acid is genomic DNA, mRNA or cDNA derived
 CC from olfactory neurons or the olfactory epithelium. The olfactory
 CC receptors are 7 transmembrane receptors, manipulation of which can
 CC modulate an animals olfactory response and can be used to generate novel
 CC odourants. The present sequence is a olfactory receptor peptide consensus
 CC sequence used design degenerate PCR primer used to amplify an olfactory
 CC receptor ligand-binding region.
 XX
 XX Sequence 6 AA;
 SQ

Query Match 30.8%; Score 4; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLLY 4
 DB 2 FLLY 5
 ||||
 ||||

RESULT 60
 ABUS8261
 ID ABUS8261 standard; Peptide; 6 AA.
 XX
 AC ABUS8261;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Peptide binding to hepatitis A virus in the presence of fibrinogen #7.
 XX
 KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
 KW surface-immobilised library; blood composition.
 XX
 OS Synthetic.
 XX
 PN US2002155106-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 01-DEC-2000; 2000US-0727963.
 XX
 PR 01-DEC-2000; 2000US-0727963.
 XX
 PA (HAMM/) HAMMOND D J.
 XX
 PI Hammond DJ;
 XX
 DR WPI; 2003-198483/19.
 XX
 PT New peptide comprising a porcine parvovirus-binding, hepatitis A
 PT virus-binding or prion-binding domain, useful for screening a library
 PT of surface-immobilized ligands that bind to target molecules -
 XX
 XX Claim 4; Page 31; 35pp; English.
 PS
 CC The invention relates to a peptide, having a sequence of less than 20
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis
 CC A virus (HAV)-binding, or prion-binding domain. Also included are
 CC a composition comprising the peptide, removing a target from a biological

CC fluid, identifying a ligand for a target or targets and identifying a
 CC peptide that binds to a virus present in a blood composition. The peptide
 CC is useful for identifying a ligand for a target or targets (Hepatitis A
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a
 CC peptide that binds to a virus present in a blood composition. It is used
 CC to screen a library of surface-immobilised ligands that bind to target
 CC molecules. The peptide allows for multiple screenings of the same
 CC surface-immobilised library for a number of different ligands.
 CC The present sequence is a peptide of the invention, targeting one
 CC of the above listed targets.
 XX
 XX Sequence 6 AA;
 SQ

Query Match 30.8%; Score 4; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLLY 4
 DB 1 FLLY 4
 ||||
 ||||

RESULT 61
 ABUS8271
 ID ABUS8271 standard; Peptide; 6 AA.
 XX
 AC ABUS8271;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Peptide binding to hepatitis A virus in the presence of fibrinogen #12.
 XX
 KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
 KW surface-immobilised library; blood composition.
 XX
 OS Synthetic.
 XX
 PN US2002155106-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 01-DEC-2000; 2000US-0727963.
 XX
 PR 01-DEC-2000; 2000US-0727963.
 XX
 PA (HAMM/) HAMMOND D J.
 XX
 PI Hammond DJ;
 XX
 DR WPI; 2003-198483/19.
 XX
 PT New peptide comprising a porcine parvovirus-binding, hepatitis A
 PT virus-binding or prion-binding domain, useful for screening a library
 PT of surface-immobilized ligands that bind to target molecules -
 XX
 XX Claim 4; Page 31; 35pp; English.
 PS
 CC The invention relates to a peptide, having a sequence of less than 20
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis
 CC A virus (HAV)-binding, or prion-binding domain. Also included are
 CC a composition comprising the peptide, removing a target from a biological
 CC fluid, identifying a ligand for a target or targets and identifying a
 CC peptide that binds to a virus present in a blood composition. The peptide
 CC is useful for identifying a ligand for a target or targets (Hepatitis A
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a
 CC peptide that binds to a virus present in a blood composition. It is used
 CC to screen a library of surface-immobilised ligands that bind to target

CC molecules. The peptide allows for multiple screenings of the same
 CC surface-immobilised library for a number of different ligands. one
 CC The present sequence is a peptide of the invention, targeting one
 CC of the above listed targets.

XX Sequence 6 AA;

Query Match 30.8%; Score 4; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4
 ||||
 Db 1 FLLY 4

RESULT 62

ABUS8273
 ID ABUS8273 standard; Peptide; 6 AA.

XX AC ABUS8273;

XX DT 14-APR-2003 (first entry)

XX Peptide binding to hepatitis A virus in the presence of fibrinogen #14.

XX Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
 KW surface-immobilised library; blood composition.

XX OS Synthetic.

XX US2002155106-A1.

XX PD 24-OCT-2002.

XX PF 01-DEC-2000; 2000US-0727963.

XX PR 01-DEC-2000; 2000US-0727963.

XX PA (HAMM/) HAMMOND D J.

XX PI Hammond DJ;

XX DR WPI; 2003-198483/19.

XX New peptide comprising a porcine parvovirus-binding, hepatitis A
 PT virus-binding or prion-binding domain, useful for screening a library
 PT of surface-immobilized ligands that bind to target molecules -

XX Claim 10; Page 31; 35pp; English.

XX The invention relates to a peptide, having a sequence of less than 20
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis
 CC A virus (HAV)-binding, or prion-binding domain. Also included are
 CC a composition comprising the peptide, removing a target from a biological
 CC fluid, identifying a ligand for a target or targets and identifying a
 CC peptide that binds to a virus present in a blood composition. The peptide
 CC is useful for identifying a ligand for a target or targets (Hepatitis A
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a
 CC peptide that binds to a virus present in a blood composition. It is used
 CC to screen a library of surface-immobilised ligands that bind to target
 CC molecules. The peptide allows for multiple screenings of the same
 CC surface-immobilised library for a number of different ligands.
 CC The present sequence is a peptide of the invention, targeting one
 CC of the above listed targets.

XX Sequence 6 AA;

Query Match 30.8%; Score 4; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4
 ||||
 Db 1 FLLY 4

RESULT 63

ABUS8291
 ID ABUS8291 standard; Peptide; 6 AA.

XX AC ABUS8291;

XX DT 14-APR-2003 (first entry)

XX Poliovirus-binding peptide #6.

XX Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
 KW surface-immobilised library; blood composition.

XX OS Synthetic.

XX US2002155106-A1.

XX PD 24-OCT-2002.

XX PF 01-DEC-2000; 2000US-0727963.

XX PR 01-DEC-2000; 2000US-0727963.

XX PA (HAMM/) HAMMOND D J.

XX PI Hammond DJ;

XX DR WPI; 2003-198483/19.

XX New peptide comprising a porcine parvovirus-binding, hepatitis A
 PT virus-binding or prion-binding domain, useful for screening a library
 PT of surface-immobilized ligands that bind to target molecules -

XX Claim 30; Page 32; 35pp; English.

XX The invention relates to a peptide, having a sequence of less than 20
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis
 CC A virus (HAV)-binding, or prion-binding domain. Also included are
 CC a composition comprising the peptide, removing a target from a biological
 CC fluid, identifying a ligand for a target or targets and identifying a
 CC peptide that binds to a virus present in a blood composition. The peptide
 CC is useful for identifying a ligand for a target or targets (Hepatitis A
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a
 CC peptide that binds to a virus present in a blood composition. It is used
 CC to screen a library of surface-immobilised ligands that bind to target
 CC molecules. The peptide allows for multiple screenings of the same
 CC surface-immobilised library for a number of different ligands.
 CC The present sequence is a peptide of the invention, targeting one
 CC of the above listed targets.

XX Sequence 6 AA;

Query Match 30.8%; Score 4; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4
 ||||
 Db 1 FLLY 4

```

RESULT 64
ABU58293
ID ABU58293 standard; Peptide; 6 AA.
XX AC ABU58293;
XX DT 14-APR-2003 (first entry)
XX DE Poliovirus-binding peptide #8.
XX KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
XX KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
XX KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
XX KW surface-immobilised library; blood composition.
XX OS Synthetic.
XX PN US2002155106-A1.
XX PD 24-OCT-2002.
XX PF 01-DEC-2000; 2000US-0727963.
XX PR 01-DEC-2000; 2000US-0727963.
XX PA (HAMM/) HAMMOND D J.
XX PI Hammond DJ;
XX PT WPI; 2003-198483/19.
XX DR
XX PT New peptide comprising a porcine parvovirus-binding, hepatitis A
XX PT virus-binding or prion-binding domain, useful for screening a library
XX PT of surface-immobilized ligands that bind to target molecules -
XX PS Claim 30; Page 32; 35pp; English.
XX CC The invention relates to a peptide, having a sequence of less than 20
XX CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis
XX CC A virus (HAV)-binding, or prion-binding domain. Also included are
XX CC a composition comprising the peptide, removing a target from a biological
XX CC fluid, identifying a ligand for a target or targets and identifying a
XX CC peptide that binds to a virus present in a blood composition. The peptide
XX CC is useful for identifying a ligand for a target or targets (Hepatitis A
XX CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine
XX CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,
XX CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a
XX CC peptide that binds to a virus present in a blood composition. It is used
XX CC to screen a library of surface-immobilised ligands that bind to target
XX CC molecules. The peptide allows for multiple screenings of the same
XX CC surface-immobilised library for a number of different ligands.
XX CC The present sequence is a peptide of the invention, targeting one
XX CC of the above listed targets.
XX SQ Sequence 6 AA;
Query Match 30.8%; Score 4; DB 24; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FLLY 4
Db 1 FLLY 4
RESULT 65
ABU58312
ID ABU58312 standard; Peptide; 6 AA.
XX AC ABU58312;
XX DT 14-APR-2003 (first entry)
XX DE
XX KW Milk derived non-anti-hypertensive peptide.
XX KW Non-anti-hypertensive; fermentation; animal milk; Lactobacillus;
XX KW microorganism; digestion; protease; reduction; blood pressure.
XX OS Mammalian spp.
XX XX EP737690-A2.

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DE Peptide binding to hepatitis A virus in the presence of fibrinogen #23.
XX Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
XX KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
XX KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
XX KW surface-immobilised library; blood composition.
XX OS Synthetic.
XX PN US2002155106-A1.
XX PD 24-OCT-2002.
XX PF 01-DEC-2000; 2000US-0727963.
XX PR 01-DEC-2000; 2000US-0727963.
XX PA (HAMM/) HAMMOND D J.
XX PI Hammond DJ;
XX PT WPI; 2003-198483/19.
XX DR
XX PT New peptide comprising a porcine parvovirus-binding, hepatitis A
XX PT virus-binding or prion-binding domain, useful for screening a library
XX PT of surface-immobilized ligands that bind to target molecules -
XX PS Claim 4; Page 31; 35pp; English.
XX CC The invention relates to a peptide, having a sequence of less than 20
XX CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis
XX CC A virus (HAV)-binding, or prion-binding domain. Also included are
XX CC a composition comprising the peptide, removing a target from a biological
XX CC fluid, identifying a ligand for a target or targets and identifying a
XX CC peptide that binds to a virus present in a blood composition. The peptide
XX CC is useful for identifying a ligand for a target or targets (Hepatitis A
XX CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine
XX CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,
XX CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a
XX CC peptide that binds to a virus present in a blood composition. It is used
XX CC to screen a library of surface-immobilised ligands that bind to target
XX CC molecules. The peptide allows for multiple screenings of the same
XX CC surface-immobilised library for a number of different ligands.
XX CC The present sequence is a peptide of the invention, targeting one
XX CC of the above listed targets.
XX SQ Sequence 6 AA;
Query Match 30.8%; Score 4; DB 24; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FLLY 4
Db 1 FLLY 4
RESULT 66
AAW04280
ID AAW04280 standard; peptide; 7 AA.
XX AC AAW04280;
XX DT 06-JUN-1997 (first entry)
XX DE Milk derived non-anti-hypertensive peptide.
XX KW Non-anti-hypertensive; fermentation; animal milk; Lactobacillus;
XX KW microorganism; digestion; protease; reduction; blood pressure.
XX OS Mammalian spp.
XX XX EP737690-A2.

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XX 16-OCT-1996.
 XX
 PF 10-APR-1996; 96EP-0302522.
 XX
 PR 10-APR-1995; 95JP-0084247.
 XX
 PA (CALV) CALPIS FOOD IND CO LTD.
 XX
 PI Maeno M;
 XX
 DR WPI; 1996-457284/46.
 XX
 XX Antihypertensive compsns. derived from milk - by fermentation or
 PT protease digestion
 XX
 XX Example 1; Page 6; 10pp; English.
 XX
 CC The present non-anti-hypertensive (NAH) peptide was prepared by
 CC fermenting an animal milk starting material with a Lactobacillus
 CC microorganism, especially L. helveticus, L. delbrueckii subspecies
 CC bulgaricus or L. acidophilus, or digesting it with a protease at
 CC 20-50 degrees C for 3-30 hours, obtaining an eluent by
 CC ultrafiltration and then fractionating the eluent by reverse phase
 CC HPLC. The change in the systolic blood pressure of spontaneously
 CC hypertensive rats treated intragastrically with 1 mg/kg of body
 CC weight of the present NAH peptide was plus 1.2 +/- 9.8 mmHg.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 30.8%; Score 4; DB 17; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LLYQ 5
 DB 1 LLYQ 4

RESULT 67
 AAW30407
 ID AAW30407 standard; peptide; 7 AA.
 AC
 AC AAW30407;
 XX
 XX 22-APR-1998 (first entry)
 DT
 XX
 DE HRE-I affinity peptide SEQ ID NO:25.
 XX
 KW Binding site; HRE-I; screening; H-Ras; target gene; plasmid;
 KW inhibition; affinity peptide.
 XX
 OS Synthetic.
 OS
 XX WO9737030-A1.
 XX
 XX 09-OCT-1997.
 PD
 XX
 XX 31-MAR-1997; 97WO-JP01105.
 PF
 XX
 XX 03-OCT-1996; 96JP-0263345.
 PR
 PR 01-APR-1996; 96JP-0101990.
 XX
 XX (YAWH) NIPPON STEEL CHEM CO.
 PA (YAWA) NIPPON STEEL CORP.
 PA
 PI Kato T;
 XX
 XX WPI; 1997-503115/46.
 DR
 XX Plasmid for screening peptide(s) which bind target genes - for
 PT treatment of conditions associated with H-Ras
 XX

PS Claim 41; Page 65; 127pp; Japanese.
 XX
 CC A novel plasmid has been developed for screening peptides which bind
 CC target genes. The plasmid comprises a sequence encoding the test
 CC peptide, a promoter comprising the target gene, and a reporter gene
 CC bound to the promoter. The present sequence represents a specifically
 CC claimed peptide with affinity to HRE-I. The plasmids are used for
 CC screening for peptides which bind to target genes. The identified
 CC peptides can be used for the treatment of conditions associated with
 CC the inhibition of the expression the genes, and treatment of conditions
 CC associated with H-Ras.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 30.8%; Score 4; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LGPV 12
 DB 1 LGPV 4

RESULT 68
 ABG60365
 ID ABG60365 standard; Peptide; 7 AA.
 XX
 AC ABG60365;
 XX
 XX 30-JUL-2002 (first entry)
 DT
 XX
 DE Selective targeting peptide #40.
 XX
 KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
 KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
 KW gene therapy.
 XX
 OS Synthetic.
 OS
 XX WO200220769-A1.
 PN
 XX 14-MAR-2002.
 PD
 XX
 PF 07-SEP-2001; 2001WO-US27692.
 XX
 XX 08-SEP-2000; 2000US-231266P.
 PR
 PR 17-JAN-2001; 2001US-0765101.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX
 XX Arap W, Pasqualini R;
 XX
 XX WPI; 2002-415731/44.
 DR
 XX
 XX Targeting peptides identified by phage display, useful for targeting
 PT delivery to an organ or tissue, particularly for treating a disease,
 PT e.g. cancer, inflammatory or autoimmune diseases, infections or
 PT cardiovascular disease -
 XX
 XX Claim 22; Page 62; 317pp; English.
 PS
 XX
 CC The invention relates to an isolated peptide of 100 amino acids or less
 CC in size useful for targeting delivery to an organ or tissue, particularly
 CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
 CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
 CC infection, cardiovascular disease or degenerative disease. The peptide is
 CC also useful for inducing apoptosis, particularly to a subject with
 CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,
 CC inflammation or macular degeneration. Furthermore, the peptide is useful
 CC for diagnosing the diseases cited above. Targeting peptides of the

CC invention can also be used to deliver an agent to a foetus, by attaching
CC a peptide to the agent and administering the peptide to a pregnant
CC subject. Sequences ABG60326-ABG60574 represent selective targeting
CC peptides of the invention.

SQ Sequence 7 AA;
Query Match 30.8%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPVR 13
Db 4 GPVR 7

RESULT 69
ABG34932
ID ABG34932 standard; Peptide; 7 AA.
XX AC ABG34932;
XX DT 15-JUL-2002 (first entry)
XX DE Human bone marrow targeting peptide #4.
XX KW Targeting peptide; cancer; Hodgkin's disease; cytostatic;
KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
KW inflammatory disease; arthritis; atherosclerosis; cancer;
KW autoimmune disease; bacterial infection; viral infection.

OS Homo sapiens.
XX WO200220722-A2.
XX PD 14-MAR-2002.
XX PF 07-SEP-2001; 2001WO-US27702.
XX PR 08-SEP-2000; 2000US-231266P.
XX PR 17-JAN-2001; 2001US-0765101.
XX PA (TEXA) UNIV TEXAS SYSTEM.

PI Arap W, Pasqualini R;
XX WPI; 2002-383050/41.
XX PT Identifying targeting peptides useful for treating e.g. diabetes
PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,
PT comprises exposing a sample to a phage display library and recovering
PT phage bound to the sample -
XX Claim 56; Page 202; 298pp; English.

XX This invention relates to a novel method for identifying disease
XX targeting peptides. The method comprises exposing a sample from an
XX organ, tissue or cell type of interest, to a phage display library and
XX recovering phage bound to the sample (the phage expresses targeting
XX peptides). The peptides identified by the method of the invention may
XX have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
XX antiatherosclerotic, antidiabetic, antibacterial and antiviral
XX activities. The methods and composition are useful for identifying
XX targeting peptides and one or more receptors for a targeting peptide.
XX The targeting peptides are used for selective delivery of therapeutic
XX agents, including gene therapy vectors and fusion proteins, to specific
XX organs, tissues, or cell types in subject. The targeting peptide may
XX also be used for treating diseases such as diabetes mellitus,
XX inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune
XX diseases, bacterial and viral infections and Hodgkin's disease. The
XX present sequence represents a targeting peptide of the invention.

SQ Sequence 7 AA;
Query Match 30.8%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
Db 4 PVLG 7

RESULT 70
ABG34933
ID ABG34933 standard; Peptide; 7 AA.
XX AC ABG34933;
XX DT 15-JUL-2002 (first entry)
XX DE Human bone marrow targeting peptide #5.
XX KW Targeting peptide; cancer; Hodgkin's disease; cytostatic;
KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
KW inflammatory disease; arthritis; atherosclerosis; cancer;
KW autoimmune disease; bacterial infection; viral infection.

OS Homo sapiens.
XX WO200220722-A2.
XX PD 14-MAR-2002.
XX PF 07-SEP-2001; 2001WO-US27702.
XX PR 08-SEP-2000; 2000US-231266P.
XX PR 17-JAN-2001; 2001US-0765101.
XX PA (TEXA) UNIV TEXAS SYSTEM.

PI Arap W, Pasqualini R;
XX WPI; 2002-383050/41.
XX PT Identifying targeting peptides useful for treating e.g. diabetes
PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,
PT comprises exposing a sample to a phage display library and recovering
PT phage bound to the sample -
XX Claim 56; Page 202; 298pp; English.

XX This invention relates to a novel method for identifying disease
XX targeting peptides. The method comprises exposing a sample from an
XX organ, tissue or cell type of interest, to a phage display library and
XX recovering phage bound to the sample (the phage expresses targeting
XX peptides). The peptides identified by the method of the invention may
XX have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
XX antiatherosclerotic, antidiabetic, antibacterial and antiviral
XX activities. The methods and composition are useful for identifying
XX targeting peptides and one or more receptors for a targeting peptide.
XX The targeting peptides are used for selective delivery of therapeutic
XX agents, including gene therapy vectors and fusion proteins, to specific
XX organs, tissues, or cell types in subject. The targeting peptide may
XX also be used for treating diseases such as diabetes mellitus,
XX inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune
XX diseases, bacterial and viral infections and Hodgkin's disease. The
XX present sequence represents a targeting peptide of the invention.

SQ Sequence 7 AA;
Query Match 30.8%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGP 11
 Db 1 VLGP 4

RESULT 71
 ABJ19880
 ID ABJ19880 standard; Peptide; 7 AA.
 XX
 AC ABJ19880;
 XX
 DT 10-APR-2003 (first entry)
 XX
 DE MHC binding peptide SEQ ID No 45.
 XX
 KW Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;
 KW antiinflammatory; major histocompatibility complex; MHC;
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
 KW inflammation; gene therapy; MHC binding peptide.
 XX
 OS Synthetic.
 XX
 PN WO200294981-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 16-MAY-2002; 2002WO-IL00383.
 XX
 PR 16-MAY-2001; 2001US-290958P.
 PR 29-MAY-2001; 2001US-0865548.
 XX
 PA (TECR) TECHNION RES & DEV FOUND LTD.
 XX
 PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;
 DR WPI; 2003-210043/20.
 XX
 XX Identifying peptides that are capable of binding to major
 PT histocompatibility complex (MHC) molecules of a particular haplotype by
 PT analyzing peptides bound to the soluble and secreted form of the MHC
 PT molecules of the particular haplotype -
 XX
 PS Claim 37; Page 61; 238pp; English.
 XX
 CC The invention relates to a novel method for identifying peptides
 CC originating from a particular cell type, which are capable of binding to
 CC major histocompatibility complex (MHC) molecules of a particular
 CC haplotype. The method comprises analysing peptides bound to the soluble
 CC and secreted form of the MHC molecules of the particular haplotype. The
 CC method is useful for identifying peptides for treating an autoimmune
 CC disease, such as T or B cell and/or allergic disease or condition,
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
 CC sequences of the invention may be used in a gene therapy application.
 CC This sequence represents a peptide relating to the method for identifying
 CC MHC binding peptides of the invention.
 XX
 SQ Sequence 7 AA;
 Query Match 30.8%; Score 4; DB 24; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 EPVL 9
 Db 4 EPVL 7

RESULT 72
 AAR58333
 ID AAR58333 standard; peptide; 8 AA.

XX AAR58333;
 AC
 XX
 DT 22-SEP-1994 (first entry)
 XX
 DE Hypotensive polypeptide.
 XX
 KW Hypotensive; antioxidative; calcium absorption; salt; food;
 KW pharmaceuticals; physiologically active agents.
 XX
 OS Lactobacillus helveticus.
 XX
 PN JP06041191-A.
 XX
 PD 15-FEB-1994.
 XX
 PF 03-MAR-1993; 93JP-0043047.
 XX
 PR 04-MAR-1992; 92JP-0047340.
 XX
 PA (CALV) CALPIS SHOKUHN KOGYO KK.
 XX
 DR WPI; 1994-089332/11.
 XX
 XX New polypeptide - used in physiologically active agents having
 PT e.g. hypotensive antioxidative and calcium absorption promoting
 PT activity
 XX
 PS Claim 1-2; Page 9; 10pp; Japanese.
 XX
 CC Sequences (AAR58319-341) are used in conjunction with
 CC physiologically active agents showing a property such as
 CC hypotensive activity, calcium absorption promoting activity and
 CC antioxidative activity. The peptides are non-toxic and can be
 CC used in physiologically active agents.
 XX
 SQ Sequence 8 AA;
 Query Match 30.8%; Score 4; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 GPVR 13
 Db 1 GPVR 4

RESULT 73
 AAR84066
 ID AAR84066 standard; peptide; 8 AA.
 XX
 AC AAR84066;
 XX
 DT 21-AUG-1996 (first entry)
 XX
 DE Retinal pigment epithelial cell growth factor N-terminal peptide.
 XX
 KW Growth factor; proliferation; retina; pigment; ophthalmic disease;
 KW retinitis pigmentosa; erythema; retinal detachment.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "X= undefined amino acid"
 FT Misc-difference 6 /note= "X= undefined amino acid"
 FT
 XX JP08053362-A.
 PN
 XX
 PD 27-FEB-1996.
 XX
 PF 11-AUG-1994; 94JP-0189147.

CC	compositions. There is evidence that the immune response to whole
CC	antigens is directed largely toward variable regions of the antigen,
CC	allowing for immune escape due to mutations. The groups for inclusion in
CC	an group-based vaccine may be selected from conserved regions of viral or
CC	tumour-associated antigens, which therefore reduces the likelihood of
CC	escape mutants. Furthermore, immunosuppressive groups that may be present
CC	in whole antigens can be avoided with the use of group-based vaccines.
CC	An additional advantage of an group-based vaccine approach is the ability
CC	to combine selected groups (CTL and HTL), and further, to modify the
CC	composition of the groups, achieving, for example, enhanced
CC	immunogenicity. Accordingly, the immune response can be modulated, as
CC	appropriate, for the target disease. Similar engineering of the response
CC	is not possible with traditional approaches. ABP1501 to ABP25412
CC	represent peptide sequences used in the exemplification of the present
CC	invention.
XX	
SQ	Sequence 8 AA;
Query Match 30.8%; Score 4; DB 22; Length 8;	
Best Local Similarity 100.0%; Pred.No. 9.3e+05;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	4 YQEP 7
Db	1 YQEP 4
RESULT 75	
ABP14660	
ID	ABP14660 standard; Peptide; 8 AA.
AC	ABP14660;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	HIV A03 super motif pol peptide #34.
XX	
KW	HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW	vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW	antigen; vaccine; HIV infection; immunisation; virucide.
XX	
OS	Human immunodeficiency virus type 1.
XX	
PN	WO200124810-A1.
XX	
PD	12-APR-2001.
XX	
PF	05-OCT-2000; 2000WO-US27766.
XX	
PR	05-OCT-1999; 99US-0412863.
XX	
PA	(EPIV-) EPIIMUNE INC.
XX	
PI	Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI	Baker DM, Celis E, Kubo RT, Grey HM;
XX	
DR	WPI; 2001-354887/37.
XX	
PT	Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT	peptide groups, useful for vaccinating against HIV-1 -
XX	
PS	Claim 32; Page 168; 448pp; English.
XX	
CC	The present invention describes a composition (I) comprising a prepared
CC	human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC	sequence selected from 51 defined amino acid sequences (ABU25347 to
CC	ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC	may be used for immunising subjects against HIV-1 infections. The use of
CC	group-based vaccines has several advantages over traditional vaccines,
CC	particularly when compared to the use of whole antigens in vaccine
CC	compositions. There is evidence that the immune response to whole
CC	antigens is directed largely toward variable regions of the antigen,
CC	allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. APr1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.

XX
SQ Sequence 8 AA;

Query Match 30.8%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQEP 7
| | | |
Db 3 YQEP 6

Search completed: November 25, 2003, 19:27:22
Job time : 34.1802 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; search time 20.8605 seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLLYQEPVLGPVR 13

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	13	100.0	13	US-10-281-652-32	Sequence 32, Appl
2	7	53.8	7	US-10-305-346-12	Sequence 12, Appl
3	7	53.8	19	US-10-280-833-7	Sequence 7, Appl
4	6	46.2	7	US-10-281-652-28	Sequence 28, Appl
5	4	30.8	6	US-09-727-963A-15	Sequence 15, Appl
6	4	30.8	6	US-09-727-963A-25	Sequence 25, Appl
7	4	30.8	6	US-09-727-963A-27	Sequence 27, Appl
8	4	30.8	6	US-09-727-963A-45	Sequence 45, Appl
9	4	30.8	6	US-09-727-963A-47	Sequence 47, Appl
10	4	30.8	6	US-09-804-291-519	Sequence 519, Appl
11	4	30.8	6	US-10-229-423-49	Sequence 49, Appl
12	4	30.8	6	US-10-156-820-48	Sequence 48, Appl
13	4	30.8	6	US-10-259-430-49	Sequence 49, Appl
14	4	30.8	7	US-09-865-548A-45	Sequence 45, Appl
15	4	30.8	8	US-09-865-548A-200	Sequence 200, Appl

16	4	30.8	8	12	US-10-137-867-382	Sequence 382, Appl
17	4	30.8	9	10	US-09-894-018-79	Sequence 79, Appl
18	4	30.8	9	10	US-09-894-018-181	Sequence 181, Appl
19	4	30.8	9	10	US-09-894-018-183	Sequence 183, Appl
20	4	30.8	9	10	US-09-835-853-11	Sequence 11, Appl
21	4	30.8	9	11	US-09-865-548A-145	Sequence 145, Appl
22	4	30.8	9	12	US-09-793-451-130	Sequence 130, Appl
23	4	30.8	9	12	US-09-793-451-156	Sequence 156, Appl
24	4	30.8	9	12	US-09-793-451-251	Sequence 251, Appl
25	4	30.8	9	12	US-09-793-451-357	Sequence 357, Appl
26	4	30.8	9	12	US-09-793-451-456	Sequence 456, Appl
27	4	30.8	9	12	US-09-793-451-460	Sequence 460, Appl
28	4	30.8	9	12	US-09-793-451-529	Sequence 529, Appl
29	4	30.8	9	12	US-09-793-451-540	Sequence 540, Appl
30	4	30.8	9	12	US-09-793-451-641	Sequence 641, Appl
31	4	30.8	9	12	US-10-283-722-130	Sequence 130, Appl
32	4	30.8	9	12	US-10-283-722-156	Sequence 156, Appl
33	4	30.8	9	12	US-10-283-722-251	Sequence 251, Appl
34	4	30.8	9	12	US-10-283-722-357	Sequence 357, Appl
35	4	30.8	9	12	US-10-283-722-456	Sequence 456, Appl
36	4	30.8	9	12	US-10-283-722-460	Sequence 460, Appl
37	4	30.8	9	12	US-10-283-722-529	Sequence 529, Appl
38	4	30.8	9	12	US-10-283-722-540	Sequence 540, Appl
39	4	30.8	9	12	US-10-283-722-641	Sequence 641, Appl
40	4	30.8	9	12	US-10-371-069-376	Sequence 376, Appl
41	4	30.8	9	12	US-10-371-069-382	Sequence 382, Appl
42	4	30.8	9	12	US-10-371-645-376	Sequence 376, Appl
43	4	30.8	9	12	US-10-371-645-382	Sequence 382, Appl
44	4	30.8	9	15	US-10-133-210-112	Sequence 112, Appl
45	4	30.8	9	15	US-10-133-210-113	Sequence 113, Appl
46	4	30.8	9	15	US-10-254-464A-122	Sequence 122, Appl
47	4	30.8	10	11	US-09-572-404B-1421	Sequence 1421, Appl
48	4	30.8	10	11	US-09-572-404B-1423	Sequence 1423, Appl
49	4	30.8	10	11	US-09-572-404B-2039	Sequence 2039, Appl
50	4	30.8	10	11	US-09-572-404B-2945	Sequence 2945, Appl
51	4	30.8	10	11	US-09-572-404B-3866	Sequence 3866, Appl
52	4	30.8	10	11	US-09-572-404B-3867	Sequence 3867, Appl
53	4	30.8	10	11	US-09-572-404B-3868	Sequence 3868, Appl
54	4	30.8	10	11	US-09-572-404B-3869	Sequence 3869, Appl
55	4	30.8	10	11	US-09-572-404B-3870	Sequence 3870, Appl
56	4	30.8	10	12	US-09-793-451-183	Sequence 183, Appl
57	4	30.8	10	12	US-09-793-451-206	Sequence 206, Appl
58	4	30.8	10	12	US-09-793-451-272	Sequence 272, Appl
59	4	30.8	10	12	US-09-793-451-303	Sequence 303, Appl
60	4	30.8	10	12	US-09-793-451-474	Sequence 474, Appl
61	4	30.8	10	12	US-09-793-451-502	Sequence 502, Appl
62	4	30.8	10	12	US-09-793-451-594	Sequence 594, Appl
63	4	30.8	10	12	US-09-793-451-596	Sequence 596, Appl
64	4	30.8	10	12	US-09-793-451-691	Sequence 691, Appl
65	4	30.8	10	12	US-10-239-313A-433	Sequence 433, Appl
66	4	30.8	10	12	US-10-200-708-132	Sequence 132, Appl
67	4	30.8	10	12	US-10-200-708-564	Sequence 564, Appl
68	4	30.8	10	12	US-10-200-708-662	Sequence 662, Appl
69	4	30.8	10	12	US-10-283-722-183	Sequence 183, Appl
70	4	30.8	10	12	US-10-283-722-206	Sequence 206, Appl
71	4	30.8	10	12	US-10-283-722-272	Sequence 272, Appl
72	4	30.8	10	12	US-10-283-722-303	Sequence 303, Appl
73	4	30.8	10	12	US-10-283-722-474	Sequence 474, Appl
74	4	30.8	10	12	US-10-283-722-502	Sequence 502, Appl
75	4	30.8	10	12	US-10-283-722-594	Sequence 594, Appl
76	4	30.8	10	12	US-10-283-722-596	Sequence 596, Appl
77	4	30.8	10	12	US-10-283-722-691	Sequence 691, Appl
78	4	30.8	10	15	US-10-001-546-18	Sequence 18, Appl
79	4	30.8	10	15	US-10-043-487-345	Sequence 345, Appl
80	4	30.8	11	12	US-10-239-313A-435	Sequence 435, Appl
81	4	30.8	12	9	US-09-739-852-11	Sequence 11, Appl
82	4	30.8	12	11	US-09-354-385-312	Sequence 312, Appl
83	4	30.8	12	12	US-10-237-852-34	Sequence 34, Appl
84	4	30.8	12	12	US-10-237-852-46	Sequence 46, Appl
85	4	30.8	12	12	US-10-405-231-11	Sequence 11, Appl
86	4	30.8	12	15	US-10-238-607-11	Sequence 11, Appl
87	4	30.8	13	11	US-09-983-802-439	Sequence 439, Appl
88	4	30.8	13	12	US-10-239-313A-436	Sequence 436, Appl

89 4 30.8 14 11 US-09-992-331-22 Sequence 22, Appl
 90 4 30.8 14 16 US-10-262-313-22 Sequence 22, Appl
 91 4 30.8 15 12 US-10-336-491-6 Sequence 6, Appl
 92 4 30.8 15 12 US-10-239-313A-499 Sequence 499, App
 93 4 30.8 15 12 US-10-350-405-197 Sequence 197, App
 94 4 30.8 15 12 US-10-376-121A-5 Sequence 5, Appl
 95 4 30.8 15 15 US-10-033-741-77 Sequence 77, Appl
 96 4 30.8 15 15 US-10-033-662-71 Sequence 71, Appl
 97 4 30.8 16 10 US-09-791-378-550 Sequence 550, App
 98 4 30.8 16 10 US-09-791-378-564 Sequence 564, App
 99 4 30.8 16 11 US-09-791-393-238 Sequence 238, App
 100 4 30.8 16 11 US-09-791-389-238 Sequence 238, App

ALIGNMENTS

RESULT 1
 US-10-281-652-32
 ; Sequence 32, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: 265,00220101
 ; CURRENT APPLICATION NUMBER: US/10/281,652
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/09/641,803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 32
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-10-281-652-32

Query Match 100.0%; Score 13; DB 15; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.8e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLYQEPVLGPVR 13
 Db 1 FLLYQEPVLGPVR 13
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RESULT 2
 US-10-305-346-12
 ; Sequence 12, Application US/10305346
 ; Publication No. US20030130195A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AMIOT, Jean
 ; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS
 ; FILE REFERENCE: 6013-57"US"-1
 ; CURRENT APPLICATION NUMBER: US/10/305,346
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide

; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk proteins
 US-10-305-346-12

Query Match 53.8%; Score 7; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LYQEPVL 9
 Db 1 LYQEPVL 7
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RESULT 3
 US-10-280-833-7
 ; Sequence 7, Application US/10280833
 ; Publication No. US20030195150A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reynolds, Charles Eric
 ; APPLICANT: Dashper, Stuart Geoffrey
 ; APPLICANT: O'Brien-Simpson, Neil Martin
 ; APPLICANT: Talbot, Gert Hoy
 ; APPLICANT: Malkoski, Marina
 ; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES
 ; FILE REFERENCE: EDWP-001CON
 ; CURRENT APPLICATION NUMBER: US/10/280,833
 ; CURRENT FILING DATE: 2002-10-24
 ; PRIOR APPLICATION NUMBER: 09/554,997
 ; PRIOR FILING DATE: 2000-08-09
 ; PRIOR APPLICATION NUMBER: PP 0514
 ; PRIOR FILING DATE: 1997-11-24
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: bovine
 US-10-280-833-7

Query Match 53.8%; Score 7; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVLGPVR 13
 Db 13 PVLGPVR 19
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RESULT 4
 US-10-281-652-28
 ; Sequence 28, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: 265,00220101
 ; CURRENT APPLICATION NUMBER: US/10/281,652
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/09/641,803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 28
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide

US-10-281-652-28

Query Match 46.2%; Score 6; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQ 6
Db 2 FLLYQ 7

RESULT 5

US-09-727-963A-15
; Sequence 15, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence : peptide
; OTHER INFORMATION: ligand
US-09-727-963A-15

Query Match 30.8%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4
Db 1 FLLY 4

RESULT 6

US-09-727-963A-25
; Sequence 25, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence : peptide
; OTHER INFORMATION: ligand
US-09-727-963A-25

Query Match 30.8%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4

Db 1 FLLY 4
|||||

RESULT 7

US-09-727-963A-27
; Sequence 27, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence : peptide
; OTHER INFORMATION: ligand
US-09-727-963A-27

Query Match 30.8%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4
Db 1 FLLY 4

RESULT 8

US-09-727-963A-45
; Sequence 45, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand
US-09-727-963A-45

Query Match 30.8%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4
Db 1 FLLY 4

RESULT 9

US-09-727-963A-47
; Sequence 47, Application US/09727963A
; Patent No. US20020155106A1

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; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand
US-09-727-963A-47

Query Match          30.8%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYY 4
Db 1 FLYY 4

RESULT 10
US-09-804-291-519
; Sequence 519, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 519
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-804-291-519

Query Match          30.8%; Score 4; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYY 4
Db 1 FLYY 4

US-09-804-291-519

Query Match          30.8%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYY 4
Db 1 FLYY 4

US-09-804-291-519

Query Match          30.8%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 9 LGPV 12
```

```
Db 2 FLYY 5

RESULT 11
US-10-259-423-49
; Sequence 49, Application US/10259423
; Publication No. US20030175744A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-wai
; APPLICANT: Krutwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/10/259,423
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/465,901
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-259-423-49

Query Match          30.8%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYY 4
Db 2 FLYY 5

RESULT 12
US-10-156-820-48
; Sequence 48, Application US/10156820
; Publication No. US20020150558A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karavan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156,820
; CURRENT FILING DATE: 2002-06-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotope
US-10-156-820-48

Query Match          30.8%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 9 LGPV 12
```


Db 1 LGPV 4

RESULT 13
US-10-259-430-49
; Sequence 49, Application US/10259430
; Publication No. US20030082615A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/10/259,430
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/465,901
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-259-430-49

Query Match 30.8%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYY 4
Db 2 FLYY 5

RESULT 14
US-09-865-548A-45
; Sequence 45, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamir
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-45

Query Match 30.8%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPVL 9
Db 4 EPVL 7

RESULT 15
US-09-865-548A-200
; Sequence 200, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamir
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-200

Query Match 30.8%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPVL 9
Db 4 EPVL 7

RESULT 16
US-10-137-867-382
; Sequence 382, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 382
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-382

Query Match 30.8%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;

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Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      8 VLGP 11
      ||||
Db      4 VLGP 7

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Transgenic mouse
US-09-894-018-181

Query Match      30.8%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      4 YOEP 7
      ||||
Db      2 YOEP 5
      ||||

RESULT 19
US-09-894-018-183
; Sequence 183, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-09-894-018-79

Query Match      30.8%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      4 YOEP 7
      ||||
Db      2 YOEP 5
      ||||

RESULT 18
US-09-894-018-181
; Sequence 181, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Transgenic mouse
US-09-894-018-183

Query Match      30.8%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      4 YOEP 7
      ||||
Db      5 YOEP 8
      ||||

RESULT 20
US-09-835-853-11
; Sequence 11, Application US/09835853
; Patent No. US20020165136A1
; GENERAL INFORMATION:
; APPLICANT: BASERGA, Renato L.
; APPLICANT: RESNICOFF, Mariana
; APPLICANT: HUANG, Ziwei
; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/835,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/704,344
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, Henry N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8459
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-09-835-853-11

Query Match 30.8%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPVL 13
DB 5 GPVR 8

RESULT 21
US-09-865-548A-145
; Sequence 145, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
;
US-09-865-548A-145

Query Match 30.8%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPVL 9
DB 4 EPVL 7

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/793,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
;
US-09-793-451-130

Query Match 30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
DB 1 LLYQ 4

RESULT 23
US-09-793-451-156
; Sequence 156, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
;
US-09-793-451-156

Query Match 30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

US-09-793-451-357
Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLYQ 5
Db 3 LLYQ 6

RESULT 26
US-09-793-451-456
; Sequence 456, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 456
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-456

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLYQ 5
Db 1 LLYQ 4

RESULT 27
US-09-793-451-460
; Sequence 460, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-457

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLYQ 5
Db 1 LLYQ 4

RESULT 25
US-09-793-451-357
; Sequence 357, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-251

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLYQ 5
Db 2 LLYQ 5

RESULT 24
US-09-793-451-251
; Sequence 251, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-251

```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 460
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-460
```

```
Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 LLYQ 5
Db 5 LLYQ 8
```

RESULT 28

```
US-09-793-451-529
; Sequence 529, Application US/09793451
; Publication No. US20030157597A1
```

GENERAL INFORMATION:

```
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 529
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-529
```

```
Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 LLYQ 5
Db 5 LLYQ 8
```

RESULT 29

```
US-09-793-451-540
; Sequence 540, Application US/09793451
; Publication No. US20030157597A1
```

GENERAL INFORMATION:

```
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
```

```
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 540
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-540
```

```
Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 LLYQ 5
Db 1 LLYQ 4
```

RESULT 30

```
US-09-793-451-641
; Sequence 641, Application US/09793451
; Publication No. US20030157597A1
```

GENERAL INFORMATION:

```
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-641
```

```
Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 LLYQ 5
Db 5 LLYQ 8
```

RESULT 31

```
US-10-283-722-130
; Sequence 130, Application US/10283722
; Publication No. US20030194407A1
```

GENERAL INFORMATION:

```
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
```

```
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-130

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLYQ 5
        ||||
Db      1 LLYQ 4

RESULT 32
US-10-283-722-156
; Sequence 156, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-156

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLYQ 5
        ||||
Db      2 LLYQ 5

RESULT 33
US-10-283-722-251
; Sequence 251, Application US/10283722
; Publication No. US20030194407A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-251

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLYQ 5
        ||||
Db      1 LLYQ 4

RESULT 34
US-10-283-722-357
; Sequence 357, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-357

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 LLYQ 5
      ||||
Db      3 LLYQ 6

RESULT 35
US-10-283-722-456
; Sequence 456, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 456
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-456

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLYQ 5
      ||||
Db      1 LLYQ 4

RESULT 36
US-10-283-722-460
; Sequence 460, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 460

Qy      2 LLYQ 5
      ||||
Db      1 LLYQ 4

RESULT 37
US-10-283-722-529
; Sequence 529, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 529
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-529

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLYQ 5
      ||||
Db      5 LLYQ 8

RESULT 38
US-10-283-722-540
; Sequence 540, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
```

```
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 540
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-540
```

```
Query Match 30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 LLYQ 5
Db 1 LLYQ 4
```

RESULT 39

```
US-10-283-722-641
; Sequence 641, Application US/10283722
; Publication No. US20030194407A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-641
```

```
Query Match 30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 LLYQ 5
Db 5 LLYQ 8
```

RESULT 40

```
US-10-371-069-376
; Sequence 376, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
```

```
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 376
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1036 (peptide 1069.60)
US-10-371-069-376
```

```
Query Match 30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 YOEP 7
Db 2 YOEP 5
```

RESULT 41

```
US-10-371-069-382
; Sequence 382, Application US/10371069
; Publication No. US20030216342A1
```

```
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1033 (peptide 1069.59)
US-10-371-069-382
```

```
Query Match 30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 YOEP 7
Db 5 YOEP 8
```



```
RESULT 42
US-10-371-645-376
; Sequence 376, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 376
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1036 (peptide 1069..60)
US-10-371-645-376

Query Match          30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YQEP 7
Db      2 YQEP 5

RESULT 43
US-10-371-645-382
; Sequence 382, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1033 (peptide 1069..59)
US-10-371-645-382

Query Match          30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YQEP 7
Db      2 YQEP 5

RESULT 44
US-10-133-210-112
; Sequence 112, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-112

Query Match          30.8%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YQEP 7
Db      5 YQEP 8

RESULT 45
US-10-133-210-113
; Sequence 113, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-113

Query Match          30.8%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YQEP 7
Db      5 YQEP 8
```

QY 4 YQEP 7
Db 2 YQEP 5

RESULT 46

US-10-254-446A-122
; Sequence 122, Application US/1025446A

; Publication No. US20030113714A1

; GENERAL INFORMATION:

; APPLICANT: Belcher, Angela M

; APPLICANT: Smalley, Richard E.

; APPLICANT: Ryan, Esther

; APPLICANT: Lee, Seung-Wuk

; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES

; FILE REFERENCE: 119927-1066

; CURRENT APPLICATION NUMBER: US/10/254,446A

; CURRENT FILING DATE: 2003-02-19

; PRIOR APPLICATION NUMBER: 60/325,664

; PRIOR FILING DATE: 2001-09-28

; NUMBER OF SEQ ID NOS: 245

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 122

; LENGTH: 9

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopan

US-10-254-446A-122

Query Match 30.8%; Score 4; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10

Db 3 PVLG 6

RESULT 47

US-09-572-404B-1421

; Sequence 1421, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 1421

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in CACNA1L3 OR CACNA1 OR CACNA1 at 1707

US-09-572-404B-1421

Query Match 30.8%; Score 4; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGP 11

Db 4 VLGP 7

RESULT 48

US-09-572-404B-1423

; Sequence 1423, Application US/09572404B

```
;
; FEATURE:
; OTHER INFORMATION: sequence located in GUCY2D OR GUC2D OR RETGC1 OR RETGC OR GUC1A4
; OTHER INFORMATION: CORD6 at 52-61 and may interact with Sequence 2946 in this patent
US-09-572-404B-2945

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLPV 11
Db 7 VLPV 10

RESULT 51
US-09-572-404B-3866
; Sequence 3866, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3866
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 394-403 and may interact with S
US-09-572-404B-3866

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 6 LGPV 9

RESULT 52
US-09-572-404B-3867
; Sequence 3867, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3867
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 394-403 and may interact with S
US-09-572-404B-3867

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 6 LGPV 9

RESULT 53
US-09-572-404B-3868
; Sequence 3868, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3868
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 395-404 and may interact with
US-09-572-404B-3868

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 5 LGPV 8

RESULT 54
US-09-572-404B-3869
; Sequence 3869, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3869
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 393-402 and may interact with
US-09-572-404B-3869

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 7 LGPV 10

RESULT 55
US-09-572-404B-3870
; Sequence 3870, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
```

; SEQ ID NO 3870
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 396-405 and may interact with S
; OTHER INFORMATION: 3871 in this patent.
US-09-572-404B-3870

Query Match 30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGPV 12
Db 4 LGPV 7

RESULT 56
US-09-793-451-183
; Sequence 183, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-183

Query Match 30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
Db 2 LLYQ 5

RESULT 57
US-09-793-451-206
; Sequence 206, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2

; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-206

Query Match 30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
Db 6 LLYQ 9

RESULT 58
US-09-793-451-272
; Sequence 272, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-272

Query Match 30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
Db 1 LLYQ 4

RESULT 59
US-09-793-451-303
; Sequence 303, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid

```
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-303
```

```
Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 LLYQ 5
         ||||
Db       2 LLYQ 5
```

RESULT 60

```
US-09-793-451-474
; Sequence 474, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-474
```

```
Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 LLYQ 5
         ||||
Db       2 LLYQ 5
```

RESULT 61

```
US-09-793-451-502
; Sequence 502, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Arthur B. Raitano
```

```
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-502
```

```
Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 LLYQ 5
         ||||
Db       6 LLYQ 9
```

RESULT 62

```
US-09-793-451-594
; Sequence 594, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-594
```

```
Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 LLYQ 5
         ||||
Db       2 LLYQ 5
```

RESULT 63

US-09-793-451-596
 ; Sequence 596, Application US/09793451
 ; Publication No. US20030157597A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Daniel E.H. Afar
 ; APPLICANT: Gazelle S. Rastegar
 ; APPLICANT: Steve Chappell Mitchell
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Pia M. Challita-Eid
 ; APPLICANT: Mary Faris
 ; APPLICANT: Aya Jakobovits
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
 ; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
 ; FILE REFERENCE: 129.2USU2
 ; CURRENT APPLICATION NUMBER: US/09/793,451
 ; CURRENT FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: 60/184,558
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/218,856
 ; PRIOR FILING DATE: 2000-07-13
 ; NUMBER OF SEQ ID NOS: 752
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 596
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-09-793-451-596

Query Match 30.8%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 LLYQ 5
 Db 6 LLYQ 9

RESULT 64
 US-09-793-451-691
 ; Sequence 691, Application US/09793451
 ; Publication No. US20030157597A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Daniel E.H. Afar
 ; APPLICANT: Gazelle S. Rastegar
 ; APPLICANT: Steve Chappell Mitchell
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Pia M. Challita-Eid
 ; APPLICANT: Mary Faris
 ; APPLICANT: Aya Jakobovits
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
 ; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
 ; FILE REFERENCE: 129.2USU2
 ; CURRENT APPLICATION NUMBER: US/09/793,451
 ; CURRENT FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: 60/184,558
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/218,856
 ; PRIOR FILING DATE: 2000-07-13
 ; NUMBER OF SEQ ID NOS: 752
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 691
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-09-793-451-691

Query Match 30.8%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 LLYQ 5

Db 5 LLYQ 8
 ||||

RESULT 65
 US-10-239-313A-433
 ; Sequence 433, Application US/10239313A
 ; Publication No. US20030175285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KLINGUER - HAMOUR, Christine
 ; APPLICANT: CORVAIA, Nathalie
 ; APPLICANT: BECK, Alain
 ; APPLICANT: GOETSCH, Liliane
 ; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
 ; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
 ; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
 ; FILE REFERENCE: 343 727 - US
 ; CURRENT APPLICATION NUMBER: US/10/239,313A
 ; CURRENT FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: FR 00/03711
 ; PRIOR FILING DATE: 2000-03-23
 ; PRIOR APPLICATION NUMBER: PCT 01/70772
 ; PRIOR FILING DATE: 2001-03-22
 ; NUMBER OF SEQ ID NOS: 697
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 433
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-239-313A-433

Query Match 30.8%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YQEP 7
 Db 3 YQEP 6
 ||||

RESULT 66
 US-10-200-708-132
 ; Sequence 132, Application US/10200708
 ; Publication No. US20030180314A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DeGroot, Anne S.
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
 ; FILE REFERENCE: 17999-001
 ; CURRENT APPLICATION NUMBER: US/10/200,708
 ; CURRENT FILING DATE: 2002-07-22
 ; PRIOR APPLICATION NUMBER: US/09/351,036
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 60/092,346
 ; PRIOR FILING DATE: 1998-07-10
 ; PRIOR APPLICATION NUMBER: 60/115,145
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: 60/130,677
 ; PRIOR FILING DATE: 1999-04-23
 ; NUMBER OF SEQ ID NOS: 672
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 132
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-200-708-132

Query Match 30.8%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YQEP 7
 Db 2 YQEP 5
 ||||

RESULT 67
 US-10-200-708-564
 ; Sequence 564, Application US/10200708
 ; Publication No. US200301803141
 ; GENERAL INFORMATION:
 ; APPLICANT: DeGroot, Anne S.
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
 ; FILE REFERENCE: 17999-001
 ; CURRENT APPLICATION NUMBER: US/10/200,708
 ; CURRENT FILING DATE: 2002-07-22
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 60/092,346
 ; PRIOR FILING DATE: 1998-07-10
 ; PRIOR APPLICATION NUMBER: 60/115,145
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: 60/130,677
 ; PRIOR FILING DATE: 1999-04-23
 ; NUMBER OF SEQ ID NOS: 672
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 564
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-200-708-564

Query Match 30.8%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred.No.7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YQEP 7
 Db 6 YQEP 9

RESULT 68
 US-10-200-708-662
 ; Sequence 662, Application US/10200708
 ; Publication No. US200301803141
 ; GENERAL INFORMATION:
 ; APPLICANT: DeGroot, Anne S.
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
 ; FILE REFERENCE: 17999-001
 ; CURRENT APPLICATION NUMBER: US/10/200,708
 ; CURRENT FILING DATE: 2002-07-22
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 60/092,346
 ; PRIOR FILING DATE: 1998-07-10
 ; PRIOR APPLICATION NUMBER: 60/115,145
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: 60/130,677
 ; PRIOR FILING DATE: 1999-04-23
 ; NUMBER OF SEQ ID NOS: 672
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 662
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-200-708-662

Query Match 30.8%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred.No.7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YQEP 7
 Db 2 YQEP 5

RESULT 69

US-10-283-722-183
 ; Sequence 183, Application US/10283722
 ; Publication No. US20030194407A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Daniel E.H. Afar
 ; APPLICANT: Gazelle S. Rastegar
 ; APPLICANT: Steve Chappell Mitchell
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Pia M. Challita-Eid
 ; APPLICANT: Mary Faris
 ; APPLICANT: Aya Jakobovits
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
 ; FILE REFERENCE: 129.2USU2
 ; CURRENT APPLICATION NUMBER: US/10/283,722
 ; CURRENT FILING DATE: 2003-02-03
 ; PRIOR APPLICATION NUMBER: US/09/793,451
 ; PRIOR FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: 60/184,558
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/218,856
 ; PRIOR FILING DATE: 2000-07-13
 ; NUMBER OF SEQ ID NOS: 752
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 183
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-283-722-183

Query Match 30.8%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred.No.7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLYQ 5
 Db 2 LLYQ 5

RESULT 70
 US-10-283-722-206
 ; Sequence 206, Application US/10283722
 ; Publication No. US20030194407A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Daniel E.H. Afar
 ; APPLICANT: Gazelle S. Rastegar
 ; APPLICANT: Steve Chappell Mitchell
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Pia M. Challita-Eid
 ; APPLICANT: Mary Faris
 ; APPLICANT: Aya Jakobovits
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
 ; FILE REFERENCE: 129.2USU2
 ; CURRENT APPLICATION NUMBER: US/10/283,722
 ; CURRENT FILING DATE: 2003-02-03
 ; PRIOR APPLICATION NUMBER: US/09/793,451
 ; PRIOR FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: 60/184,558
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/218,856
 ; PRIOR FILING DATE: 2000-07-13
 ; NUMBER OF SEQ ID NOS: 752
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 206
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-283-722-206

Query Match 30.8%; Score 4; DB 12; Length 10;

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Best Local Similarity 100.0%; Pred. No. 7.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 2 LLYQ 5
   ||||
Db 6 LLYQ 9

RESULT 71
US-10-283-722-272
; Sequence 272, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-272

Query Match 30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
   ||||
Db 1 LLYQ 4

RESULT 72
US-10-283-722-303
; Sequence 303, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
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; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-303

Query Match 30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
   ||||
Db 2 LLYQ 5

RESULT 73
US-10-283-722-474
; Sequence 474, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-474

Query Match 30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
   ||||
Db 2 LLYQ 5

RESULT 74
US-10-283-722-502
; Sequence 502, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
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; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 502
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-502

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```

Query Match      30.8%  Score 4;  DB 12;  Length 10;
Best Local Similarity 100.0%;  Pred. No. 7.4e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      2 LLYQ 5
Db      6 LLYQ 9

```

```

RESULT 75
US-10-283-722-594
; Sequence 594, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-594

```

```

Query Match      30.8%  Score 4;  DB 12;  Length 10;
Best Local Similarity 100.0%;  Pred. No. 7.4e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      2 LLYQ 5
Db      2 LLYQ 5

```

```

Search completed: November 25, 2003, 20:37:08
Job time : 21.8605 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 10.5058 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLLYQEPVLGPR 13

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	%	ID	Description
1	13	100.0	13	4	US-09-641-803-32
2	7	53.8	7	4	US-09-492-766-12
3	6	46.2	7	4	US-09-641-803-28
4	5	38.5	10	2	US-08-617-929-14
5	5	38.5	13	5	PCT-US94-10257A-16
6	5	38.5	14	2	US-08-617-923-16
7	5	38.5	20	1	US-08-399-646-6
8	5	38.5	20	1	US-08-399-646-10
9	5	38.5	20	1	US-08-607-321-6
10	5	38.5	20	1	US-08-607-321-10
11	5	38.5	20	2	US-08-961-240-6
12	5	38.5	20	2	US-08-961-240-10
13	5	38.5	20	2	US-08-605-501-6
14	5	38.5	20	2	US-08-605-501-10
15	5	38.5	20	5	PCT-US94-10257A-91
16	4	30.8	6	4	US-09-155-613A-48
17	4	30.8	6	4	US-09-465-901-49
18	4	30.8	7	1	US-08-212-433A-46
19	4	30.8	7	3	US-08-716-256-46
20	4	30.8	7	5	PCT-US95-03239-46
21	4	30.8	9	3	US-08-159-339A-366
22	4	30.8	9	3	US-08-159-339A-516
23	4	30.8	9	3	US-08-159-339A-517
24	4	30.8	9	3	US-08-660-092-110
25	4	30.8	9	3	US-08-660-092-121
26	4	30.8	9	3	US-08-660-092-125
27	4	30.8	9	3	US-08-704-344-11

28	4	30.8	9	4	US-09-160-513-110	Sequence 110, App
29	4	30.8	9	4	US-09-160-513-121	Sequence 121, App
30	4	30.8	9	4	US-09-160-513-125	Sequence 125, App
31	4	30.8	9	4	US-09-311-784A-376	Sequence 376, App
32	4	30.8	9	4	US-09-311-784A-382	Sequence 382, App
33	4	30.8	10	1	US-08-203-716-17	Sequence 17, Appl
34	4	30.8	10	1	US-08-440-179-17	Sequence 17, Appl
35	4	30.8	10	3	US-08-159-339A-375	Sequence 375, App
36	4	30.8	10	3	US-09-039-657-17	Sequence 17, Appl
37	4	30.8	10	4	US-08-980-523-1	Sequence 1, Appl
38	4	30.8	10	4	US-08-403-459-18	Sequence 18, Appl
39	4	30.8	11	3	US-08-159-339A-641	Sequence 641, App
40	4	30.8	11	3	US-08-159-339A-1159	Sequence 1159, App
41	4	30.8	11	6	5177197-24	Patent No. 5177197
42	4	30.8	12	1	US-08-260-582-63	Sequence 63, Appl
43	4	30.8	12	1	US-08-442-063A-23	Sequence 23, Appl
44	4	30.8	12	2	US-08-750-856A-9	Sequence 9, Appl
45	4	30.8	12	2	US-08-617-929-17	Sequence 17, Appl
46	4	30.8	12	2	US-08-659-984A-8	Sequence 8, Appl
47	4	30.8	12	3	US-09-075-257A-20	Sequence 20, Appl
48	4	30.8	12	3	US-09-133-341-11	Sequence 11, Appl
49	4	30.8	12	3	US-08-660-531-8	Sequence 8, Appl
50	4	30.8	12	3	US-09-534-639-20	Sequence 20, Appl
51	4	30.8	12	4	US-09-739-852-11	Sequence 11, Appl
52	4	30.8	12	4	US-09-692-170C-11	Sequence 11, Appl
53	4	30.8	12	5	PCT-US95-05471-63	Sequence 63, Appl
54	4	30.8	13	1	US-08-064-400B-16	Sequence 16, Appl
55	4	30.8	13	1	US-08-291-601-1	Sequence 1, Appl
56	4	30.8	13	1	US-08-291-601-2	Sequence 2, Appl
57	4	30.8	13	1	US-08-291-601-3	Sequence 3, Appl
58	4	30.8	13	4	US-09-227-357-439	Sequence 439, App
59	4	30.8	14	1	US-07-956-700B-82	Sequence 82, Appl
60	4	30.8	14	1	US-07-956-700B-92	Sequence 92, Appl
61	4	30.8	14	1	US-08-476-537-82	Sequence 82, Appl
62	4	30.8	14	1	US-08-476-537-92	Sequence 92, Appl
63	4	30.8	14	1	US-08-485-607-82	Sequence 82, Appl
64	4	30.8	14	2	US-08-485-607-92	Sequence 92, Appl
65	4	30.8	14	2	US-08-659-984A-11	Sequence 11, Appl
66	4	30.8	14	2	US-08-475-873-82	Sequence 82, Appl
67	4	30.8	14	2	US-08-475-873-92	Sequence 92, Appl
68	4	30.8	14	3	US-08-660-531-11	Sequence 11, Appl
69	4	30.8	14	4	US-09-433-043B-82	Sequence 82, Appl
70	4	30.8	14	4	US-09-433-043B-92	Sequence 92, Appl
71	4	30.8	15	1	US-07-794-288D-20	Sequence 20, Appl
72	4	30.8	15	1	US-09-501-612A-6	Sequence 6, Appl
73	4	30.8	16	1	US-07-794-288D-19	Sequence 19, Appl
74	4	30.8	16	1	US-08-077-797A-36	Sequence 36, Appl
75	4	30.8	16	3	US-08-602-999A-207	Sequence 207, App
76	4	30.8	16	4	US-09-009-953-36	Sequence 36, Appl
77	4	30.8	16	4	US-09-500-124-207	Sequence 207, App
78	4	30.8	16	5	PCT-US94-01238-36	Sequence 36, Appl
79	4	30.8	17	1	US-07-794-288D-18	Sequence 18, Appl
80	4	30.8	18	1	US-07-794-288D-17	Sequence 17, Appl
81	4	30.8	18	1	US-07-794-288D-214	Sequence 214, Appl
82	4	30.8	18	1	US-08-244-116B-9	Sequence 9, Appl
83	4	30.8	18	2	US-08-816-105A-11	Sequence 11, Appl
84	4	30.8	18	6	5258287-50	Patent No. 5258287
85	4	30.8	19	1	US-07-794-288D-16	Sequence 16, Appl
86	4	30.8	19	1	US-07-794-288D-126	Sequence 126, App
87	4	30.8	19	1	US-08-507-124-5	Sequence 5, Appl
88	4	30.8	19	3	US-08-928-213B-35	Sequence 35, Appl
89	4	30.8	20	1	US-07-794-288D-15	Sequence 15, Appl
90	4	30.8	20	1	US-07-794-288D-118	Sequence 118, App
91	4	30.8	20	1	US-07-794-288D-125	Sequence 125, App
92	4	30.8	20	1	US-08-484-635-140	Sequence 140, App
93	4	30.8	20	2	US-08-484-631-140	Sequence 140, App
94	4	30.8	20	2	US-08-617-929-1	Sequence 1, Appl
95	4	30.8	20	3	US-08-827-570-140	Sequence 140, App
96	4	30.8	20	3	US-09-247-527-17	Sequence 17, Appl
97	4	30.8	20	5	PCT-US94-10257A-90	Sequence 90, Appl
98	3	23.1	4	1	US-07-657-769B-14	Sequence 14, Appl
99	3	23.1	4	1	US-07-657-769B-54	Sequence 54, Appl
100	3	23.1	4	1	US-07-729-353-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
 US-09-641-803-32
 ; Sequence 32, Application US/09641803
 ; Patent No. 6500798
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/09/641,803
 ; CURRENT FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 32
 ; LENGTH: 13
 ; TYPE: PPT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-09-641-803-32

Query Match 100.0%; Score 13; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQEPVLGPVR 13
 |||||
 Db 1 FLLYQEPVLGPVR 13

RESULT 2
 US-09-492-766-12
 ; Sequence 12, Application US/09492766
 ; Patent No. 6506732
 ; GENERAL INFORMATION:
 ; APPLICANT: AMIOT, Jean
 ; TITLE OF INVENTION: ENZYMIC HYDROLYSATE OF MILK PROTEINS
 ; FILE REFERENCE: 6013-57"US"
 ; CURRENT APPLICATION NUMBER: US/09/492,766
 ; CURRENT FILING DATE: 2000-01-27
 ; EARLIER APPLICATION NUMBER: 60/117,661
 ; EARLIER FILING DATE: 1999-01-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 7
 ; TYPE: PPT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk
 ; OTHER INFORMATION: proteins
 US-09-492-766-12

Query Match 53.8%; Score 7; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQEPVL 9
 |||||
 Db 1 LYQEPVL 7

RESULT 3

US-09-641-803-28
 ; Sequence 28, Application US/09641803
 ; Patent No. 6500798
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/09/641,803
 ; CURRENT FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 28
 ; LENGTH: 7
 ; TYPE: PPT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-09-641-803-28

Query Match 46.2%; Score 6; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQ 6
 |||||
 Db 2 FLLYQ 7

RESULT 4
 US-08-617-929-14
 ; Sequence 14, Application US/08617929
 ; Patent No. 5895771
 ; GENERAL INFORMATION:
 ; APPLICANT: KUMAZAWA, Toshiaki
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND
 ; TITLE OF INVENTION: IMMUNOASSAY
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/617,929
 ; FILING DATE: 24-APR-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/JP94/01823
 ; FILING DATE: 28-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6/207695
 ; FILING DATE: 31-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 5/272864
 ; FILING DATE: 29-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saxe, Bernhard D.
 ; REGISTRATION NUMBER: 28,665
 ; REFERENCE/DOCKET NUMBER: 77384/109
 ; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-617-929-14

Query Match      38.5%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLYQE 6
Db      3 LLYQE 7
      |||||

RESULT 5
PCT-US94-10257A-16
; Sequence 16, Application PC/TUS9410257A
; GENERAL INFORMATION:
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
; APPLICANT: BRIGITTE DEVAUX
; APPLICANT: JONATHAN B. ROTHBARD
; APPLICANT: DAWN SMILEK
; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
; TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A
; FILING DATE: 1 SEPTEMBER 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824
; FILING DATE: 03-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 071.1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US94-10257A-16

Query Match      38.5%; Score 5; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PVLGP 11
      |||||

; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-617-929-14

Query Match      38.5%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLYQE 6
Db      3 LLYQE 7
      |||||

RESULT 5
PCT-US94-10257A-16
; Sequence 16, Application PC/TUS9410257A
; GENERAL INFORMATION:
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
; APPLICANT: BRIGITTE DEVAUX
; APPLICANT: JONATHAN B. ROTHBARD
; APPLICANT: DAWN SMILEK
; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
; TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A
; FILING DATE: 1 SEPTEMBER 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824
; FILING DATE: 03-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 071.1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US94-10257A-16

Query Match      38.5%; Score 5; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PVLGP 11
      |||||

; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-617-929-14

Query Match      38.5%; Score 5; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLYQE 6
Db      10 LLYQE 14
      |||||

RESULT 7
US-08-399-646-6
; Sequence 6, Application US/08399646
; Patent No. 5556781
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE

```

```

Db      8 PVLGP 12

RESULT 6
US-08-617-929-16
; Sequence 16, Application US/08617929
; Patent No. 5885771
; GENERAL INFORMATION:
; APPLICANT: KUMAZAWA, Toshiaki
; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND
; TITLE OF INVENTION: IMMUNOASSAY
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,929
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01823
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6/207695
; FILING DATE: 31-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5/272864
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 77384/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-617-929-16

Query Match      38.5%; Score 5; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LLYQE 6
Db      10 LLYQE 14
      |||||

RESULT 7
US-08-399-646-6
; Sequence 6, Application US/08399646
; Patent No. 5556781
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE

```

```

; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,646
; FILING DATE: 07-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-399-646-6

```

```

Query Match 38.5%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 PVLGP 11
    |||||
Db 11 PVLGP 15

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RESULT 8
US-08-399-646-10
; Sequence 10, Application US/08399646
; Patent No. 5556781
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuo
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,646
; FILING DATE: 07-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-399-646-10

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```

Query Match 38.5%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 7 PVLGP 11
    |||||
Db 1 PVLGP 5

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RESULT 9
US-08-607-321-6
; Sequence 6, Application US/08607321
; Patent No. 5716813
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuo
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,321
; FILING DATE: 26-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:

```

```
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-607-321-6

Query Match      38.5%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PVLGP 11
Db      11 PVLGP 15

RESULT 10
US-08-607-321-10
; Sequence 10, Application US/08607321
; Patent No. 5715813
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,321
; FILING DATE: 26-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid

; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-961-240-6

Query Match      38.5%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PVLGP 11
Db      1 PVLGP 5

RESULT 11
US-08-961-240-6
; Sequence 6, Application US/08961240
; Patent No. 5830715
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,240
; FILING DATE: 30-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-961-240-6

Query Match      38.5%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PVLGP 11
Db      1 PVLGP 5
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```

Db          11 PVLGP 15

RESULT 12
US-08-961-240-10
; Sequence 10, Application US/08961240
; Patent No. 5830715
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,240
; FILING DATE: 30-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-961-240-10

Query Match          38.5%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 PVLGP 11
           |||||
Db          1 PVLGP 5

RESULT 13
US-08-605-501-6
; Sequence 6, Application US/08605501
; Patent No. 5834287
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

Query Match          38.5%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 PVLGP 11
           |||||
Db          1 PVLGP 5

RESULT 14
US-08-605-501-10
; Sequence 10, Application US/08605501
; Patent No. 5834287
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

Query Match          38.5%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 PVLGP 11
           |||||
Db          11 PVLGP 15

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,501
; FILING DATE: 26-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-605-501-10

Query Match 38.5%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11
DB 1 PVLGP 5

RESULT 15
PCT-US94-10257A-91
; Sequence 91, Application PC/TUS9410257A
; GENERAL INFORMATION:
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
; APPLICANT: BRIGITTE DEVAUX
; APPLICANT: JONATHAN B. ROTHBARD
; APPLICANT: DAWN SMILEK
; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
; TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A
; FILING DATE: 1 SEPTEMBER 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824
```

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; FILING DATE: 03-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 071.1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; PCT-US94-10257A-91

Query Match 38.5%; Score 5; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11
DB 7 PVLGP 11

RESULT 16
US-09-155-613A-48
; Sequence 48, Application US/09155613A
; Patent No. 6420120
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/09/155,613A
; CURRENT FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 6
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotope
; US-09-155-613A-48

Query Match 30.8%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGPV 12
DB 1 LGPV 4

RESULT 17
US-09-465-901-49
; Sequence 49, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
```


;; TITLE OF INVENTION: ad Methods of Making and Using Them
;; FILE REFERENCE: 001107.00105
;; CURRENT APPLICATION NUMBER: US/09/465,901
;; CURRENT FILING DATE: 2001-12-17
;; PRIOR APPLICATION NUMBER: 60/112,605
;; PRIOR FILING DATE: 1998-12-17
;; NUMBER OF SEQ ID NOS: 57
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 49
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Mus musculus
;; FEATURE:
;; OTHER INFORMATION: PCR primer
US-09-465-901-49

Query Match 30.8%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYY 4
Db 2 FLYY 5

RESULT 18
US-08-212-433A-46
; Sequence 46, Application US/08212433A
; Patent No. 553897
; GENERAL INFORMATION:
; APPLICANT: Yates, III, John R.
; APPLICANT: Eng, James K.
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS OF PEPTIDES TO IDENTIFY AMINO ACID SEQUENCES IN
; TITLE OF INVENTION: DATABASES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart St. Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,433A
FILING DATE: 14-MAR-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Hughes, Richard L.
REGISTRATION NUMBER: 31,264
REFERENCE/DOCKET NUMBER: 16336-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-212-433A-46

Query Match 30.8%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 FVLG 10

Db 3 FVLG 6
RESULT 19
US-08-716-256-46
; Sequence 46, Application US/08716256
; Patent No. 6017693
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,256
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03239
FILING DATE: 14-MAR-1995
APPLICATION NUMBER: US 08/212,433
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 16336-2PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-256-46

Query Match 30.8%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 FVLG 10
Db 3 FVLG 6

RESULT 20
PCT-US95-03239-46
; Sequence 46, Application PC/TUS9503239
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03239
FILING DATE: 14-MAR-1995
CLASSIFICATION:

```
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/212,433
/ FILING DATE: 14-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parmelee, Steven W.
/ REGISTRATION NUMBER: 31,990
/ REFERENCE/DOCKET NUMBER: 16336-2PC
/ TELEPHONE: 206-467-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ PCT-US95-03239-46

Query Match 30.8%; Score 4; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
DB 3 PVLG 6

RESULT 21
US-08-159-339A-366
/ Sequence 366, Application US/08159339A
/ Patent No. 6037135
/ GENERAL INFORMATION:
/ APPLICANT: Kubo, Ralph T.
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Celis, Esteban
/ TITLE OF INVENTION: HLA Binding peptides and Their
/ NUMBER OF INVENTIONS: Uses
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: Fast-SEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/159,339A
/ FILING DATE: 29-NOV-1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/926,666
/ FILING DATE: 07-AUG-1992
/ APPLICATION NUMBER: US 08/027,746
/ FILING DATE: 05-MAR-1993
/ APPLICATION NUMBER: US 08/103,396
/ FILING DATE: 06-AUG-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Weber, Ellen Lauver
/ REGISTRATION NUMBER: 32,762
/ REFERENCE/DOCKET NUMBER: 018623-0050300S
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 366:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-159-339A-366

Query Match 30.8%; Score 4; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
DB 3 PVLG 6

RESULT 22
US-08-159-339A-516
/ Sequence 516, Application US/08159339A
/ Patent No. 6037135
/ GENERAL INFORMATION:
/ APPLICANT: Kubo, Ralph T.
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Celis, Esteban
/ TITLE OF INVENTION: HLA Binding peptides and Their
/ NUMBER OF INVENTIONS: Uses
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: Fast-SEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/159,339A
/ FILING DATE: 29-NOV-1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/926,666
/ FILING DATE: 07-AUG-1992
/ APPLICATION NUMBER: US 08/027,746
/ FILING DATE: 05-MAR-1993
/ APPLICATION NUMBER: US 08/103,396
/ FILING DATE: 06-AUG-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Weber, Ellen Lauver
/ REGISTRATION NUMBER: 32,762
/ REFERENCE/DOCKET NUMBER: 018623-0050300S
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 516:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-159-339A-516

Query Match 30.8%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQEP 7
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```
/
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-159-339A-366

Query Match 30.8%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
DB 1 LLYQ 4

RESULT 22
US-08-159-339A-516
/ Sequence 516, Application US/08159339A
/ Patent No. 6037135
/ GENERAL INFORMATION:
/ APPLICANT: Kubo, Ralph T.
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Celis, Esteban
/ TITLE OF INVENTION: HLA Binding peptides and Their
/ NUMBER OF INVENTIONS: Uses
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: Fast-SEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/159,339A
/ FILING DATE: 29-NOV-1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/926,666
/ FILING DATE: 07-AUG-1992
/ APPLICATION NUMBER: US 08/027,746
/ FILING DATE: 05-MAR-1993
/ APPLICATION NUMBER: US 08/103,396
/ FILING DATE: 06-AUG-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Weber, Ellen Lauver
/ REGISTRATION NUMBER: 32,762
/ REFERENCE/DOCKET NUMBER: 018623-0050300S
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 516:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-159-339A-516

Query Match 30.8%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQEP 7
```

```

Db      5 YQEP 8
|||||
RESULT 23
US-08-159-339A-517
; Sequence 517, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 517:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-517
Query Match      30.8%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      4 YQEP 7
|||||
Db      2 YQEP 5

RESULT 24
US-08-660-092-110
; Sequence 110, Application US/08660092
; Patent No. 6207160
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; TITLE OF INVENTION:
; TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

Query Match      30.8%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      7 PVLG 10
|||||
Db      3 PVLG 6

RESULT 25
US-08-660-092-121
; Sequence 121, Application US/08660092
; Patent No. 6207160
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION:
; TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```
/ APPLICATION NUMBER: US/08/660,092
/ FILING DATE: 06-JUN-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Park, Freddie K.
/ REGISTRATION NUMBER: 35,636
/ REFERENCE/DOCKET NUMBER: 25231-20061.20
/ TELEPHONE: (415) 813-5600
/ TELEFAX: (415) 494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 121:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-660-092-121

Query Match 30.8%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
Db 3 PVLG 6

RESULT 26
US-08-660-092-125
; Sequence 125, Application US/08660092
; Patent No. 6207160
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION: APL IMMUNOREACTIVE PEPTIDES, CONJUGATES
; TITLE OF INVENTION: THREEOF AND METHODS OF TREATMENT FOR APL ANTIBODY-MEDIATED
; TITLE OF INVENTION: PATHOLOGIES
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,092
; FILING DATE: 06-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Park, Freddie K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 25231-20061.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-660-092-125
; Sequence 125, Application US/08704344
; Patent No. 6218363
; GENERAL INFORMATION:
; APPLICANT: BASERGA, Renato L.
; APPLICANT: RESNICOFF, Mariana
; APPLICANT: HUANG, Ziwei
; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,344
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, Henry N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.196
; TELEPHONE: (202) 942-8459
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-704-344-11

Query Match 30.8%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPVR 13
Db 5 GPVR 8

RESULT 28
US-09-160-513-110
; Sequence 110, Application US/09160513
; Patent No. 6410775
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
```

```
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-160-513-110

Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
DB 3 PVLG 6

RESULT 29
US-09-160-513-121
; Sequence 121, Application US/09160513
; Patent No. 6410775
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-160-513-125

Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
DB 3 PVLG 6

RESULT 30
US-09-160-513-125
; Sequence 125, Application US/09160513
; Patent No. 6410775
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-160-513-125

Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVLG 11
```

```
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-160-513-121

Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
DB 3 PVLG 6

RESULT 30
US-09-160-513-125
; Sequence 125, Application US/09160513
; Patent No. 6410775
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-160-513-125

Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVLG 11
```

Db 4 VLGP 7
|||||
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 YOEP 7
Db 2 YOEP 5
|||||
US-09-311-784A-376
; Sequence 382, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.01
; CURRENT FILING DATE: 1999-05-13
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 376
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1036 (peptide 1069.60)
US-09-311-784A-376
Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 YOEP 7
Db 2 YOEP 5
|||||
US-09-311-784A-382
; Sequence 382, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.01
; CURRENT FILING DATE: 1999-05-13
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1033 (peptide 1069.59)
US-09-311-784A-382
Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 YOEP 7
Db 5 YOEP 8
|||||
US-08-203-716-17
; Sequence 17, Application US/08203716
; Patent No. 5416013
; GENERAL INFORMATION:
; APPLICANT: BLACK, ROY A
; APPLICANT: SLEATH, PAUL R
; APPLICANT: KRONHEIM, SHIRLEY R
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &
; STREET: 180 N. STETSON
; CITY: CHICAGO
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/203,716
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/750,644
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KATZ, MARTIN L. 25011
; REGISTRATION NUMBER: IMMUNEX2108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165400
; TELEFAX: 3126165460
; TELEX: 9102211206
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-203-716-17
Query Match 30.8%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GPVR 13
Db 6 GPVR 9
|||||
US-08-440-179-17
; Sequence 17, Application US/08440179
; Patent No. 5756465
; GENERAL INFORMATION:
; APPLICANT: BLACK, ROY A
; APPLICANT: SLEATH, PAUL R
; APPLICANT: KRONHEIM, SHIRLEY R
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &

ADDRESSEE: MILNAMOW
STREET: 180 N. STETSON
CITY: CHICAGO
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,179
FILING DATE: 12-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,644
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: KATZ, MARTIN L.
REGISTRATION NUMBER: 25011
REFERENCE/DOCKET NUMBER: IMMUNEX2108
TELEPHONE: 3126165400
TELEFAX: 3126165460
TELEX: 9102211206
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-179-17

Query Match 30.8%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 10 GPCR 13
Db 6 GPCR 9

RESULT 35
US-08-159-339A-375
Sequence 375, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessadro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 375:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-375

Query Match 30.8%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 2 LLYQ 5
Db 2 LLYQ 5

RESULT 36
US-09-039-657-17
Sequence 17, Application US/09039657
Patent No. 6136787
GENERAL INFORMATION:
APPLICANT: Black, Roy A.
APPLICANT: Sleath, Paul R.
APPLICANT: Kronheim, Shirley R.
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN
TITLE OF INVENTION: 1B PROTEASE INHIBITORS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,657
FILING DATE: 16-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI/SW002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-039-657-17

Query Match 30.8%; Score 4; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 10 GPVR 13
 ||||
 Db 6 GPVR 9

RESULT 37

US-08-980-523-1
 ; Sequence 1, Application US/08980523
 ; Patent No. 6310181
 ; GENERAL INFORMATION:
 ; APPLICANT: Kouhara, Haruhiko
 ; APPLICANT: Spivak-Kroizman, Taly
 ; APPLICANT: Lax, Irit
 ; APPLICANT: Schlössinger, Joseph
 ; TITLE OF INVENTION: ADAPTOR PROTEIN PRS2 AND
 ; TITLE OF INVENTION: RELATED PRODUCTS AND METHODS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/980,523
 FILING DATE: December 1, 1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/21851
 FILING DATE: December 1, 1997
 APPLICATION NUMBER: 60/032,093
 FILING DATE: December 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 230/045
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-980-523-1

Query Match 30.8%; Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 VLGP 11
 ||||
 Db 2 VLGP 5

RESULT 38

US-08-403-459-18

; Sequence 18, Application US/08403459
 ; Patent No. 6514942
 ; GENERAL INFORMATION:
 ; APPLICANT: Ioannides, Constantin G.
 ; APPLICANT: Fisk, Bryan A.
 ; APPLICANT: Ioannides, Maria G.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
 ; TITLE OF INVENTION: T-LYMPHOCYTES
 ; NUMBER OF SEQUENCES: 68
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: United States of America
 ; ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/403,459
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: UTSC:390/KIT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (713) 789-2679
 TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-403-459-18

Query Match 30.8%; Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 LLYQ 5
 ||||
 Db 2 LLYQ 5

RESULT 39

US-08-159-339A-641

; Sequence 641, Application US/08159339A

; Patent No. 6037135

GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.
 APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Esteban
 TITLE OF INVENTION: HLA Binding peptides and Their
 TITLE OF INVENTION: Uses
 NUMBER OF SEQUENCES: 1254
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible


```

; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159.339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 641:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-641

Query Match 30.8%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YOEP 7
Db 6 YOEP 9

RESULT 40
US-08-159-339A-1159
; Sequence 1159, Application US/08/159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159.339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396

```

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; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1159

Query Match 30.8%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YOEP 7
Db 3 YOEP 6

RESULT 41
5177197-24
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUO;OLOFSSON, ANDERS;MOREN, ANITA;
; WERNSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESON-WELSH,
; LENA;HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO:24:
; LENGTH: 11
5177197-24

Query Match 30.8%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
Db 5 PVLG 8

RESULT 42
US-08-260-582-63
; Sequence 63, Application US/08260582
; Patent No. 5635182
; GENERAL INFORMATION:
; APPLICANT: McCoy, John M.
; APPLICANT: Lu, Zhijian
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND
; TITLE OF INVENTION: INTERACTIONS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/260.582
;; FILING DATE: 16-JUN-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meinert, M. C.
;; REGISTRATION NUMBER: 31,544
;; REFERENCE/DOCKET NUMBER: GI 5236
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 876-1170
;; TELEFAX: (617) 876-5851
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEetical: NO
;; ANTI-SENSE: NO
US-08-260-582-63

Query Match 30.8%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLPV 11
Db 3 VLPV 6

RESULT 43
US-08-442-063A-23
;; Sequence 23, Application US/08442063A
;; Patent No. 5705609
;; GENERAL INFORMATION:
;; APPLICANT: RUOSLAHTI, ERKKI I.
;; APPLICANT: PIERSCHACHER, MICHAEL D.
;; APPLICANT: CARDENAS, JOSE
;; APPLICANT: CRAIG, WILLIAM
;; APPLICANT: MULLEN, DANIEL G.
;; TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
;; TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
;; NUMBER OF SEQUENCES: 62
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: CAMPBELL AND FLORES
;; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
;; CITY: SAN DIEGO
;; STATE: CALIFORNIA
;; COUNTRY: UNITED STATES
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/442.063A
;; FILING DATE: 16-MAY-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION INFORMATION:
;; APPLICANT NUMBER: US 07/865,652
;; FILING DATE: 03-APR-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAMPBELL, CATHRYN A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LA 1454
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-535-9001
;; TELEFAX: 619-535-8949
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
US-08-442-063A-23

Query Match 30.8%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 5 LGPV 8

RESULT 44
US-08-750-856A-9
;; Sequence 9, Application US/08750856A
;; Patent No. 5858672
;; GENERAL INFORMATION:
;; APPLICANT: SONIGO, PIERRE
;; APPLICANT: PANCINO, GIANFRANCO
;; APPLICANT: PETERHANS, ERNST
;; APPLICANT: BERTONI, GIUSEPPE
;; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS AND CORRESPONDING
;; TITLE OF INVENTION: PEPTIDE FRAGMENTS FROM THE CAPRINE ARTHRITIS-ENCEPHALITIS
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCELLELAND, MAIER & NEUSTADT,
;; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;; CITY: ARLINGTON
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/750.856A
;; FILING DATE: 30-DEC-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 94/07933
;; FILING DATE: 28-JUN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, NORMAN F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 917-052-0 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-413-3000
;; TELEFAX: 703-413-2220
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-750-856A-9

Query Match 30.8%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LYQE 6
Db 9 LYQE 12

RESULT 45
 US-08-617-929-17
 ; Sequence 17, Application US/08617929
 ; Patent No. 5885771
 ; GENERAL INFORMATION:
 ; APPLICANT: KUMAZAWA, Toshiaki
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND
 ; TITLE OF INVENTION: IMMUNOSSAY
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/617,929
 ; FILING DATE: 24-APR-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/JP94/01823
 ; FILING DATE: 28-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6/207695
 ; FILING DATE: 31-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 5/272864
 ; FILING DATE: 29-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SAXE, Bernhard D.
 ; REGISTRATION NUMBER: 28,665
 ; REFERENCE/DOCKET NUMBER: 77384/109
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-617-929-17
 Query Match 30.8%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.6e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 2 LLYQ 5
 Db 9 LLYQ 12

RESULT 46
 US-08-659-984A-8
 ; Sequence 8, Application US/08659984A
 ; Patent No. 5942400
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Jacobson-Croak, Kirsten L.
 ; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
 ; TITLE OF INVENTION: Inhibition
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Ctr., 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/659,984A
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,152
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002810US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-659-984A-8
 Query Match 30.8%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.6e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 6 EPVL 9
 Db 6 EPVL 9

RESULT 47
 US-09-075-257A-20
 ; Sequence 20, Application US/09075257A
 ; Patent No. 6074645
 ; GENERAL INFORMATION:
 ; APPLICANT: DIAMOND, DON JEFFREY
 ; APPLICANT: YORK, JOANNE
 ; TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES
 ; TITLE OF INVENTION: OF HUMAN CYTOMEGALOVIRUS
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BART G. NEWMAN
 ; STREET: 555 13TH STREET, NW SUITE 701E
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/075,257A
 ; FILING DATE: 11-MAY-1998
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/021,298
 ; FILING DATE: 10-FEB-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/950,064

;
; FILING DATE: 14-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/747,488
; FILING DATE: 12-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: NEWLAND, BART G
; REGISTRATION NUMBER: 31,282
; REFERENCE/DOCKET NUMBER: 1954-112CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-075-257A-20

Query Match 30.8%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLPG 11
Db 2 VLPG 5

RESULT 48

US-09-133-341-11
; Sequence 11, Application US/09133341A
; Patent No. 6162440
; GENERAL INFORMATION:
; APPLICANT: Hayward, Diane S.
; APPLICANT: Ling, Paul D.
; TITLE OF INVENTION: EBNA2 PEPTIDES AND METHODS OF USING SAME
; FILE REFERENCE: 87512
; CURRENT APPLICATION NUMBER: US/09/133,341A
; CURRENT FILING DATE: 1998-08-13
; EARLIER APPLICATION NUMBER: WO 97US2243
; EARLIER FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
; US-09-133-341-11

Query Match 30.8%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVLG 10
Db 8 PVLG 11

RESULT 49

US-08-660-531-8
; Sequence 8, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysier, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

;
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-660-531-8

Query Match 30.8%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EPVL 9
Db 6 EPVL 9

RESULT 50

US-09-534-639-20
; Sequence 20, Application US/09534639
; Patent No. 6251399
; GENERAL INFORMATION:
; APPLICANT: Diamond, Don J
; APPLICANT: York, Joanne
; TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN
; TITLE OF INVENTION: CYTOMEGALOVIRUS
; FILE REFERENCE: 1954-343
; CURRENT APPLICATION NUMBER: US/09/534,639
; CURRENT FILING DATE: 2000-03-27
; EARLIER APPLICATION NUMBER: 09/075,257
; EARLIER FILING DATE: 1998-05-11
; EARLIER APPLICATION NUMBER: 09/021,298
; EARLIER FILING DATE: 1998-02-10
; EARLIER APPLICATION NUMBER: 08/950,064
; EARLIER FILING DATE: 1997-10-14
; EARLIER APPLICATION NUMBER: 08/747,488
; EARLIER FILING DATE: 1996-11-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human Cytomegalovirus
; US-09-534-639-20

Query Match 30.8%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      8 VLGP 11
DB      2 VLGP 5

RESULT 51
US-09-739-852-11
; Sequence 11, Application US/09739852
; Patent No. 6495144
; GENERAL INFORMATION:
; APPLICANT: Hayward, Diane S.
; TITLE OF INVENTION: EBN2 PEPTIDES AND METHODS OF USING SAME
; FILE REFERENCE: 87512
; CURRENT APPLICATION NUMBER: US/09/739,852
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/133,341
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
US-09-739-852-11

Query Match      30.8%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PVLG 10
DB      8 PVLG 11

RESULT 52
US-09-692-170C-11
; Sequence 11, Application US/09692170C
; Patent No. 6562345
; GENERAL INFORMATION:
; APPLICANT: Diamond, Don J.
; TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
; FILE REFERENCE: 1954-346
; CURRENT APPLICATION NUMBER: US/09/692,170C
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 09/534,639
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/075,257
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: US 09/021,298
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 08/950,064
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: US 08/747,488
; PRIOR FILING DATE: 1996-11-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human cytomegalovirus
US-09-692-170C-11

Query Match      30.8%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VLGP 11
DB      2 VLGP 5

us-09-641-801-32.oligo.ra1

RESULT 53
PCT-US95-05471-63
; Sequence 63, Application PC/TUS9505471
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS
; NUMBER OF SEQUENCES: 76
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05471
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
PCT-US95-05471-63

Query Match      30.8%; Score 4; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VLGP 11
DB      3 VLGP 6

RESULT 54
US-08-064-400B-16
; Sequence 16, Application US/08064400B
; Patent No. 5559028
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: Regulation of Antigen Presentation
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,400B
; FILING DATE: May 19, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH93-01
; TELEPHONE: 207-363-0558
; TELEFAX: 207-363-0528
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-064-400B-16
```

Query Match 30.8%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 LYQE 6
|||
DB 1 LYQE 4

RESULT 55
US-08-291-601-1
; Sequence 1, Application US/08291601
; Patent No. 5679527
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: US
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,601
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9401M
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-291-601-1

Query Match 30.8%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 LYQE 6
|||
DB 1 LYQE 4

RESULT 56
US-08-291-601-2
; Sequence 2, Application US/08291601
; Patent No. 5679527
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: US
; ZIP: 03911

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,601
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9401M
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-291-601-2

Query Match 30.8%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 LYQE 6
|||
DB 1 LYQE 4

RESULT 57
US-08-291-601-3
; Sequence 3, Application US/08291601
; Patent No. 5679527
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: US
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,601
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9401M
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-291-601-3

Query Match 30.8%; Score 4; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 3 LYQE 6
|||
Db 1 LYQE 4

RESULT 58
US-09-227-357-439
; Sequence 439, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984

; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 439
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-439

Query Match 30.8%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 FLYY 4
|||
Db 7 FLYY 10

RESULT 59
US-07-956-700B-82
; Sequence 82, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-07-956-700B-82

Query Match 30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

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QY      4 YOEP 7
Db      1 YOEP 4

RESULT 60
US-07-956-700B-92
; Sequence 92, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-07-956-700B-92

Query Match      30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YOEP 7
Db      1 YOEP 4

RESULT 61
US-08-476-537-82
; Sequence 82, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-07-956-700B-92

Query Match      30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YOEP 7
Db      1 YOEP 4

RESULT 62
US-08-476-537-92
; Sequence 92, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-476-537-82

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; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-476-537-82

Query Match      30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YOEP 7
Db      1 YOEP 4

RESULT 62
US-08-476-537-92
; Sequence 92, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-476-537-82

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;
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-92

Query Match 30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YQEP 7
Db 1 YQEP 4

RESULT 63
US-08-485-607-82
; Sequence 82, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485.607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-485-607-92

Query Match 30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YQEP 7
Db 1 YQEP 4

RESULT 64
US-08-485-607-92
; Sequence 92, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485.607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-485-607-82

Query Match 30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YQEP 7
Db 1 YQEP 4

RESULT 65
US-08-659-984A-11
; Sequence 11, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659.984A
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;
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 14
; OTHER INFORMATION: /note="C-terminal Lys is
; OTHER INFORMATION: amidated."
US-08-659-984A-11

Query Match 30.8%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 6 BPVL 9
Db 8 BPVL 11

RESULT 66
US-08-475-879-82
; Sequence 82, Application US/08475879
; Patent No. 5972644
; Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5972644 5786170th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-475-879-92

Query Match 30.8%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 4 YQEP 7
Db 1 YQEP 4

RESULT 68
US-08-660-531-11
; Sequence 11, Application US/08660531
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;
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-475-879-82

Query Match 30.8%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 4 YQEP 7
Db 1 YQEP 4

RESULT 67
US-08-475-879-92
; Sequence 92, Application US/08475879
; Patent No. 5972644
; Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5972644 5786170th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-475-879-92

Query Match 30.8%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 4 YQEP 7
Db 1 YQEP 4

RESULT 68
US-08-660-531-11
; Sequence 11, Application US/08660531
```

; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(14)
; OTHER INFORMATION: /note= "C-terminal Lys is
; OTHER INFORMATION: amidated."
US-08-660-531-11

Query Match 30.8%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPVL 9
Db 8 EPVL 11
|||
|||

RESULT 69
US-09-433-043B-82
; Sequence 82, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-433-043B-82

Query Match 30.8%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQEP 7
Db 1 YQEP 4
|||
|||

RESULT 70
US-09-433-043B-92
; Sequence 92, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-433-043B-92

Query Match 30.8%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQEP 7
Db 1 YQEP 4
|||
|||

RESULT 71
US-07-794-288D-20
; Sequence 20, Application US/07794288D
; Patent No. 5580953
; GENERAL INFORMATION:
; APPLICANT: ELISABETH ALBRECHT,
; APPLICANT: HOWARD JONES,
; APPLICANT: LAURA S.L. GAETA,
; APPLICANT: KATHRYN S. PRICKETT and
; APPLICANT: KEVIN BEAUMONT
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: First Interstate World
; STREET: Center
; STREET: 633 West Fifth Street,
; STREET: Suite 4700

```

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44
; MEDIUM TYPE: Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: IBM M.S. DOS (Version
; OPERATING SYSTEM: 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA: US/07/794,288D
; APPLICATION NUMBER: 07/794,288D
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/794,288
; FILING DATE: 19-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Duft, Bradford, J.
; REGISTRATION NUMBER: 32,219
; REFERENCE/DOCKET NUMBER: 193/153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FEATURE:
; OTHER INFORMATION:
; US-07-794-288D-20

```

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Query Match 30.8%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 9 LGPV 12
Db 1 LGPV 4

```

```

RESULT 72
US-09-501-612A-6
; Sequence 6, Application US/09501612A
; Patent No. 6544765
; GENERAL INFORMATION:
; APPLICANT: Hjoert, Carsten M.
; APPLICANT: Pedersen, Henrik
; TITLE OF INVENTION: Oxaloacetate Hydrolase Deficient Fungal Host Cells
; FILE REFERENCE: 5789.200-US
; CURRENT APPLICATION NUMBER: US/09/501.612A
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-09-501-612A-6

```

```

Query Match 30.8%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 QEPV 8
Db 4 QEPV 7

```

```

RESULT 73
US-07-794-288D-19
; Sequence 19, Application US/07794288D
; Patent No. 5580953
; GENERAL INFORMATION:
; APPLICANT: ELISABETH ALBRECHT,
; APPLICANT: HOWARD JONES,
; APPLICANT: LAURA S. L. GAETA,
; APPLICANT: KATHRYN S. PRICKETT and
; APPLICANT: KEVIN BEAUMONT
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: First Interstate World
; STREET: Center
; STREET: 633 West Fifth Street,
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44
; MEDIUM TYPE: Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: IBM M.S. DOS (Version
; OPERATING SYSTEM: 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/794,288D
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/794,288
; FILING DATE: 19-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Duft, Bradford, J.
; REGISTRATION NUMBER: 32,219
; REFERENCE/DOCKET NUMBER: 193/153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FEATURE:
; OTHER INFORMATION:
; US-07-794-288D-19

```

```

Query Match 30.8%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 9 LGPV 12
Db 2 LGPV 5

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RESULT 74
US-08-077-797A-36
; Sequence 36, Application US/0807797A
; Patent No. 5679548
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Rosenblum, Jonathan
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL

```

;/ TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
;/ NUMBER OF SEQUENCES: 65
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: The Scripps Research Institute, Office of
;/ ADDRESSEE: Patent Counsel
;/ STREET: 10666 No. 5679548th Torrey Pines Road, TPC8
;/ CITY: La Jolla
;/ STATE: CA
;/ COUNTRY: USA
;/ ZIP: 92037
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/077,797A
;/ FILING DATE: 14-JUN-1993
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/012,566
;/ FILING DATE: 02-FEB-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Fitting, Thomas
;/ REGISTRATION NUMBER: 34,163
;/ REFERENCE/DOCKET NUMBER: SCRI276P
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 619-554-2937
;/ TELEFAX: 619-554-6312
;/ INFORMATION FOR SEQ ID NO: 36:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 16 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ FRAGMENT TYPE: internal
;/ US-08-077-797A-36

Query Match 30.8%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 10 GPCR 13
Db 1 GPCR 4

RESULT 75
US-08-602-999A-207
;/ Sequence 207, Application US/08602999A
;/ Patent No. 6184205
;/ GENERAL INFORMATION:
;/ APPLICANT: SPARKS, Andrew B.
;/ APPLICANT: KAY, Brian K.
;/ APPLICANT: THORN, Judith M.
;/ APPLICANT: QUILLIAM, Lawrence A.
;/ APPLICANT: DER, Channing J.
;/ APPLICANT: FOWLKES, Dana M.
;/ APPLICANT: RIDER, James E.
;/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;/ TITLE OF INVENTION: ISOLATING AND USING SAME
;/ NUMBER OF SEQUENCES: 467
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Pennie & Edmonds
;/ STREET: 1155 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10036-2711
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS

;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/602,999A
;/ FILING DATE: 16-FEB-1996
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Misrock, S. Leslie
;/ REGISTRATION NUMBER: 18,872
;/ REFERENCE/DOCKET NUMBER: 1101-202
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212) 790-9090
;/ TELEFAX: (212) 869-9741/8864
;/ TELEX: 66141 PENNIE
;/ INFORMATION FOR SEQ ID NO: 207:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 16 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: peptide
;/ US-08-602-999A-207

Query Match 30.8%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 VLGP 11
Db 3 VLGP 6

Search completed: November 25, 2003, 20:30:08
Job time : 11.5058 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 : Search time 2.05814 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3

Sequence: 1 LNF 3

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76:**

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	100.0	8	2	Ac1348
2	3	100.0	8	2	red pigment-concen
3	3	100.0	8	2	hypertrehalosemic
4	3	100.0	9	2	hypertrehalosemic
5	3	100.0	10	2	calsequestrin, car
6	3	100.0	11	2	Fc mu (IgM) recept
7	3	100.0	12	2	T-cell receptor al
8	3	100.0	15	2	Fc mu (IgM) recept
9	3	100.0	16	2	T-cell receptor be
10	3	100.0	16	2	crystal protein, 2
11	3	100.0	17	2	T cell receptor al
12	3	100.0	18	2	phage antigenic de
13	3	100.0	20	2	T-cell receptor al
14	2	66.7	6	2	creatine kinase (E
15	2	66.7	7	2	neuropeptide GMRFR
16	2	66.7	7	2	glutathione transf
17	2	66.7	7	2	callifMRamide 11
18	2	66.7	7	2	acetylcholinestera
19	2	66.7	7	2	pullulanase (EC 3.
20	2	66.7	8	2	probable H+-transp
21	2	66.7	8	2	adipokinetic hormo
22	2	66.7	8	2	hypertrehalosemic
23	2	66.7	8	2	adipokinetic hormo
24	2	66.7	8	2	adipokinetic hormo
25	2	66.7	8	2	neuropeptide Led-C
26	2	66.7	8	2	adipokinetic hormo
27	2	66.7	8	2	adipokinetic hormo
28	2	66.7	8	2	adipokinetic hormo
29	2	66.7	8	2	capsid protein Vp-

30	2	66.7	8	2	A05169	neuropeptide M-I -
31	2	66.7	8	2	S21563	neuropeptide - flo
32	2	66.7	8	2	A39892	P element, P cytot
33	2	66.7	9	2	A14683	aspartate transami
34	2	66.7	9	1	AKLQIM	locustamycininhibi
35	2	66.7	9	2	S19523	orf AB protein - S
36	2	66.7	9	2	A57444	neuropeptide Grb-A
37	2	66.7	9	2	B57444	neuropeptide Grb-A
38	2	66.7	9	2	S78420	gene NF2 protein -
39	2	66.7	9	2	S154379	ribosomal protein
40	2	66.7	10	2	A60421	hypertrehalosemic
41	2	66.7	10	2	S08997	hypertrehalosemic
42	2	66.7	10	2	S08998	hypertrehalosemic
43	2	66.7	10	2	A26381	hypertrehalosemic
44	2	66.7	10	2	C60788	sperm-activating p
45	2	66.7	10	2	C60787	sperm-activating p
46	2	66.7	10	2	A60787	sperm-activating p
47	2	66.7	10	2	A60527	sperm-activating p
48	2	66.7	10	2	G60527	sperm-activating p
49	2	66.7	10	2	G60589	sperm-activating p
50	2	66.7	10	2	I60527	sperm-activating p
51	2	66.7	10	2	S42282	parasporal crystal
52	2	66.7	10	2	F44644	neurotoxin-associa
53	2	66.7	10	2	B39308	glycine reductase
54	2	66.7	10	2	S38304	lectin GNL1 alpha
55	2	66.7	10	2	PN0165	triiose-phosphate i
56	2	66.7	10	2	C44787	callifMRamide 12
57	2	66.7	10	2	C39111	Ig heavy chain C r
58	2	66.7	10	2	PT0289	Ig heavy chain CRD
59	2	66.7	10	2	PT0284	Ig heavy chain CRD
60	2	66.7	10	2	S36849	Ig heavy chain V r
61	2	66.7	10	2	A47364	placental lactogen
62	2	66.7	10	2	S53789	neuropeptide Pec-H
63	2	66.7	11	2	I41138	acetyl ornithine d
64	2	66.7	11	2	S35490	type II site-speci
65	2	66.7	11	2	S71304	amine oxidase (cop
66	2	66.7	11	2	PN0664	dystrophin-associa
67	2	66.7	12	2	A29169	phospholipase A2 (
68	2	66.7	12	2	I64829	gene HEXA protein
69	2	66.7	12	2	S29859	gene p10 protein -
70	2	66.7	12	2	B58502	43.2K bile stone p
71	2	66.7	12	2	S71034	potB protein - Sal
72	2	66.7	12	2	B61497	seed protein ws-17
73	2	66.7	12	2	A56878	light yellow cell
74	2	66.7	12	2	F61308	hemocyanin chain 5
75	2	66.7	12	2	PH1567	cerebrin 28 - huma
76	2	66.7	12	2	PH1454	T-cell receptor al
77	2	66.7	12	2	S23168	Z protein - Guinea
78	2	66.7	12	4	PC2123	aminotransferase c
79	2	66.7	13	1	NTKXAS	alpha-conotoxin SI
80	2	66.7	13	2	G44644	neurotoxin-associa
81	2	66.7	13	2	S29488	GTP-binding protei
82	2	66.7	13	2	B28810	glutathione transf
83	2	66.7	13	2	G56046	urinary tract ston
84	2	66.7	13	2	PH0787	T-cell receptor al
85	2	66.7	13	2	S54344	glyceraldhyde-3-p
86	2	66.7	13	4	I70076	glycophorin B/glyc
87	2	66.7	14	1	QMVHP2	mastoparan C - Eur
88	2	66.7	14	2	C60414	somatostatin - sli
89	2	66.7	14	2	B60842	somatostatin I - c
90	2	66.7	14	2	A60840	somatostatin I - E
91	2	66.7	14	2	S00172	somatostatin I - S
92	2	66.7	14	2	A42473	ermK leader peptid
93	2	66.7	14	2	A41589	25K elastin-bindin
94	2	66.7	14	2	B56919	PS I complex subun
95	2	66.7	14	2	PA0007	lectin B1 - Psopho
96	2	66.7	14	2	F61497	seed protein ws-21
97	2	66.7	14	2	PS0252	16K protein 5404 -
98	2	66.7	14	2	S29486	GTP-binding protei
99	2	66.7	14	2	I56493	endothelial growth
100	2	66.7	14	2	S41601	interferon alpha r

ALIGNMENTS

RESULT 1

A61348
red pigment-concentrating hormone - northern shrimp
N/Alternate names: blanching hormone
C/Species: Pandanus borealis (northern shrimp)
C/Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C/Accession: A61348, S07139
R/Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A/Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A/Reference number: A61348; MUID:7228738; PMID:5041363
A/Accession: A61348
A/Molecule type: protein
A/Residues: 1-8 <FERI>

R/Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A/Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandanus borealis
A/Reference number: S07139; MUID:75054965; PMID:4433569
A/Accession: S07139
A/Molecule type: protein
A/Residues: E', 2-8 <FER2>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-
zed pigment-containing cells.
C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami
F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 100.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 2

A43976
hypertrehalosemic hormone - yellow mealworm
C/Species: Tenebrio molitor (yellow mealworm)
C/Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C/Accession: A43976

R/Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A/Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be
A/Reference number: A43976; MUID:90341081; PMID:2381871
A/Accession: A43976

A/Molecule type: protein
A/Residues: 1-8 <GAE>
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 100.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 3

B43976
hypertrehalosemic hormone - beetle (Zophobas rugipes)
C/Species: Zophobas rugipes
C/Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999

C/Accession: B43976
R/Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A/Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be
A/Reference number: A43976; MUID:90341081; PMID:2381871
A/Accession: B43976
A/Molecule type: protein
A/Residues: 1-8 <GAE>

C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 100.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 4

A61230
calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (fragment)
N/Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin
C/Species: Rana pipiens (northern leopard frog)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C/Accession: A61230

R/McLeod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.
Circ. Res. 69, 344-359, 1991
A/Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular
rdium.

A/Reference number: A61230; MUID:91316784; PMID:1860177
A/Accession: A61230
A/Molecule type: protein
A/Residues: 1-9 <MCL>

C/Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding prote
C/Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to
C/Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in v
C/Superfamily: calsequestrin
C/Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; skelet

Query Match 100.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 1 LNF 3
|||
Db 4 LNF 6

RESULT 5

C39398
Fc mu (IgM) receptor surface complex gamma chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 20-Mar-1998
C/Accession: C39398

R/Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991
A/Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1
A/Reference number: A39398; MUID:91219496; PMID:2023945
A/Accession: C39398

A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <CAM>

Query Match 100.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 1 LNF 3
|||

Db - 6 LNF 8

RESULT 6

S23364
T-cell receptor alpha chain J region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S23364
R:Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman, Eur. J. Immunol. 21, 2749-2754, 1991
A:Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheumatoid arthritis
A:Reference number: S23364; MUID:92037820; PMID:1657615
A:Accession: S23364
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-11 <PLU>
A:Cross-references: EMBL:X58164
C:Keywords: T-cell receptor

Query Match 100.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

Db 9 LNF 11

RESULT 7

B60228
Fc mu (IgM) receptor surface complex beta chain - mouse (fragment)
N:Alternate names: membrane protein B29
C:Species: Mus musculus (house mouse)
C>Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 20-Mar-1998
C:Accession: B60228; B39398
R:Hombach, J.; Lottspeich, F.; Reth, M. Eur. J. Immunol. 20, 2795-2799, 1990
A:Title: Identification of the genes encoding the IgM-alpha and Ig-beta components of the B cell receptor
A:Reference number: A60228; MUID:91099432; PMID:2269334
A:Accession: B60228
A:Molecule type: protein
A:Residues: 1-12 <HOM>
R:Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C. Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991
A:Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1 genes
A:Reference number: A39398; MUID:91219496; PMID:2023945
A:Accession: B39398
A:Molecule type: protein
A:Residues: 'XX', 3-10 <CAM>
C:Keywords: membrane protein

Query Match 100.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

Db 6 LNF 8

RESULT 8

C36198
T-cell receptor beta chain J region - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 21-Jul-2000
C:Accession: C36198
R:Tjoelker, L.W.; Carlson, L.M.; Lee, K.; Lahti, J.; McCormack, W.T.; Leiden, J.M.; Chen, Proc. Natl. Acad. Sci. U.S.A. 87, 7856-7860, 1990
A:Title: Evolutionary conservation of antigen recognition: the chicken T-cell receptor beta chain
A:Reference number: A36198; MUID:91045896; PMID:2236002
A:Accession: C36198
A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <TJO>

A:Cross-references: EMBL:M37799; NID:g212737; PIDN:AAA62754.1; PID:g555475

C:Keywords: T-cell receptor

Query Match 100.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

Db 4 LNF 6

RESULT 9

A24099
crystal protein, 28K - Bacillus thuringiensis (fragment)
C:Species: Bacillus thuringiensis
C>Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Jun-2000
C:Accession: A24099
R:Chetukhina, G.G.; Zalunin, I.A.; Kostina, L.I.; Bormatova, M.E.; Klepikova, F.S.; Kl PBS Lett. 190, 345-348, 1985
A:Title: Structural features of crystal-forming proteins produced by Bacillus thuringiensis
A:Reference number: A91347
A:Accession: A24099
A:Molecule type: protein
A:Residues: 1-16 <CHE>

Query Match 100.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

Db 4 LNF 6

RESULT 10

PH1770
T cell receptor alpha chain V region (clone 2V alpha 23-1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1770
R:Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P. J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood lymphocytes

A:Reference number: PH1754; MUID:93301585; PMID:8391057

A:Accession: PH1770

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-16 <POR>

Query Match 100.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

Db 13 LNF 15

RESULT 11

B48943
phage antigenic determinant (clone pOA79) - phage phi-197 (fragment)
C:Species: phage phi-197
C>Date: 13-Aug-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997
C:Accession: B48943
R:Schouler, C.; Bouet, C.; Ritzenhaler, P.; Drouet, X.; Mata, M. Appl. Environ. Microbiol. 58, 2479-2484, 1992
A:Title: Characterization of Lactococcus lactis phage antigens.
A:Reference number: A48943; MUID:92384563; PMID:1514794
A:Contents: Lactococcus lactis

A;Accession: B48943

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-17 <SCH>

A;Note: sequence modified after extraction from NCBI backbone

A;Note: sequence extracted from NCBI backbone (NCBIN:114551)

Query Match 100.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db 5 LNF 7

RESULT 12

C32537

T-cell receptor alpha chain J region (HAJTL17) - human

C;Species: Homo sapiens (man)

C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 30-May-1997

C;Accession: C32537

R;Kimura, N.; Toyonaga, B.; Yoshikai, Y.; Du, R.P.; Mak, T.W.

Eur. J. Immunol. 17, 375-383, 1987

A;Title: Sequences and repertoire of the human T cell receptor alpha- and beta-chain var

A;Reference number: A91263; MUID:87190670; PMID:3494611

A;Accession: C32537

A;Molecule type: mRNA

A;Residues: 1-18 <KIM>

A;Cross-references: GB:M27378

C;Keywords: T-cell receptor

Query Match 100.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db 2 LNF 4

RESULT 13

A53875

creatine kinase (EC 2.7.3.2) CK-MM - coho salmon (fragment)

C;Species: Oncorhynchus kisutch (coho salmon)

C;Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997

C;Accession: A53875

R;White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.

J. Protein Chem. 11, 489-494, 1992

A;Title: The principal islet of the Coho salmon (Oncorhynchus kisutch) contains the BB is

A;Reference number: A53875; MUID:93080727; PMID:1449598

A;Accession: A53875

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-20 <WHI>

A;Experimental source: Brockmann body, principal islet

A;Note: sequence extracted from NCBI backbone (NCBIP:120599)

C;Superfamily: creatine kinase; creatine kinase repeat homology

C;Keywords: phosphotransferase

Query Match 100.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db 11 LNF 13

RESULT 14

A43129

neuropeptide GNFRFamide - tapeworm (Moniezia expansa)

C;Species: Moniezia expansa

C;Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 14-Nov-1997

C;Accession: A43129

R;Maule, A.; Shaw, C.; Halton, D.; Thim, L.

Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993

A;Title: GNFRFamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep

A;Reference number: A43129; MUID:93312289; PMID:8323531

A;Accession: A43129

A;Molecule type: protein

A;Residues: 1-6 <MAU>

C;Keywords: amidated carboxyl end; neuropeptide

F;6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 66.7%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

Db 2 NF 3

RESULT 15

S71867

glutathione transferase (EC 2.5.1.18) class alpha 5 - pig (fragment)

N;Alternate names: glutathione S-transferase class alpha 5

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999

C;Accession: S71867

R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.

Biochem. J. 317, 879-884, 1996

A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospr.

A;Reference number: S71864; MUID:96332484; PMID:8760377

A;Accession: S71867

A;Molecule type: protein

A;Residues: 1-7 <ROU>

C;Comment: At least five species-independent classes of cytosolic glutathion transferas

s mitochondrial form are known.

C;Complex: dimer

C;Function:

A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a

A;Pathway: detoxification; xenobiotics metabolism

A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism

C;Superfamily: glutathione transferase

C;Keywords: dimer; transferase

Query Match 66.7%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

Db 3 LN 4

RESULT 16

B44787

calliFMRFamide 11 - bluebottle fly (Calliphora vomitoria)

C;Species: Calliphora vomitoria

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999

C;Accession: B44787

R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorp

Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (des

A;Reference number: A41978; MUID:92196111; PMID:1549595

A;Accession: B44787

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <DUV>

C;Keywords: amidated carboxyl end; neuropeptide

F;7/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0

QY 2 NF 3
||
3 NF 4

Db

RESULT 17
A34026
acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)
C:Species: Torpedo californica (Pacific electric ray)
C>Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C:Accession: A34026
R:Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedrick, T.; Low, M.G.; Taylor, S.S.; T
J. Biol. Chem. 263, 1140-1145, 1988
A:Title: Divergence in primary structure between the molecular forms of acetylcholinester
A:Reference number: A34026; MUID:88087239; PMID:3335534
A:Accession: A34026
A:Molecule type: protein
A:Residues: 1-7 <GIB>
C:Keywords: alternative splicing; carboxylic ester hydrolase

Query Match 66.7%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
2 LN 3

Db

RESULT 18
PN0649
pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)
C:Species: Bacillus sp.
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-Jun-2002
C:Accession: PN0649
R:Kim, C.H.; Choi, H.I.; Lee, D.S.
Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993
A:Title: Purification and biochemical properties of an alkaline pullulanase from alkalop
A:Reference number: PN0649; MUID:94080025; PMID:7764261
A:Accession: PN0649
A:Molecule type: protein
A:Residues: 1-7 <KIM>
C:Comment: This enzyme is used together with glucoamylase to improve the efficiency of st
nent in high maltose syrups.
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 66.7%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
2 LN 3

Db

RESULT 19
PC2370
probable H⁺-transporting two-sector ATPase (EC 3.6.3.14) alpha chain [similarity] - Baci
N:Alternate names: unidentified 78K protein
C:Species: Bacillus cereus
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 03-Jun-2002
C:Accession: PC2370
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulation i
A:Reference number: PC2369; MUID:95218265; PMID:7766022
A:Accession: PC2370
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAS>

C:Keywords: ATP biosynthesis; hydrolase

Query Match 66.7%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
3 LN 4

Db

RESULT 20

A28004

adipokinetic hormone G - two-spotted cricket

N:Alternate names: AKI-G

C:Species: Gryllus bimaculatus (two-spotted cricket)

C>Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997

C:Accession: A28004

R:Gaede, G.; Rinehart, K.L.

Biochem. Biophys. Res. Commun. 149, 908-914, 1987

A:Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a pept

A:Reference number: A28004; MUID:88106553; PMID:3426616

A:Accession: A28004

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A>Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we hav

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3

||

3 NF 4

Db

RESULT 21

S08995

hypertrehalosemic hormone I - oriental cockroach

N:Alternate names: Pea-CAH-I

C:Species: Blatta orientalis (oriental cockroach)

C>Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997

C:Accession: S08995

R:Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corp

entails and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bomb

A:Reference number: S08995; MUID:90253659; PMID:2340112

A:Accession: S08995

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A>Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we hav

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3

||

3 NF 4

Db

RESULT 22

S10596

adipokinetic hormone - pond skimmer

C;Species: Libellula auripennis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997
C;Accession: S10596
R;Gaede, G.
Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone
A;Reference number: S10596; MUID:90359055; PMID:2390213
A;Accession: S10596
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Comment: This peptide has both adipokinetic and hypertrahalosemic activities.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyroglutamic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
||
Db 3 NF 4

RESULT 23
A49823
adipokinetic hormone I - American cockroach
N;Alternate names: periplanetin CC-1
C;Species: Periplaneta americana (American cockroach)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: A49823
R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.; Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive activities
A;Reference number: A49823; MUID:84298179; PMID:6591205
A;Accession: A49823
A;Molecule type: protein
A;Residues: 1-8 <SCA>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyroglutamic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
||
Db 3 NF 4

RESULT 24
A44960
neuropeptide Led-CC-I - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and their role in feeding regulation
A;Reference number: A44960; MUID:90160053; PMID:2576128
A;Accession: A44960
A;Molecule type: protein
A;Residues: 1-8 <GAB>
C;Superfamily: adipokinetic hormone
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyroglutamic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
||
Db 3 NF 4

RESULT 25
S15422
adipokinetic hormone - cockchafer
C;Species: Melolontha melolontha (cockchafer)
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: S15422
R;Gaede, G. 275, 671-677, 1991
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone family
A;Reference number: S15422; MUID:91248100; PMID:2039445
A;Accession: S15422
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyroglutamic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
||
Db 2 LN 3

RESULT 26
S55310
adipokinetic hormone - damselfly (Pseudagrion inconspicuum)
N;Alternate names: Psi-AKH
C;Species: Pseudagrion inconspicuum
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C;Accession: S55310
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum and Zygoptera
A;Reference number: S55310; MUID:94379987; PMID:8093008
A;Accession: S55310
A;Molecule type: protein
A;Residues: 1-8 <JAN>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyroglutamic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
||
Db 3 NF 4

RESULT 27
A58641
adipokinetic hormone - dor beetle
C;Species: Geotrupes stercorosus (dor beetle)
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: A58641
R;Gaede, G. 275, 671-677, 1991
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone family
A;Reference number: S15422; MUID:91248100; PMID:2039445
A;Accession: A58641

A:Molecule type: protein

A;Residues: 1-8 <BIO>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

Db 2 LN 3

RESULT 28

A58620

A;Title: adipokinetic hormone - damselfly (*Ischnura senegalensis*)

C;Species: *Ischnura senegalensis*

C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999

C;Accession: A58620

R;Janssens, M.P.E.; Kellner, R.; Gaede, G.

Biochem. J. 302, 539-543, 1994

A;Title: A novel adipokinetic octapeptide found in the damselflies *Pseudagrion inconspicuum*

A;Reference number: S55310; MUID:94379987; PMID:8093008

A;Accession: A58620

A:Molecule type: protein

A;Residues: 1-8 <JAN>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

Db 3 NF 4

RESULT 29

PL0184

A;Title: capsid protein VP-1 - murine poliovirus (fragment)

C;Species: murine poliovirus, Theiler's encephalomyelitis virus

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995

C;Accession: PL0184

R;Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.

J. Exp. Med. 170, 2037-2049, 1989

A;Title: Alteration of amino acid 101 within capsid protein VP-1 changes the pathogenicity

A;Reference number: PL0184; MUID:90063468; PMID:2479706

A;Accession: PL0184

A:Molecule type: genomic RNA

A;Residues: 1-8 <ZUR>

C;Keywords: capsid protein

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

Db 6 NF 7

RESULT 30

A05169

A;Title: neuropeptide M-I - American cockroach

C;Species: *Periplaneta americana* (American cockroach)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993

C;Accession: A05169

R;Witten, J.L.; Schafer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.

Biochem. Biophys. Res. Commun. 124, 350-358, 1984

A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment ma

A;Reference number: A90118; MUID:85046530; PMID:6548628

A;Accession: A05169

A:Molecule type: protein

A;Residues: 1-8 <WIT>

C;Keywords: neuropeptide

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

Db 3 NF 4

RESULT 31

S21663

A;Title: neuropeptide - flower beetle (*Pachnoda marginata*)

C;Species: *Pachnoda marginata*

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C;Accession: S21663

R;Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 373, 133-142, 1992

A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of vari

ectrometry. A;Reference number: S21663; MUID:92265187; PMID:1586453

A;Accession: S21663

A;Status: preliminary

A:Molecule type: protein

A;Residues: 1-8 <GAE>

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

Db 2 LN 3

RESULT 32

A39892

A;Title: P cytotyping-determining - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Feb-1997

C;Accession: A39892

R;Nitasaka, E.; Mukai, T.; Yamazaki, T.

Proc. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987

A;Title: Repressor of P elements in *Drosophila melanogaster*: cytotyping determination by

A;Reference number: A39892

A;Accession: A39892

A;Status: preliminary

A:Molecule type: DNA

A;Residues: 1-8 <NIT>

C;Genetics:

A;Gene: *FlyBase:P-element*

A;Cross-references: *FlyBase:FBgn0003055*

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

Db 4 NF 5

RESULT 33

A14683

A;Title: aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (frag

N;Alternate names: aspartate aminotransferase, mitochondrial
C;Species: Gallus gallus (chicken)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C;Accession: A14683
R;Wilson, K.J.; Hunziker, P.; Hughes, G.J.
FEBS Lett. 108, 98-102, 1979
A;Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.
A;Reference number: A14683; MUID:80092116; PMID:520566
A;Accession: A14683
A;Molecule type: protein
A;Residues: 1-8 <WIL>
C;Keywords: aminotransferase; mitochondrion

Query Match 66.7%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
||
Db 4 NF 5

RESULT 34
AKLQIM
locustamyo-inhibiting peptide - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998
C;Accession: A60065
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
Regul. Pept. 36, 111-119, 1991
A;Title: Isolation, identification and synthesis of locustamyo-inhibiting peptide (LOM-MI)
A;Reference number: A60065; MUID:92179466; PMID:1796179
A;Accession: A60065
A;Molecule type: protein
A;Residues: 1-9 <SCH>
C;Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and c
C;Superfamily: locustamyo-inhibiting peptide
C;Keywords: amidated carboxyl end; hormone
F;9/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
Db 5 LN 6

RESULT 35
S19523
orf AB protein - Shigella dysenteriae insertion sequence IS911
C;Species: Shigella dysenteriae
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1998
C;Accession: S19523
R;Polard, P.; Prere, M.F.; Chandler, M.; Fayet, O.
J. Mol. Biol. 222, 465-477, 1991
A;Title: Programmed translational frameshifting and initiation at an AUU codon in gene e
A;Reference number: S19523; MUID:92085268; PMID:1660923
A;Accession: S19523
A;Molecule type: protein
A;Residues: 1-9 <POL>
C;Genetics:
A;Mobile element: insertion sequence IS911

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
||
Db 5 NF 6

RESULT 36
A57444
neuropeptide Grb-AST B1 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: A57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cr
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: A57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
Db 5 LN 6

RESULT 37
B57444
neuropeptide Grb-AST B2 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: B57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cr
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: B57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
Db 5 LN 6

RESULT 38
I54379
gene NF2 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C;Accession: I54379
R;Arai, E.; Ikeuchi, T.; Nakamura, Y.
Hum. Mol. Genet. 3, 937-939, 1994
A;Title: Characterization of the translocation breakpoint on chromosome 22q12.2 in a pa
A;Reference number: I54379; MUID:95038750; PMID:7951241
A;Accession: I54379
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-9 <RES>
A;Cross-references: GB:S75841; NID:G861532; PIDN:AAI14190.1; PID:G4261890
C;Genetics:
A;Gene: GDB:NF2
A;Cross-references: GDB:120232; OMIM:101000
A;Map position: 22q12.2-22q12.2

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
||
Db 1 LN 2

RESULT 39

S08997

hypertrehalosemic neuropeptide Bld-HrTH - cockroach (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C:Accession: S78420
R:Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A:Reference number: S78411
A:Accession: S78420
A:Molecule type: protein
A:Residues: 1-9 <GGL>
A:Note: the protein is designated as mitochondrial ribosomal protein L41
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
||
Db 1 LN 2

RESULT 40

A60421

hypertrehalosemic hormone - German cockroach
N:Alternate names: Bld-HrTH
C:Species: Blattella germanica (German cockroach)
C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 31-Oct-1997
C:Accession: A60421; S09137
R:Veestra, J.A.; Camps, F.
Neuropeptides 15, 107-109, 1990
A:Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blattella germanica
A:Reference number: A60421; MUID:91179584; PMID:2080017
A:Accession: A60421
A:Molecule type: protein
A:Residues: 1-10 <VEE>
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S09137
A:Molecule type: protein
A:Residues: 1-10 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
||
Db 3 NF 4

RESULT 41

S08997

hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)
C:Species: Gromphadorina portentosa
C:Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C:Accession: S08997
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S08997
A:Molecule type: protein
A:Residues: 1-10 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
||
Db 3 NF 4

RESULT 42

S08998

hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)
C:Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C:Accession: S08998
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S08998
A:Molecule type: protein
A:Residues: 1-10 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
||
Db 3 NF 4

RESULT 43

A26381

hypertrehalosemic hormone - gray cockroach
C:Species: Nauphoeta cinerea (gray cockroach)
C:Date: 31-Mar-1988 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C:Accession: A26381
R:Gaede, G.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 141, 774-781, 1986
A:Title: Amino acid sequence of a hypertrehalosemic neuropeptide from the corpus cardiaca of the cockroach Nauphoeta cinerea
A:Reference number: A26381; MUID:87100208; PMID:3801028
A:Accession: A26381
A:Molecule type: protein
A:Residues: 1-10 <GAD>
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have used the sequence of the mature peptide
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
||

A;Residues: 1-10 <Y02>
 C;Superfamily: unassigned animal peptides
 C;Keywords: bromine
 P;2/Modified site: 2'-bromophenylalanine or 4'-bromophenylalanine (Phe) (partial) #status

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 4 LN 5

RESULT 49
 G60589
 sperm-activating peptide (Tyr-2, Asn-3, Asp-7,10, Arg-8, Ile-9 SAP-I) - Echinomera math
 C;Species: Echinomera mathaei
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C;Accession: G60589
 R;Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe
 otus nudus, Echinomera mathaei and Heterocentrotus mammillatus.
 A;Reference number: A60527
 A;Accession: G60589
 A;Molecule type: protein
 A;Residues: 1-10 <Y0S>
 C;Superfamily: unassigned animal peptides

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 4 LN 5

RESULT 50
 I60527
 sperm-activating peptide (SAP-I) - sea urchin (Strongylocentrotus nudus)
 N;Alternate names: speract
 C;Species: Strongylocentrotus nudus
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C;Accession: I60527
 R;Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe
 otus nudus, Echinomera mathaei and Heterocentrotus mammillatus.
 A;Reference number: A60527
 A;Accession: I60527
 A;Molecule type: protein
 A;Residues: 1-10 <Y0S>
 C;Superfamily: unassigned animal peptides

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 4 LN 5

RESULT 51
 S42282
 parasporal crystal protein cryIIB - Bacillus thuringiensis plasmid (fragment)
 N;Alternate names: delta-endotoxin
 C;Species: Bacillus thuringiensis
 C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 24-Jul-1998
 C;Accession: S42282
 R;Crickmore, N.; Wheeler, V.C.; Ellar, D.J.

Mol. Gen. Genet. 242, 365-368, 1994
 A;Title: Use of an operon fusion to induce expression and crystallisation of a Bacillus
 A;Reference number: S42282; MUID:94150472; PMID:7906381
 A;Accession: S42282
 A;Molecule type: protein
 A;Residues: 1-10 <CRI>
 A;Experimental source: subsp. gallerae 916
 C;Genetics:
 A;Gene: cryIIB
 A;Genome: plasmid
 C;Keywords: delta-endotoxin

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 5 LN 6

RESULT 52
 F44644
 neurotoxin-associated protein type B Hn+ 35K chain, band 3a - Clostridium botulinum (fr
 C;Species: Clostridium botulinum
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
 C;Accession: F44644
 R;Somers, E.; Dasgupta, B.R.
 J. Protein Chem. 10, 415-425, 1991
 A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without h
 A;Reference number: A44644; MUID:92143938; PMID:1781887
 A;Contents: type B
 A;Accession: F44644
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <SOM>
 A;Note: sequence extracted from NCBI backbone (NCBIP:83787)
 C;Keywords: hemagglutinin

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 5 LN 6

RESULT 53
 B39308
 glycine reductase (EC 1.4.99.-) sulphydryl protein C, beta chain - Clostridium sticklan
 C;Species: Clostridium sticklandii
 C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
 C;Accession: B39308
 R;Stadtman, T.C.; Davis, J.N.
 J. Biol. Chem. 266, 22147-22153, 1991
 A;Title: Glycine reductase protein C. Properties and characterization of its role in th
 A;Reference number: A39308; MUID:92042141; PMID:1939235
 A;Accession: B39308
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <STA>
 C;Function:
 A;Description: glycine reductase complex catalyzes the reductive deamination of glycine
 C;Keywords: ATP; oxidoreductase

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 3 LN 4


```

Db          ||
           6 NF 7

RESULT 54
S38304
lectin GNLI alpha chain - kidney bean (fragment)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C;Accession: S38304
R;Kamemura, K.; Furuichi, Y.; Umekawa, H.; Takahaashi, T.
Biochim. Biophys. Acta 1158, 181-188, 1993
A;Title: Purification and characterization of novel lectins from Great Northern bean, PH
A;Reference number: S38304; MUID:94002183; PMID:8399319
A;Accession: S38304
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <KAM>

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
Db 7 NF 8

RESULT 55
PN0165
triose-phosphate isomerase (EC 5.3.1.1) - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C;Accession: PN0165
R;Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A;Reference number: PN0160
A;Accession: PN0165
A;Molecule type: protein
A;Residues: 1-10 <FDK>
A;Experimental source: strain M-1-1
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
Db 9 NF 10

RESULT 56
C44787
Calliphora vomitoria 12 - bluebottle fly (Calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: C44787
R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A;Reference number: A41978; MUID:92196111; PMID:1549595
A;Accession: C44787
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <DUV>
A;Keywords: amidated carboxyl end; neuropeptide
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3

Db          ||
           6 NF 7

RESULT 57
C39111
Ig heavy chain C region - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: C39111
R;Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simi
A;Reference number: A39111; MUID:91156684; PMID:2000382
A;Accession: C39111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <VAR>
C;Keywords: heterotetramer; immunoglobulin

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 1 LN 2

RESULT 58
PT0289
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0289
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0289
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 2 LN 3

RESULT 59
PT0284
Ig heavy chain CRD3 region (clone 4-97) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0284
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0284
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3

```

```
Qy      2 NF 3
      ||
Db      7 NF 8

RESULT 60
S36849
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1996 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C:Accession: S36849
R:Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl
A:Reference number: S25024
A:Accession: S36849
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-10 <JAC>
A:Cross-references: EMBL:X67382; NID:G50070; PIDN:CAA47794.1; PID:e51590; PID:gl333861
C:Keywords: heterotetramer; immunoglobulin

Query Match      66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NF 3
      ||
Db      9 NF 10

RESULT 61
A47364
Placental lactogen-I precursor - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C:Accession: A47364
R:Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.
Mol. Endocrinol. 7, 181-188, 1993
A>Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene pro
A:Reference number: A47364; MUID:93225959; PMID:8469232
A:Accession: A47364
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <RES>
A:Cross-references: GB:S58124; NID:G299449

Query Match      66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LN 2
      ||
Db      5 LN 6

RESULT 62
S53789
neuropeptide Pec-HrTH - Platypaleura capensis
C:Species: Platypaleura capensis
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C:Accession: S53789
R:Gaede, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A>Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalo
A:Reference number: S53789; MUID:95225985; PMID:7710694
A:Accession: S53789
A:Molecule type: protein
A:Residues: 1-10 <GAE>
C:Keywords: blocked amino end; blocked carboxyl end

Query Match      66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LN 2
      ||
Db      5 LN 6

Query Match      66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NF 3
      ||
Db      10 NF 11

RESULT 65
S71304
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)
C:Species: Aspergillus niger
C:Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 07-May-1999
C:Accession: S71304
R:Freibort, I.; Tanaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Halata, M.; Asar
Eur. J. Biochem. 237, 255-265, 1996
A>Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the my
A:Reference number: S71303; MUID:96201933; PMID:8620892
A:Accession: S71304
A:Molecule type: protein
A:Residues: 1-11 <FRE>
```

```
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NF 3
      ||
Db      3 NF 4

RESULT 63
I41138
acetyl ornithine deacetylase (argE) - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 08-Oct-1999
C:Accession: I41138
R:Charlier, D.; Piette, J.; Glansdorff, N.
Nucleic Acids Res. 10, 5935-5948, 1982
A>Title: 183 can function as a mobile promoter in e.coli.
A:Reference number: I41137; MUID:83064529; PMID:16292860
A:Accession: I41138
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:J01589; NID:G145346; PIDN:AAA23485.1; PID:G551788

Query Match      66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LN 2
      ||
Db      2 LN 3

RESULT 64
S35490
type II site-specific deoxyribonuclease (EC 3.1.21.4) PvuI - Proteus vulgaris
A:Alternate names: PvuI endonuclease
C:Species: Proteus vulgaris
C:Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
C:Accession: S35490
R:Smith, M.D.; Longo, M.; Gerard, G.F.; Chatterjee, D.K.
Nucleic Acids Res. 20, 5743-5747, 1992
A>Title: Cloning and characterization of genes for the PvuI restriction and modificati
A:Reference number: S35490; MUID:93087186; PMID:1454536
A:Accession: S35490
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-11 <SMI>
A:Cross-references: EMBL:L04163; NID:G150901; PIDN:AAA25660.1; PID:G150902
C:Keywords: hydrolase

Query Match      66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NF 3
      ||
Db      10 NF 11

RESULT 65
S71304
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)
C:Species: Aspergillus niger
C:Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 07-May-1999
C:Accession: S71304
R:Freibort, I.; Tanaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Halata, M.; Asar
Eur. J. Biochem. 237, 255-265, 1996
A>Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the my
A:Reference number: S71303; MUID:96201933; PMID:8620892
A:Accession: S71304
A:Molecule type: protein
A:Residues: 1-11 <FRE>
```

C;Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquinone

Query Match 66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
Db 6 LN 7

RESULT 66
A29169
dystrophin-associated glycoprotein A3a-III - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C;Accession: FN0664
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
A;Reference number: FN0662; MUID: 94156881; PMID: 8113213
A;Accession: FN0664
A;Molecule type: protein
A;Residues: 1-11 <YOS>
C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C;Keywords: glycoprotein; skeletal muscle

Query Match 66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
Db 4 LN 5

RESULT 67
A29169
phospholipase A2 (EC 3.1.1.4) precursor - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 31-Oct-1997
C;Accession: A29169
R;Dutilh, C.E.; Van Doren, P.J.; Verheul, F.E.A.M.; De Haas, G.H.
Eur. J. Biochem. 53, 91-97, 1975
A;Title: Isolation and properties of phospholipase A2 from ox and sheep pancreas.
A;Reference number: A94661
A;Accession: A29169
A;Molecule type: protein
A;Residues: 1-12 <DUT>
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
Db 4 LN 5

RESULT 68
I64829
gene HEXA protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I64829
R;Boles, D.J.; Proia, R.L.
Am. J. Hum. Genet. 56, 716-724, 1995
A;Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sachs
A;Reference number: I51882; MUID: 95193801; PMID: 7887427
A;Accession: I64829

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-12 <RES>
A;Cross-references: GB:S76984; NID:G912781; PIDN:AAD14243.1; PID:G4261943
C;Genetics:
A;Gene: GDB:HEXA
A;Cross-references: GDB:120040; OMIM:272800
A;Map position: 15q23-15q24
C;Superfamily: beta-hexosaminidase

Query Match 66.7%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
Db 4 LN 5

RESULT 69
S29859
gene p10 protein - Choristoneura fumiferana nuclear polyhedrosis virus (fragment)
C;Species: Choristoneura fumiferana nuclear polyhedrosis virus, CFMNPV
C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Accession: S29859
R;Hill, J.E.; Kuzio, J.; Wilson, J.A.; MacKinnon, E.A.; Faulkner, P.
Biochim. Biophys. Acta 1172, 187-189, 1993
A;Title: Nucleotide sequence of the p74 gene of a baculovirus pathogenic to the spruce
A;Reference number: S29849; MUID: 93176808; PMID: 8439559
A;Accession: S29859
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-12 <HIL>
A;Experimental source: strain Ireland

Query Match 66.7%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
Db 5 LN 6

RESULT 70
E58502
43.2K bile stone protein - unidentified bacterium (fragment)
C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: E58502
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: E58502
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <BIN>
A;Experimental source: human bile with stones
A;Note: a secondary sequence DVKIGVAGS was also found

Query Match 66.7%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
Db 5 LN 6

RESULT 71
S71034
potB protein - Salmonella typhimurium (fragment)

C;Species: Salmonella typhimurium
 C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
 C;Accession: S71034
 R;Stein, M.A.; Leung, K.Y.; Zwick, M.; Garcia-del Portillo, F.; Finlay, B.B.
 Mol. Microbiol. 20, 151-164, 1996
 A;Title: Identification of a Salmonella virulence gene required for formation of filamen
 A;Reference number: S71033; MUID:97014378; PMID:8861213
 A;Accession: S71034
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-12 <STE>
 A;Cross-references: EMBL:U51867; NID:gl272352; PIDN:AAA97466.1; PID:gl272353
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1996
 C;Genetics:
 A;Gene: potB

Query Match 66.7%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 3 LN 4

Db

RESULT 72
 B61497
 seed protein ws-17 - winged bean (fragment)
 C;Species: Psophocarpus tetragonolobus (winged bean)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
 C;Accession: B61497
 R;Hirano, H.
 J. Protein Chem. 8, 115-130, 1989
 A;Title: Microsequence analysis of winged bean seed proteins electroblooded from two-dim
 A;Reference number: A61491; MUID:89351606; PMID:2765119
 A;Accession: B61497
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <HR>
 C;Keywords: seed

Query Match 66.7%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 6 NF 7

Db

RESULT 73
 A56878
 light yellow cell peptide A - great pond snail
 N;Contains: light yellow cell peptide B
 C;Species: Lymanaea stagnalis (great pond snail)
 C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Aug-1999
 C;Accession: A56878
 R;Hoek, R.M.; Li, K.W.; van Minnen, J.; Geraerts, W.P.
 Brain Res. Mol. Brain Res. 16, 71-74, 1992
 A;Title: Chemical characterization of a novel peptide from the neuroendocrine light yell
 A;Reference number: A56878; MUID:93095719; PMID:1334202
 A;Accession: A56878
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <HOE>
 A;Cross-references: PIDN:AA24433.1; PID:G261422
 A;Note: sequence extracted from NCBI backbone (NCBIP:120090)
 C;Keywords: neuropeptide
 F;1-12/Product: light yellow cell peptide A #status experimental <YCPA>
 F;12-12/Product: light yellow cell peptide B #status experimental <YCPB>

Query Match 66.7%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 9 LN 10

Db

RESULT 74
 F61308
 hemocyanin chain 5B - Sahara scorpion (fragment)
 C;Species: Androctonus australis (Sahara scorpion)
 C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
 C;Accession: F61308
 R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
 FEBS Lett. 106, 289-291, 1979
 A;Title: Structural characterization of seven different subunits in Androctonus austral
 A;Reference number: A61308; MUID:80047238; PMID:499512
 A;Accession: F61308
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <JOL>

Query Match 66.7%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 2 LN 3

Db

RESULT 75
 PH1567
 cerebrin 28 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
 C;Accession: PH1567
 R;Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.
 J. Neurochem. 61, 533-540, 1993
 A;Title: Micropurification of two human cerebrospinal fluid proteins by high performanc
 A;Reference number: PH1566; MUID:93329419; PMID:8336140
 A;Accession: PH1567
 A;Molecule type: protein
 A;Residues: 1-12 <LEO>

Query Match 66.7%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 11 NF 12

Db

Search completed: November 25, 2003, 19:36:14
 Job time : 2.05814 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 1.06395 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3

Sequence: 1 LNF 3

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	100.0	8	1	HTF_TENMO
2	3	100.0	8	1	RPCB_PANBO
3	2	66.7	6	1	FARP_MONEX
4	2	66.7	7	1	FAR1_MACRS
5	2	66.7	7	1	FAR1_PROCL
6	2	66.7	7	1	FAR2_PROCL
7	2	66.7	7	1	FAR4_PANRE
8	2	66.7	7	1	FARB_CALVO
9	2	66.7	8	1	AKHG_GRYBI
10	2	66.7	8	1	AKH_LIBAU
11	2	66.7	8	1	AKH_MELML
12	2	66.7	8	1	ALL1_CYOPO
13	2	66.7	8	1	ALL6_CYOPO
14	2	66.7	8	1	FAR1_PANRE
15	2	66.7	8	1	FAR1_PENNO
16	2	66.7	8	1	FAR2_MACRS
17	2	66.7	8	1	FAR3_HOMAM
18	2	66.7	8	1	FAR4_HOMAM
19	2	66.7	8	1	HTF1_PERAM
20	2	66.7	9	1	FAR2_PANRE
21	2	66.7	9	1	FAR3_MACRS
22	2	66.7	9	1	FAR6_MACRS
23	2	66.7	9	1	FAR8_MACRS
24	2	66.7	9	1	LMP_LOOMI
25	2	66.7	9	1	PTSP_BOMMO
26	2	66.7	9	1	UPA6_HUMAN
27	2	66.7	10	1	FAR2_PENNO
28	2	66.7	10	1	FAR7_MACRS
29	2	66.7	10	1	FARC_CALVO
30	2	66.7	10	1	HTF1_ROMMI
31	2	66.7	10	1	HTF_NAUCI
32	2	66.7	10	1	URA7_HUMAN
33	2	66.7	10	1	UXA6_CHLTR

34	2	66.7	11	1	CS15_BACSU
35	2	66.7	11	1	RRPL_CHAV
36	2	66.7	11	1	T2P1_PROVU
37	2	66.7	11	1	ULAG_HUMAN
38	2	66.7	12	1	FIF1_SARBU
39	2	66.7	12	1	UR2_SCYCA
40	2	66.7	13	1	CXAA_CONST
41	2	66.7	13	1	FARB_ASCSU
42	2	66.7	13	1	ITB5_BOVIN
43	2	66.7	13	1	ORCK_ORCLI
44	2	66.7	13	1	ROCK_MWCGA
45	2	66.7	13	1	TEJA_RANJA
46	2	66.7	13	1	TEMC_RANTE
47	2	66.7	13	1	TEMD_RANTE
48	2	66.7	13	1	TEME_RANTE
49	2	66.7	13	1	YENP_PHOLU
50	2	66.7	14	1	LECB_PSOSC
51	2	66.7	14	1	LPER_BACLI
52	2	66.7	14	1	MAST_VESCR
53	2	66.7	14	1	PSAG_CUCSA
54	2	66.7	14	1	SMS1_MYOSC
55	2	66.7	14	1	SMS_ALLMI
56	2	66.7	15	1	ECDA_LYMDI
57	2	66.7	15	1	FRE2_LITIN
58	2	66.7	15	1	LEC1_PSOSC
59	2	66.7	15	1	LEC2_PSOSC
60	2	66.7	15	1	LEC3_AXIPO
61	2	66.7	15	1	LEC3_PSOSC
62	2	66.7	15	1	MAOX_CHICK
63	2	66.7	15	1	PC20_BRANA
64	2	66.7	15	1	UBL1_MONDO
65	2	66.7	15	1	UC17_MAIZE
66	2	66.7	15	1	UC28_MAIZE
67	2	66.7	15	1	UE15_HORVU
68	2	66.7	16	1	ALL1_CALVO
69	2	66.7	16	1	MDH_SYNY4
70	2	66.7	16	1	ODPB_SOLTU
71	2	66.7	17	1	PATS_ANASP
72	2	66.7	17	1	PSBL_SYNVU
73	2	66.7	18	1	A2M_OCTVU
74	2	66.7	18	1	AHD2_TETPY
75	2	66.7	18	1	ALL2_CYDPO
76	2	66.7	18	1	LCTN_LAMGL
77	2	66.7	18	1	LUXB_KRYAS
78	2	66.7	19	1	HI70_BAT
79	2	66.7	19	1	ITHA_PERAM
80	2	66.7	19	1	LGRP_PETMA
81	2	66.7	19	1	LPGE_ECOLI
82	2	66.7	19	1	MIFH_TRISP
83	2	66.7	19	1	RL10_CITFR
84	2	66.7	20	1	AROQ_AMYME
85	2	66.7	20	1	CATA_ACIRA
86	2	66.7	20	1	FLA_VIBAL
87	2	66.7	20	1	ITRA_ALEJU
88	2	66.7	20	1	PSBH_SYNVU
89	2	66.7	20	1	RL10_PROVU
90	2	66.7	20	1	STVA_STYCL
91	2	66.7	20	1	STYB_STYCL
92	2	66.7	20	1	THIO_CANFA
93	2	66.7	20	1	TRYL_STREX
94	1	33.3	4	1	ACH1_ACHFV
95	1	33.3	4	1	FAR3_HIRME
96	1	33.3	4	1	FAR4_HIRME
97	1	33.3	4	1	FFKA_ANTEL
98	1	33.3	4	1	FLRF_HIRME
99	1	33.3	4	1	FLRN_ANTEL
100	1	33.3	4	1	FMRF_MACNI

ALIGNMENTS

RESULT 1

HTF TENMO
 ID _HTF TENMO STANDARD; PRT; 8 AA.
 AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hypertrehalosemic factor (HOTH) (Hypertrehalosemic neuropeptide).
 OS Tenebrio molitor (Yellow mealworm), and
 OS Zophobas rugipes.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067, 7075;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=T.molitor, and Z.rugipes;
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Rosinski G.;
 RT "The primary structure of the hypertrehalosemic neuropeptide from
 RT tenebrionid beetles: a novel member of the AKH/RPCH family.";
 RL Peptides 11:455-459(1990).
 CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A43976; A43976.
 DR PIR; B43976; B43976.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;
 Query Match 100.0%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 DB 2 LNF 4

RESULT 2
 RPCH_PANBO
 ID _RPCH_PANBO STANDARD; PRT; 8 AA.
 AC P08939;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Red pigment concentrating hormone (RPCH).
 OS Pandanus borealis (Northern red shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
 OC Pandallidae; Pandalus.
 OX NCBI_TaxID=6703;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75054965; PubMed=4433569;
 RA Fernlund P.;
 RT "Structure of the red-pigment-concentrating hormone of the shrimp,
 RT Pandalus borealis.";
 RL Biochim. Biophys. Acta 371:304-311(1974).
 CC -1- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY
 CC STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-
 CC CHROMATOPHORES.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A61348; A61348.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Pigment; Hormone; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;
 Query Match 100.0%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 DB 2 LNF 4

RESULT 3
 FARP_MONEX
 ID _FARP_MONEX STANDARD; PRT; 6 AA.
 AC F41966;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE FMRamide-like neuropeptide GNFRP-amide.
 OS Moniezia expansa (Sheep tapeworm)
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidae; Anoplocephalidae; Moniezia.
 OX NCBI_TaxID=28841;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93312289; PubMed=8323531;
 RA Maule A.G., Shaw C., Halton D.W., Thim L.;
 RT "GNFRamide: a novel FMRamide-immunoreactive peptide isolated from
 RT the sheep tapeworm, Moniezia expansa.";
 RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; A43129; A43129.
 KW Neuropeptide; Amidation.
 FT MOD_RES 6 6
 SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NF 3
 DB 2 NF 3

RESULT 4
 FARI_MACRS
 ID _FARI_MACRS STANDARD; PRT; 7 AA.
 AC P8327A;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FLPI (DRNFLRP-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE. AND MASS SPECTROMETRY.
 RC TISSUE=Eye stalk;
 RA Sithigongul P., Sarathongkum W., Jaideechoey S., Longyant S.,
 RA Sithigongul W.;
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn Macrobrachium rosenbergii.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -1- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.

FT MOD RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;
Query Match 66.7%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NF 3
Db 3 NF 4
RESULT 5
FAR1_PROCL STANDARD; PRT; 7 AA.
AC P38459;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cardioexcitatory FMRFamide homolog NF1.
OS Procamburus clarkii (Red swamp crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Cambaridae; Procamburus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=93248032; PubMed=8387183;
RA Mercier A.J.; Orchard I.; Tebrugge V.; Skerrett M.;
RT "Isolation of two FMRFamide-related peptides from crayfish
pericardial organs."
RL Peptides 14:137-143(1993).
CC -I- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;
Query Match 66.7%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NF 3
Db 3 NF 4
RESULT 6
FAR2_PROCL STANDARD; PRT; 7 AA.
AC P38498;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cardioexcitatory FMRFamide homolog DF2.
OS Procamburus clarkii (Red swamp crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Cambaridae; Procamburus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=93248032; PubMed=8387183;
RA Mercier A.J.; Orchard I.; Tebrugge V.; Skerrett M.;
RT "Isolation of two FMRFamide-related peptides from crayfish
pericardial organs."
RL Peptides 14:137-143(1993).
CC -I- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS

CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;
Query Match 66.7%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NF 3
Db 3 NF 4
RESULT 7
FAR4_PANRE STANDARD; PRT; 7 AA.
AC P41875;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF4 (KPNFIRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimidae; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95232026; PubMed=7716079;
RA Maule A.G.; Shaw C.; Bowman J.W.; Halton D.W.; Thompson D.P.;
RA Thim L.; Kubiak T.M.; Martin R.A.; Geary T.G.;
RT "Isolation and preliminary biological characterization of
KPNFIRFamide, a novel FMRFamide-related peptide from the free-living
nematode, Panagrellus redivivus."
RL Peptides 16:87-93(1995).
CC -I- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
CC MUSCLE TENSION INCREASE.
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;
Query Match 66.7%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NF 3
Db 3 NF 4
RESULT 8
FARB_CALVO STANDARD; PRT; 7 AA.
AC P41866;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CallifMRFamide 11.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H.; Johnsen A.H.; Sewell J.C.; Scott A.G.; Orchard I.,

RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliphrinamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FARFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; B44787;
 KW Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 926 MW; 69D40693C44AB700 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
 ||
 Db 3 NF 4

RESULT 9
 AKHG GRVBI STANDARD; PRT; 8 AA.
 AC P14086;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adipokinetic hormone G (AKH-G) (RO II).
 OS Gryllus bimaculatus (Two-spotted cricket), and
 OS Romalea microptera (Lubber grasshopper).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
 OC Gryllus.
 OX NCBI_TaxID=6993, 7007;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
 RX MEDLINE=88106553; PubMed=3426616;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary sequence analysis by fast atom bombardment mass spectrometry
 RT of a peptide with adipokinetic activity from the corpora cardiaca of
 RT the cricket Gryllus bimaculatus.";
 RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
 RN [2]
 RP SEQUENCE.

RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
 RX MEDLINE=89145002; PubMed=3226948;
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
 RT the lubber grasshopper, Romalea microptera.";
 RL Peptides 9:681-688(1988).
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A28004; A28004.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
 ||
 Db 3 NF 4

RESULT 10
 AKH LIBAU STANDARD; PRT; 8 AA.
 AC P25418;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adipokinetic hormone (AKH).
 OS Libellula auripennis (Skimmer dragonfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Palaepoteria; Odonata; Anisoptera; Libellulidae; Libellula.
 OX NCBI_TaxID=6966;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90359055; PubMed=2390213;
 RA Gaede G.;
 RT "The putative ancestral peptide of the adipokinetic/red-pigment-
 RT concentrating hormone family isolated and sequenced from a
 RT dragonfly.";
 RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; S10596; S10596.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
 ||
 Db 3 NF 4

RESULT 11
 AKH MELML STANDARD; PRT; 8 AA.
 AC P25423;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adipokinetic hormone (AKH).
 OS Melolontha melolontha (Cockchafer),
 OS Geotrupes stercorosus (Dor beetle), and
 OS Pachnoda marginata (Flower beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;
 OC Scarabaeidae; Melolonthinae; Melolontha.
 OX NCBI_TaxID=7061, 7087, 7058;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
 RX MEDLINE=91248100; PubMed=2039445;
 RA Gaede G.;
 RT "A unique charged tyrosine-containing member of the adipokinetic
 RT hormone/red-pigment-concentrating hormone peptide family isolated and
 RT sequenced from two beetle species.";
 RL Biochem. J. 275:671-677(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
 RX MEDLINE=92265187; PubMed=1586453;
 RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;

RT "Primary structures of neuropeptides isolated from the corpora
 RT cardiaca of various cetonid beetle species determined by
 RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
 RT spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A58641; A58641.
 DR PIR; S15422; S15422.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 2 LN 3

RESULT 12
 ALL1 CYDPO STANDARD; PRT; 8 AA.
 ID -FAR1 PANRE
 AC P41872;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiaastatin 1.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OK NCBI_TaxID=82600;
 [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC -!- FUNCTION: MYOACTIVE.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 5 NF 6

RESULT 13
 ALL6 CYDPO STANDARD; PRT; 8 AA.
 ID -FAR1 PANRE
 AC P8316;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiaastatin 6.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OK NCBI_TaxID=82600;
 [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC -!- FUNCTION: MYOACTIVE.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 5 NF 6

RESULT 14
 FAR1 PANRE STANDARD; PRT; 8 AA.
 ID -FAR1 PANRE
 AC P41872;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide PF1 (SDENFLRP-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OK NCBI_TaxID=6233;
 [1]
 RP SEQUENCE.
 RX MEDLINE=93027659; PubMed=1408999;
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
 RA Garrison R.D., Williams J.F., Friedman A.R.;
 RT "Two FMRFamide-like peptides from the free-living nematode
 RT Panagrellus redivivus.";
 RL Peptides 13:209-214(1992).
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
 CC CAUDALLY TO THE BASE OF THE PHARYNX.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 4 NF 5

RESULT 15
 FAR1 PENMO STANDARD; PRT; 8 AA.
 ID -FAR1 PENMO
 AC P8316;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLP1 (GDRNFLRP-amide).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Rumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupum J., Krungkasek C., Longyant S.,
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 of the giant tiger prawn, Penaeus monodon.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NF 3
 DB [1]
 4 NF 5
 RESULT 16
 FAR2 MACRS
 ID FAR2_MACRS STANDARD; PRT; 8 AA.
 AC P83275;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLP2 (ADKNFURF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX Sithigorngul P., Sarathongkum W., Jaidechchoey S., Longyant S.,
 RA Sithigorngul W.;
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
 freshwater prawn Macrobrachium rosenbergii.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -!- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR GO:0007218; P-neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C433AAD CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NF 3
 DB [1]
 4 NF 5
 RESULT 17
 FAR3 HOMAM
 ID FAR3_HOMAM STANDARD; PRT; 8 AA.
 AC P41486;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide 3 (FLI 3) (F2).
 OS Homarus americanus (American lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Nephropoidea; Nephropidae; Homarus.
 OX NCBI_TaxID=6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=88116164; PubMed=3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT "Purification and characterization of FMRFamide-like immunoreactive
 substances from the lobster nervous system: isolation and sequence
 analysis of two closely related peptides.";
 RL J. Comp. Neurol. 266:16-26(1987).
 CC -!- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 MM
 POTASSIUM IN THE PRESENCE OF CALCIUM.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NF 3
 DB [1]
 4 NF 5
 RESULT 18
 FAR4 HOMAM
 ID FAR4_HOMAM STANDARD; PRT; 8 AA.
 AC P41487;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide 4 (FLI 4) (F1).
 OS Homarus americanus (American lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Nephropoidea; Nephropidae; Homarus.
 OX NCBI_TaxID=6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=88116164; PubMed=3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT "Purification and characterization of FMRFamide-like immunoreactive
 substances from the lobster nervous system: isolation and sequence
 analysis of two closely related peptides.";
 RL J. Comp. Neurol. 266:16-26(1987).
 CC -!- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
 NEUROMUSCULAR JUNCTIONS.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NF 3
 DB [1]
 4 NF 5
 RESULT 19

HTF1 PERAM
ID HTF1 PERAM STANDARD; PRT; 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Hypertrihaloaemic factor I (Neuropeptide M-I) (Periplaneta CC-I)
DE (PeA-CAH-I) (Led-CC-I) (Hypertrihaloaemic neuropeptide I).
OS Periplaneta americana (American cockroach).
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blattella orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=L.decemlineata;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish P., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrihaloaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: HYPERTRITHALOEAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR: A44960; A44960.
DR PIR: A49823; A49823.
DR PIR: S08995; S08995.
DR PROSITE: PS002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 931 MW; 86745775B9C452D6 CRC64;
Query Match 66.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 NF 4
RESULT 20
FAR2 PANRE
ID FAR2 PANRE STANDARD; PRT; 9 AA.
AC P41873;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, last sequence update)
DT 01-NOV-1995 (Rel. 32, last annotation update)
DE FMRFamide-like neuropeptide PF2 (SADPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RA Garrison R.D., Williams J.F., Friedman A.R.;
RT "Two FMRFamide-like peptides from the free-living nematode
RT Panagrellus redivivus.";
RL Peptides 13:209-214(1992).
CC -!- FUNCTION: MYOACTIVE.
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
CC CAUDALLY TO THE BASE OF THE PHARYNX.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;
Query Match 66.7%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
Db 5 NF 6
RESULT 21
FAR3 MACRS
ID FAR3 MACRS STANDARD; PRT; 9 AA.
AC P83276;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, last sequence update)
DE FMRFamide-like neuropeptide FLP3 (NYDKNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigongul P., Sarathongkum W., Jaidechoey S., Longyant S.,
RA Sithigongul W.;
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -!- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433ABB CRC64;
Query Match 66.7%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
 Db 5 NF 6

RESULT 22
 FAR6 MACRS
 ID FAR6 MACRS STANDARD; PRT; 9 AA.
 AC P83279;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE FMRamide-like neuropeptide FLP6 (DGRNPLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21107394; PubMed=11179812;
 RA Sithigorngul W., Sarathongkum W., Longyant S., Panchan N.,
 RA Sithigorngul W., Petson A.;
 RT "Three more novel FMRamide-like neuropeptide sequences from the
 RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
 RL Peptides 22:191-197(2001).
 CC -I- MASS SPECTROMETRY: MW=1080.7; METHOD=WALDI.
 CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR GO:0007218; P:neuropeptide signaling pathway; IDA.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1081 MW; 26800723C4540878 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
 Db 5 NF 6

RESULT 23
 FAR8 MACRS
 ID FAR8 MACRS STANDARD; PRT; 9 AA.
 AC P83281;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE FMRamide-like neuropeptide FLP8 (VSHNNPLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21107394; PubMed=11179812;
 RA Sithigorngul W., Sarathongkum W., Longyant S., Panchan N.,
 RA Sithigorngul W., Petson A.;
 RT "Three more novel FMRamide-like neuropeptide sequences from the
 RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
 RL Peptides 22:191-197(2001).
 CC -I- MASS SPECTROMETRY: MW=1133.8; METHOD=WALDI.
 CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR GO:0007218; P:neuropeptide signaling pathway; IDA.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1081 MW; 26800723C4540878 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
 Db 5 NF 6

RESULT 24
 LMIP LOCM
 ID LMIP LOCM STANDARD; PRT; 9 AA.
 AC P31799;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Locustamyo-inhibiting peptide (LOM-MIP).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92179466; PubMed=1796179;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, identification and synthesis of locustamyo-inhibiting
 RT peptide (LOM-MIP), a novel biologically active neuropeptide from
 RT Locusta migratoria.";
 RL Regul. Pept. 36:111-119(1991).
 CC -I- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND
 CC OVIDUCT.
 CC -I- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS
 CC IN THE SUBESOPHAGEAL GANGLION.
 DR PIR; A60065; AKLQIM.
 KW Amidation; Neuropeptide.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
 Db 5 LN 6

RESULT 25
 PTSP BOMMO
 ID PTSP BOMMO STANDARD; PRT; 9 AA.
 AC P82003;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Prothoracicostatic peptide (Bom-PTSP).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=C145 X N140; TISSUE=Brain;
 RX MEDLINE=2002634; PubMed=10531308;
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
 RA Kataoka H.;
 RT "Identification of a prothoracicostatic peptide in the larval brain of
 RT the silkworm, Bombyx mori.";
 RL J. Biol. Chem. 274:31169-31173(1999).
 RN [2]

RP ERRATUM.
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
 RA Kataoka H.,
 RL J. Biol. Chem. 275:9892-9892(2000).
 CC -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
 CC gland.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.
 KW Hormone; Amidation.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1090 MW; 3878C5B4472AB6C3 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 5 LN 6

RESULT 26
 UP06 HUMAN
 ID UP06 HUMAN STANDARD; PRT; 9 AA.
 AC P30092;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 14) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=9302937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5, ITS MW IS: 48 kDa.
 CC SWISS-2DPAGE: P30092; HUMAN.
 FT NON_TER 1 9
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 935 MW; 5282F2CAA8676447 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 2 LN 3

RESULT 27
 FAR2 PENMO
 ID FAR2 PENMO STANDARD; PRT; 10 AA.
 AC P8317;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FLP2 (AYSNLNLVRF-amide).
 OS Penaeus monodon (Pencoid shrimp).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 CC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn Penaeus monodon.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1260.0; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1260 MW; 88F9023B54472455 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 5 LN 6

RESULT 28
 FAR7 MACRS
 ID FAR7 MACRS STANDARD; PRT; 10 AA.
 AC P83280;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FLP7 (GYGDRNFLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 CC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21107394; PubMed=11179812;
 RA Sithigorngul P., Saraihongkum W., Longyant S., Panchan N.,
 RA Sithigorngul P., Petsom A.;
 RT "Three more novel FMRamide-like neuropeptide sequences from the
 RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
 RL Peptides 22:191-197(2001).
 CC -!- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC GO: GO:0007218; P:neuropeptide signaling pathway; IDA.
 DR Neuropeptide; Amidation.
 KW MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540A8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 6 NF 7

RESULT 29
 FARC CALVO
 ID FARC CALVO STANDARD; PRT; 10 AA.
 AC P41867;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CallifMRamide 12.
 OS Calliphora vomitoria (Blue blowfly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion; PubMed=1549595;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRFamides) from the blowfly
 RT Calliphora vomitoria";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC PIR; C44787; C44787.
 DR Neuropeptide; Amidation.
 KW MOD RES 10 10
 FT SEQUENCE 10 AA; 1156 MW; 2281039C44AB6D8 CRC64;
 SQ
 Query Match 66.7%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NF 3
 Db ||
 6 NF 7
 RESULT 30
 HTF1_ROMMI STANDARD; PRT; 10 AA.
 ID P18110;
 AC 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RO I (Hypertrehalosemic factor).
 OS Romalea microptera (Lubber grasshopper).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Romaleidae; Romalea.
 OX NCBI_TaxID=7007;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89145002; PubMed=3226948;
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
 RT the lubber grasshopper, Romalea microptera";
 RL Peptides 9:681-688(1988).
 CC -!- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 FT MOD RES 10 10
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NF 3
 Db ||
 3 NF 4
 RESULT 31
 HTF1_NAUCI STANDARD; PRT; 10 AA.
 ID HTF1_NAUCI

AC P10939;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypertrehalosemic hormone (HTH) (Hypertrehalosemic neuropeptide).
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
 OS Leucophaea maderae (Madeira cockroach),
 OS Blattella germanica (German cockroach), and
 OS Gromphadorhina portentosa (Madagascan hissing cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Nauphoeta.
 OX NCBI_TaxID=6990, 6988, 6973, 36953;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=N.cinerea; TISSUE=Corpora cardiaca;
 RX MEDLINE=87100208; PubMed=3801028;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Amino acid sequence of a hypertrehalosemic neuropeptide from the
 RT corpus cardiacum of the cockroach, Nauphoeta cinerea";
 RL Biochem. Biophys. Res. Commun. 141:774-781(1986).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=L.maderae, G.portentosa, and B.germanica;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=B.germanica;
 RX MEDLINE=91179584; PubMed=2080017;
 RA Veenstra J.A., Camps F.;
 RT "Structure of the hypertrehalosemic neuropeptide of the German
 RT cockroach, Blattella germanica";
 RL Neuropeptides 15:107-109(1990).
 CC -!- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A26381; A26381.
 DR PIR; A60421; A60421.
 DR PIR; S08997; S08997.
 DR PIR; S08998; S08998.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 FT MOD RES 10 10
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1092 MW; 056236786775B9C4 CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NF 3
 Db ||
 3 NF 4
 RESULT 32
 UR7_HUMAN STANDARD; PRT; 10 AA.
 ID UR7_HUMAN
 AC P34990;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of red blood cells (Spot 2D-006HO)
 DE (fragment).

OS Homo sapiens (Human) .
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Erythrocyte;
 RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
 RA Balant L., Hochstrasser D.F.;
 RL Submitted (FEB-1994) to the SWISS-PROT data bank.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.77, ITS MW IS: 26 kDa.
 DR SWISS-2DPAGE; P34990; HUMAN.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1161 MW; F72D82E9C44B1871 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 6 NF 7

RESULT 33
 UXA6_CHLTR STANDARD; PRT; 10 AA.
 AC P38007;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Unknown protein from 2D-page from elementary body (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=L2/434/Bu;
 RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
 RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
 RA Pallini V.;
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
 DR Siena-2DPAGE; P38007; -.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1243 MW; DAD39A33304B5339 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 2 NF 3

RESULT 34
 CS15_BACSU STANDARD; PRT; 11 AA.
 AC P81095;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=168 / JH642;

RA Graumann P.L., Schmid R., Marahiel M.A.;
 RL Submitted (OCT-1997) to the SWISS-PROT data bank.
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=168 / JH642;
 RX MEDLINE=96345629; PubMed=8755892;
 RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
 RT "Cold shock stress-induced proteins in *Bacillus subtilis*.";
 RL J. Bacteriol. 178:4611-4619(1996).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- INDUCTION: In response to low temperature.
 CC -!- CAUTION: Could not be found in the genome of *B. subtilis* 168.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1360 MW; 15F6ECE6322C330 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 10 LN 11

RESULT 35
 RRPL_CHAV STANDARD; PRT; 11 AA.
 AC P13179;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
 DE (L protein) (Fragment).
 GN L.
 OS Chandipura virus (strain 1653514).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Vesiculovirus.
 OX NCBI_TaxID=11273;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89299473; PubMed=2741347;
 RA Masters P.S., Shella R.S., Butcher M., Patel B., Ghosh H.P.,
 RA Banerjee A.K.;
 RT "Structure and expression of the glycoprotein gene of Chandipura
 virus."; 171:285-290(1989).
 RL Virology 171:285-290(1989).
 CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
 CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
 CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(N).
 CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
 CC NUCLEOCASID (N) PROTEIN.
 CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
 CC PARAMYXOVIRUSES.

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 EMBL; J04350; AAA42917.1; -.
 Transferase; RNA-directed RNA polymerase.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
 Db 3 LN 4

RESULT 36
 T2P1_PROVU STANDARD; PRT; 11 AA.
 AC P31031;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
 DE (R.PvuI) (Fragment).
 GN PVUIR.
 OS Proteus vulgaris.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Proteus.
 OX NCBI_TaxID=585;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13315;
 RX MEDLINE=93087186; PubMed=1454536;
 RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
 RT "Cloning and characterization of genes for the PvuI restriction and
 modification system."
 RL Nucleic Acids Res. 20:5743-5747(1992).
 CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
 CLEAVES AFTER T-4.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
 specific double-stranded fragments with terminal 5'-phosphates.
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 CC -----
 DR EMBL; L04163; AAA25660.1; -.
 DR PIR; S35490; S35490.
 DR REBASE; 1541; PvuI.
 KW Restriction system; Hydrolase; Nuclease; Endonuclease.
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1300 MW; 9FC0DE7955B72B1A CRC64;

Query Match 66.7%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
 Db 10 NF 11

RESULT 37
 ULAG_HUMAN STANDARD; PRT; 11 AA.
 AC P31933;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,

RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993."
 RL Electrophoresis 14:1216-1222(1993).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.5, ITS MW IS: 34 kDa.
 DR SWISS-2DPAGE; P31933; HUMAN.
 DR Sienna-2DPAGE; P31933; -.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 66.7%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
 Db 8 LN 9

RESULT 38
 FIF1_SARBU STANDARD; PRT; 12 AA.
 AC P83349;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neb-FIRamide 1.
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AMIDATION, AND FUNCTION.
 CC TISSUE=CNS;
 RX MEDLINE=22342733; PubMed=12438685;
 RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
 RT "Identification in Drosophila melanogaster of the invertebrate G
 protein-coupled FWRamide receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
 CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular
 junctions.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FWRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 12 12
 SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
 Db 8 NF 9

RESULT 39
 UR2_SCYCA STANDARD; PRT; 12 AA.
 AC P35490;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urotensin II (U-II) (UII).
 OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyllorhinidae; Scyllorhinus.
 OX NCBI_TaxID=7830;
 RN [1]


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RP SEQUENCE.
RC TISSUE=Spinal cord;
RX MEDLINE=92319231; PubMed=1620290;
RA Conlon J.M., O'Harte F., Smith D.D., Balmert R.J., Hazon N.;
RT "Purification and characterization of urotensin II and parvalbumin
RL from an elasmobranch fish, Scyliorhinus canicula (common dogfish).";
RL Neuroendocrinology 55:230-235(1992).
CC -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
CC -!- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.
DR InterPro; IPR001483; Urotensin II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROSENSIN_II; 1.
KW HORMONE.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1526 MW; 804729F9D579CEBA CRC64;

Query Match 66.7%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
Db 2 NF 3

RESULT 40
CXAA CONST STANDARD; PRT; 13 AA.
AC P28878;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin SIA (SIA).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91369955; PubMed=1892838;
RA Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
RA Oliveira B.M.;
RT "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
RT receptors.";
RL Biochemistry 30:9370-9377(1991).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; A40312; NTKRAS.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 7
FT MOD_RES 3 13
FT DISULFID 3 13
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
Db 10 NF 11

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RESULT 41
FARB ASCSU STANDARD; PRT; 13 AA.
AC P43173;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide APL1.
DE FMRamide-like neuropeptide APL1.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1495 MW; 9CAEC650D688B05 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
Db 9 NF 10

RESULT 42
ITB5 BOVIN STANDARD; PRT; 13 AA.
AC P80747;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrin beta-5 (Fragment).
GN ITGB5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=97299777; PubMed=9154926;
RA Andersen M.H., Berglund L., Rasmussen J.T., Petersen T.E.;
RT "Bovine PAS-6/7 binds alpha v beta 5 integrins and anionic
RT phospholipids through two domains.";
RL Biochemistry 36:5441-5446(1997).
CC -!- FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
CC -!- IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
CC ASSOCIATES WITH ALPHA-V.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
DR InterPro; IPR001169; Integrin beta C.
DR PROSITE; PS00243; INTEGRIN_BETA; PARTIAL.
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW Repeat.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1299 MW; 844197D005B9B65 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LN 2
Db      1 LN 2

RESULT 43
ORCK ORCLI STANDARD; PRT; 13 AA.
AC P37086; 1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Orcokinin.
OS Orconectes limosus (Spinycheek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacidea; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;
RN [1]
RP SEQUENCE.
RC TISSUE=Abdominal nerve cord;
RX MEDLINE=93126144; PubMed=1480511;
RA Stangler J., Hilbich C., Burdick S., Keller R.;
RT "Orcokinin: a novel myotropic peptide from the nervous system of the
RT crayfish, Orconectes limosus.";
RL Peptides 13:859-864(1992).
CC -!- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
CC -!- AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS.
CC -!- TISSUE SPECIFICITY: ABDOMINAL NERVE CORD AND HINDGUT.
KW Neuropeptide.
SQ SEQUENCE 13 AA; 1518 MW; 8A318D7B4A93A40A CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NF 3
Db      1 NF 2

RESULT 44
RPOC MYCGA STANDARD; PRT; 13 AA.
AC P47716;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit) (Fragment).
GN RPOC.
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A5969Var B;
RA Skarmov A.V., Feoktistova E.S., Gol'dman M.A., Feoktistova E.S.,
RA Bibilashvili R.S.;
RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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CC EMBL; L38402; AAB40952.1;
KW Transferase; DNA-directed RNA polymerase; Transcription.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1630 MW; 4BEC27C7480D4333 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
Db      4 LN 5

RESULT 45
TEJA_RANJA STANDARD; PRT; 13 AA.
AC P83307;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin-1Ja.
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=21826910; PubMed=11835990;
RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;
RT "Antimicrobial peptides with atypical structural features from the
RT skin of the Japanese brown frog Rana japonica.";
RL Peptides 23:419-425(2002).
CC -!- FUNCTION: Antibacterial activity against the Gram-negative
CC bacterium E.coli and the Gram-positive bacterium S.aureus.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1405; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the breviniin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1407 MW; 3EF113EA610A2448 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
Db      9 LN 10

RESULT 46
TEMC_RANTE STANDARD; PRT; 13 AA.
AC P56918;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin C.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;

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RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporaria,";
RT "Temporaria,";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION
SQ SEQUENCE 13 AA; 1363 MW; 2201403AG55B2448 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 9 LN 10

RESULT 47
TEMP_RANTE
ID TEMP_RANTE STANDARD; PRT; 13 AA.
AC P56919;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin D.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OC NCBI_TaxID=8407;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporaria,";
RT "Temporaria,";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has no antibacterial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1379 MW; 3BF35DFA655B2448 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 9 LN 10

RESULT 48
TEMP_RANTE
ID TEMP_RANTE STANDARD; PRT; 13 AA.
AC P56920;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin E.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

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OX NCBI_TaxID=8407;
RX [1]
RP SEQUENCE.
RT TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporaria,";
RT "Temporaria,";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 9 LN 10

RESULT 49
YPNP_PHOLU
ID YPNP_PHOLU STANDARD; PRT; 13 AA.
AC P41122;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in pnp 3'region (ORF3) (Fragment).
OS Photobacterium luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photobacterium.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K122;
RX MEDLINE=94266731; PubMed=8206856;
RA Clarke D.J., Dowds B.C.A.;
RT "The gene coding for polynucleotide phosphorylase in Photobacterium sp. strain K122 is induced at low temperatures.";
RL J. Bacteriol. 176:3775-3784(1994).
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CC -----
CC EMBL; X76069; CAA53672.1; -
KW Hypothetical protein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1634 MW; 64774A4F6267A364 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
Db 2 NF 3

RESULT 50
LECB_PSOC

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ID LECB PSOSC STANDARD; PRT; 14 AA.
 AC P22584;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Basic lectin B1 (Fragment).
 OS Psophocarpus scandens.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 OC Psophocarpus.
 OX NCBI_TaxID=3890;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RA Kortt A.A.;
 RT "Isolation and characterization of the lectins from the seeds of
 RT Psophocarpus scandens.";
 RL Phytochemistry 27:2847-2855(1988).
 CC -!- SUBUNIT: DIMER OF TWO IDENTICAL OR NEARLY IDENTICAL SUBUNITS OF
 CC ABOUT 32000 APPARENT MW.
 CC -!- PTM: CONTAINS ABOUT 9% CARBOHYDRATE. HETEROGENEITY IN CARBOHYDRATE
 CC COMPOSITION MAY RESULT IN DIFFERENT ISOLECTIN FORMS.
 CC -!- SIMILARITY: WITH P.TETRAONOLOBUS BASIC LECTINS IN N-TERMINAL
 CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.
 DR PIR; PA0007; PA0007.
 KW Lectin; Glycoprotein.
 FT NON TER 14
 SQ SEQUENCE 14 AA; 1732 MW; D804CE43B487C549 CRC64;

 Query Match 66.7%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 NF 3
 Db 6 NF 7

 RESULT 51
 LPER_BACLI STANDARD; PRT; 14 AA.
 ID_Q04303;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Erythromycin resistance leader peptide (23S rRNA methylase leader
 DE peptide).
 OS Bacillus licheniformis, and
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1402, 1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.licheniformis;
 RX MEDLINE=84245158; PubMed=6429477;
 RA Gryczan T., Israeli-Reches M., del Bue M., Dubnau D.;
 RT "DNA sequence and regulation of ermD, a macrolide-lincosamide-
 RT streptogramin B resistance element from Bacillus licheniformis.";
 RL Mol. Gen. Genet. 194:349-356(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.licheniformis; STRAIN=EMR-1;
 RX MEDLINE=91310580; PubMed=1713206;
 RA Kwak J.-K., Choi E.-C., Weisblum B.;
 RT "Transcriptional attenuation control of ermK, a
 RT macrolide-lincosamide-streptogramin B resistance determinant from
 RT Bacillus licheniformis.";
 RL J. Bacteriol. 173:4725-4735(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.anthraxis; STRAIN=590;
 RX MEDLINE=913232776; PubMed=8473865;

RA Kim H.-S., Choi E.-C., Kim B.-K.;
 RT "A macrolide-lincosamide-streptogramin B resistance determinant from
 RT Bacillus anthracis 590: cloning and expression of ermJ.";
 RL J. Gen. Microbiol. 139:601-607(1993).
 CC -!- FUNCTION: THIS PEPTIDE IS INVOLVED IN THE CONTROL MECHANISM OF
 CC THE SYNTHESIS OF THE MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B
 CC RESISTANCE PROTEIN. IT ACTS AS A TRANSCRIPTIONAL ATTENUATOR.
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 CC -----
 DR EMBL; L08389; AAA22596.1; -;
 DR EMBL; M29832; AAA22598.1; -;
 DR PIR; A42473; A42473.
 KW Antibiotic resistance; Leader peptide.
 SQ SEQUENCE 14 AA; 1732 MW; 5D1138B59F32ED07 CRC64;

 Query Match 66.7%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 LN 2
 Db 12 LN 13

 RESULT 52
 MAST_VESCR STANDARD; PRT; 14 AA.
 ID_P01516;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mastoparan C.
 OS Vespa crabro (European hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7445;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Venom; PubMed=6206053;
 RX MEDLINE=84289390;
 RA Argiolas A., Pisano J.J.;
 RT "Isolation and characterization of two new peptides, mastoparan C and
 RT crabrolin, from the venom of the European hornet, Vespa crabro.";
 RL J. Biol. Chem. 259:10106-10111(1984).
 CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
 CC that couple to phospholipase C.
 DR PIR; A01779; QMVHP2.
 KW Mast cell degranulation; Amidation.
 FT MOD RES 14
 SQ SEQUENCE 14 AA; 1508 MW; 550C05CA1D6AB1D7 CRC64;

 Query Match 66.7%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 LN 2
 Db 1 LN 2

 RESULT 53
 PSAG_CUCSA STANDARD; PRT; 14 AA.
 ID_P42049;
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Photosystem I reaction center subunit V (PSI-G) (Photosystem I 6.8 kDa
 DE protein) (PS I subunit 10) (Fragment).
 GN PSAG.
 OS *Cucumis sativus* (Cucumber).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 OX NCBI_TaxID=3659;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cotyledon;
 RX MEDLINE=91355209; PubMed=1883835;
 RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
 RT "Characterization of genes that encode subunits of cucumber PS I
 RT complex by N-terminal sequencing.";
 RL Biochim. Biophys. Acta 1059:141-148(1991).
 CC -!- FUNCTION: NOT YET KNOWN.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CHLOROPLAST
 CC THYLAKOID MEMBRANE; ASSOCIATED WITH THE STROMAL SIDE OF THE
 CC THYLAKOID MEMBRANE.
 CC -!- SIMILARITY: Belongs to the psag / psak family.
 CC PIR; B56819; B56819.
 DR InterPro; IPR000549; PSI_Psag/K.
 DR PROSITE; PS01026; PHOTOSYSTEM_I_PsAGK; PARTIAL.
 KW Photosynthesis; Photosystem I; Transmembrane; Chloroplast; Thylakoid.
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1452 MW; D712F0B91F1CA142 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 Db ||
 2 LN 3

RESULT 54
 SMS1 MYOSC
 ID SMS1_MYOSC STANDARD; PRT; 14 AA.
 AC P20750;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin I.
 OS *Myoxocephalus scorpius* (Shorthorn sculpin) (Daddy sculpin),
 OS *Oncorhynchus kisutch* (Coho salmon), and
 OS *Anguilla anguilla* (European freshwater eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Teleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
 OC Cottoidae; Cottidae; Myoxocephalus.
 OX NCBI_TaxID=8097, 8019, 7936;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=M.scorpius; TISSUE=Pancreas;
 RX MEDLINE=88029486; PubMed=2889597;
 RA Conlon J.M., Davis M.S., Falkner S., Thim L.;
 RT "Structural characterization of peptides derived from
 RT prosomatostatins I and II isolated from the pancreatic islets of two
 RT species of teleostean fish: the daddy sculpin and the flounder.";
 RL Eur. J. Biochem. 168:647-652(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=O.kisutch; TISSUE=Pancreas;
 RX MEDLINE=87055212; PubMed=2877919;
 RA Plietsekaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
 RA Kimmel J.R., Andrews P.C., Gorman A.;
 RT "Characterization of coho salmon (*Oncorhynchus kisutch*) islet
 RT somatostatins.";
 RL Gen. Comp. Endocrinol. 63:252-263(1986).

RN [3]
 RP SEQUENCE.
 RC SPECIES=A.anguilla; TISSUE=Pancreas;
 RX MEDLINE=89065329; PubMed=2904391;
 RA Conlon J.M., Deacon C.F., Hazon N., Henderson I.W., Thim L.;
 RT "Somatostatin-related and glucagon-related peptides with unusual
 RT structural features from the European eel (*Anguilla anguilla*).";
 RL Gen. Comp. Endocrinol. 72:181-189(1988).
 CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 DR PIR; A60840; A60840.
 DR PIR; B60842; B60842.
 DR PIR; S00172; S00172.
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin; 1.
 KW Hormone; Multigene family.
 FT DISULFID 3 14
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 Db ||
 5 NF 6

RESULT 55
 SMS ALLMI
 ID SMS ALLMI STANDARD; PRT; 14 AA.
 AC P31885; 1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin-14.
 OS *Alligator mississippiensis* (American alligator), and
 OS *Trachemys scripta* (Red-eared slider turtle) (*Pseudemys scripta*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496, 34903;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=A.mississippiensis; TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=T.scripta;
 RX MEDLINE=90341082; PubMed=1974347;
 RA Conlon J.M., Hicks J.W.;
 RT "Isolation and structural characterization of insulin, glucagon and
 RT somatostatin from the turtle, *Pseudemys scripta*.";
 RL Peptides 11:461-466(1990).
 CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 DR PIR; C60414; C60414.
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin; 1.
 KW Hormone.
 FT DISULFID 3 14
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

```

Db          1 LN 2
           ||
           10 LN 11

RESULT 56
ECDA_LYMDI STANDARD; PRT; 15 AA.
AC P80938;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis ecdysiotropin peptide A (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC OF LARVAE AND PUPAE.
SQ SEQUENCE 15 AA; 1712 MW; 12EBD8246B74EE26 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LN 2
           ||
           11 LN 12

RESULT 57
PRE2_LITIN STANDARD; PRT; 15 AA.
AC P82022;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Frenatin 2.
OS Litoria infraenata (Giant tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=61195;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97386837; PubMed=9225251;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of
RT the giant tree frog Litoria infraenata.";
RL J. Pept. Sci. 2:117-124(1996).
CC -!- FUNCTION: Wide spectrum antimicrobial peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
CC glands.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 15
SQ SEQUENCE 15 AA; 1425 MW; 06D4B7BB1650CBF CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1 LN 2
           ||
           10 LN 11

RESULT 58
LEC1_PSOSC STANDARD; PRT; 15 AA.
AC P22582;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Acidic lectin A1 (Fragment).
OS Psophocarpus scandens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3890;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Kortt A.A.;
RT "Isolation and characterization of the lectins from the seeds of
RT Psophocarpus scandens.";
RL Phytochemistry 27:2847-2855(1988).
CC -!- SUBUNIT: DIMER. THE SUBUNITS SHOW APPARENT MW HETEROGENEITY
CC (32000-35000 MW), WHICH MAY RESULT FROM DIFFERENT CARBOHYDRATE
CC CONTENT, AA SEQUENCE, OR POLYPEPTIDE LENGTH.
CC -!- PTM: CONTAINS 5-6% CARBOHYDRATE.
CC -!- SIMILARITY: WITH P.TETRAGONOLOBUS ACIDIC LECTINS IN N-TERMINAL
CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.
DR PIR; PA0005; PA0005.
KW Lectin; Glycoprotein.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1743 MW; D6EB9FE9C6B0254D CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 NF 3
           ||
           7 NF 8

RESULT 59
LEC2_PSOSC STANDARD; PRT; 15 AA.
AC P22585;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Basic lectin B2 (Fragment).
OS Psophocarpus scandens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3890;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Kortt A.A.;
RT "Isolation and characterization of the lectins from the seeds of
RT Psophocarpus scandens.";
RL Phytochemistry 27:2847-2855(1988).
CC -!- SUBUNIT: DIMER OF TWO IDENTICAL OR NEARLY IDENTICAL SUBUNITS OF
CC ABOUT 32000 APPARENT MW.
CC -!- PTM: CONTAINS ABOUT 9% CARBOHYDRATE. HETEROGENEITY IN CARBOHYDRATE
CC COMPOSITION MAY RESULT IN DIFFERENT ISOLECTIN FORMS.
CC -!- SIMILARITY: WITH P.TETRAGONOLOBUS BASIC LECTINS IN N-TERMINAL
CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.

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DR PIR; PA0008; PA0006.
KW Lectin; Glycoprotein.
FT NON TER 15
SQ SEQUENCE 15 AA; 1847 MW; D194CE400C832796 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
   ||
Db 7 NF 8

RESULT 60
LEC3 AXIPO
ID _LEC3_AXIPO STANDARD; PRT; 15 AA.
AC P28588;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Lectin III (Fragment).
OS Axinella polyoides (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Halichondrida; Axinellidae; Axinella.
OX NCBI_TaxID=12959;
[1]
RN
RP SEQUENCE.
RX MEDLINE=93003351; PubMed=1390906;
RA Buck F., Luth C., Strupat K., Bretting H.;
RT "Comparative investigations on the amino-acid sequences of different
RT isolectins from the sponge Axinella polyoides (Schmidt).";
RL Biochim. Biophys. Acta 1159:1-8(1992).
CC -!- FUNCTION: POSSESSES D-GALACTOSE BINDING SPECIFICITY.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: STORED IN SPHERULOUS CELLS IN THE SPONGE
CC TISSUE.
DR PIR; S29174; S29174.
KW Lectin.
FT NON TER 15
SQ SEQUENCE 15 AA; 1744 MW; DC05E47E3F8DC5F3 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
   ||
Db 13 LN 14

RESULT 61
LEC3 PSOSC
ID _LEC3_PSOSC STANDARD; PRT; 15 AA.
AC P22583;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Acidic lectin A3 (Fragment).
OS Psophocarpus scandens.
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3890;
[1]
RN
RP SEQUENCE.
RX Kott A.A.;
RA "Isolation and characterization of the lectins from the seeds of
RT Psophocarpus scandens.";
RL Phytochemistry 27:2847-2855(1988).
CC -!- SUBUNIT: DIMER. THE SUBUNITS SHOW APPARENT MW HETEROGENEITY
```

```
CC (32000-35000 MW), WHICH MAY RESULT FROM DIFFERENT CARBOHYDRATE
CC CONTENT, AA SEQUENCE, OR POLYPEPTIDE LENGTH.
CC -!- PTM: CONTAINS 5-6% CARBOHYDRATE.
CC -!- SIMILARITY: WITH P.TETRAONOLOBUS ACIDIC LECTINS IN N-TERMINAL
CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.
DR PIR; PA0006; PA0006.
KW Lectin; Glycoprotein.
FT NON TER 15
SQ SEQUENCE 15 AA; 1803 MW; D6EB9FF00C83954D CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
   ||
Db 7 NF 8

RESULT 62
MAOX CHICK
ID _MAOX_CHICK STANDARD; PRT; 15 AA.
AC Q92060;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DB NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Fragment).
GN MEL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=97056061; PubMed=8900406;
RA Hodnett D.W., Fantozzi D.A., Thurmond D.C., Klautsky S.A.,
RA Macphree K.G., Estrem S.T., Xu G., Goodridge A.G.;
RT "The chicken malic enzyme gene: structural organization and
RT identification of triiodothyronine response elements in the
RT 5'-flanking DNA.";
RL Arch. Biochem. Biophys. 334:309-324(1996).
CC -!- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2) +
CC NADPH.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U49693; AAA92721.1;
DR InterPro; IPR001891; Malic_oxred.
DR PROSITE; PS00331; MALIC_ENZYMES; PARTIAL.
KW Oxidoreductase; NADP.
FT NON TER 15
SQ SEQUENCE 15 AA; 1842 MW; CFEF180B2BA84C2B CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
   ||
Db 13 LN 14

RESULT 63
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PC20_BRANA
ID PC20_BRANA STANDARD; PRT; 15 AA.
AC P81096;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 20 kDa pollen coat protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Topas; TISSUE=Pollen;
RX MEDLINE=98345939; PubMed=9680961;
RA Murphy D.J., Ross J.H.;
RT "Biosynthesis, targeting and processing of oleosin-like proteins,
RT which are major pollen coat components in Brassica napus.";
RL Plant J. 13:1-16(1998).
CC -!- FUNCTION: MAJOR COMPONENT OF THE POLLEN COAT.
CC -!- TISSUE SPECIFICITY: POLLEN.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1756 MW; 4C9B7C58ED18A442 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
DB ||
8 LN 9

RESULT 64
UBLL_MONDO
ID USLL_MONDO STANDARD; PRT; 15 AA.
AC P50103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
DE L1) (Ubiquitin thioesterase L1) (Neuron cytoplasmic protein 9.5)
DE (PGP 9.5) (PGP9.5) (Fragment).
GN UCHL1.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96102916; PubMed=8522974;
RA Mann D.A., Trowern A.R., Lavender F.L., Whittaker P.A.,
RA Thompson R.J.;
RT "Identification of evolutionary conserved regulatory sequences in the
RT 5' untranslated region of the neural-specific ubiquitin C-terminal
RT hydrolase (PGP9.5) gene.";
RL J. Neurochem. 66:35-46(1996).
CC -!- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS.
CC THIS ENZYME IS A THIOL PROTEASE THAT RECOGNIZE AND HYDROLYZE
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
CC
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
PC20_BRANA
ID PC20_BRANA STANDARD; PRT; 15 AA.
AC P81096;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 20 kDa pollen coat protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Topas; TISSUE=Pollen;
RX MEDLINE=98345939; PubMed=9680961;
RA Murphy D.J., Ross J.H.;
RT "Biosynthesis, targeting and processing of oleosin-like proteins,
RT which are major pollen coat components in Brassica napus.";
RL Plant J. 13:1-16(1998).
CC -!- FUNCTION: MAJOR COMPONENT OF THE POLLEN COAT.
CC -!- TISSUE SPECIFICITY: POLLEN.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1756 MW; 4C9B7C58ED18A442 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
DB ||
8 LN 9

RESULT 64
UBLL_MONDO
ID USLL_MONDO STANDARD; PRT; 15 AA.
AC P50103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
DE L1) (Ubiquitin thioesterase L1) (Neuron cytoplasmic protein 9.5)
DE (PGP 9.5) (PGP9.5) (Fragment).
GN UCHL1.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96102916; PubMed=8522974;
RA Mann D.A., Trowern A.R., Lavender F.L., Whittaker P.A.,
RA Thompson R.J.;
RT "Identification of evolutionary conserved regulatory sequences in the
RT 5' untranslated region of the neural-specific ubiquitin C-terminal
RT hydrolase (PGP9.5) gene.";
RL J. Neurochem. 66:35-46(1996).
CC -!- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS.
CC THIS ENZYME IS A THIOL PROTEASE THAT RECOGNIZE AND HYDROLYZE
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
CC
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CC -----
 CC ENBL: U32208; AAA9059.1; -
 DR InterPro; IPR001578; UCH_1.
 DR PROSITE; PS00140; UCH_1; PARTIAL.
 KW Ub1 conjugation pathway; Hydrolase; Thiol protease; Multigene family.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1816 MW; 1B7A3B6E623F6E79 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
 DB ||
 13 LN 14

RESULT 65
 UC17_MAIZE
 ID UC17_MAIZE STANDARD; PRT; 15 AA.
 AC P80623;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 32) (Fragment).
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.

TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.5, ITS MW IS: 42.7 kDa.
 DR Maize-2DPAGE; P80623; COLEOPTILE.
 DR MaizeDB; 123949; -
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1554 MW; COAFFP15FFCECEC8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
 DB ||
 12 LN 13

RESULT 66
 UC28_MAIZE
 ID UC28_MAIZE STANDARD; PRT; 15 AA.
 AC P80634;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (spot 984) (Fragment).
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]


```

RN RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Parnollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.2, ITS MW IS: 27.7 kDa.
DR Maize-2DPAGE; P80634; COLBOPTILE.
DR MaizeDB; 123959; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1631 MW; 45C554E40BE9E77F CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 8 LN 9

RESULT 67
UE15 HORVU
ID UE15 HORVU STANDARD; PRT; 15 AA.
AC P34938;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown endosperm protein E-15/E-16/E-17 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. H354-295-2-5; TISSUE=Starchy endosperm;
RX MEDLINE=94170739; PubMed=8125056;
RA Flengsrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional
RT electrophoresis.";
RL Electrophoresis 14:1060-1066(1993).
CC -|- TISSUE SPECIFICITY: STARCHY ENDOSPERM.
CC -|- DEVELOPMENTAL STAGE: GERMINATION.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1735 MW; 2669969DDEAFD97F CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 11 LN 12

RESULT 68
ALL1 CALVO
ID ALL1 CALVO STANDARD; PRT; 16 AA.
AC P41839;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Callatostatin 1 (Leu-callatostatin 1) [Contains: Callatostatin 2 (Leu-
DE Callatostatin 2); Callatostatin 3 (Leu-callatostatin 3)].
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;

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RN RP SEQUENCE.
RC TISSUE=Brain, Head, and Thoracic ganglion;
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=94291167; PubMed=8020069;
RA Duve H., Thorpe A.;
RT "Distribution and functional significance of Leu-callatostatins in
RT the blowfly Calliphora vomitoria.";
RL Cell Tissue Res. 276:367-379(1994).
CC -|- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -|- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEREBRAL
CC COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
CC SYSTEM AND INTESTINE.
CC -|- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; A47393; A47393.
KW Neuropeptide; Amidation.
FT PEPTIDE 1 16 CALLATOSTATIN 1.
FT PEPTIDE 3 16 CALLATOSTATIN 2.
FT PEPTIDE 9 16 CALLATOSTATIN 3.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1907 MW; A435B68C26EC3D09 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 3 LN 4

RESULT 69
MDH SYN4
ID MDH SYN4 STANDARD; PRT; 16 AA.
AC P80460;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
GN MDH.
OS Synechocystis sp. (strain PCC 6714).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1147;
RN [1]
RP SEQUENCE.
RA Naterstad K., Synstad B., Sirevag R.;
RL Submitted (SEP-1996) to the SWISS-PROT data bank.
CC -|- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR InterPro; IPR001252; Mdh.
DR PROSITE; PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1780 MW; 61D1896F14E81984 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 1 LN 2

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Db          2 LN 3
RESULT 70
ODPB_SOLUTU STANDARD; PRT; 16 AA.
AC P81419;
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial
DE (EC 1.2.4.1) (PHE1-B) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
SEQUENCE.
RP STRAIN=cv. Romano; TISSUE=Tuber;
RC MEDLINE=98399821; PubMed=9729464;
RX Millar A.H., Knorr C., Leaver C.J., Hill S.A.;
RA "Plant mitochondrial pyruvate dehydrogenase complex: purification and
RT identification of catalytic components in potato.";
RL Biochem. J. 334:571-576 (1998).
CC -1- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -1- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
CC acetyldihydrolipoamide + CO(2).
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.
CC -1- SUBUNIT: Tetramer of two alpha and two beta subunits (by
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW Phosphorylation; Mitochondrion.
FT NON TER 16
SQ SEQUENCE 16 AA; 1705 MW; FF6ED80EC804F797 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 13 LN 14

RESULT 71
PATS ANASP STANDARD; PRT; 17 AA.
AC Q52748;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heterocyst inhibition signaling peptide.
GN PATS OR ASL2301.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
SEQUENCE FROM N.A., AND FUNCTION.
RP MEDLINE=99011350; PubMed=9794762;
RX Yoon H.-S., Golden J.W.;
RA "Heterocyst pattern formation controlled by a diffusible peptide.";
RT Science 282:935-938 (1998).
RL [2]
SEQUENCE FROM N.A.
RP MEDLINE=21595285; PubMed=11759840;
RX Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213 (2001).
RN [3]
FUNCTION.
RP MEDLINE=21172878; PubMed=11274121;
RX Yoon H.-S., Golden J.W.;
RA "Pats and products of nitrogen fixation control heterocyst pattern.";
RL J. Bacteriol. 183:2605-2613 (2001).
CC -1- FUNCTION: Inhibits heterocyst differentiation. Seems to control
CC heterocyst pattern formation through intercellular signaling
CC mechanisms. In Anabaena filaments every 10th vegetative cell
CC terminally differentiates into a heterocyst specialized for
CC nitrogen fixation. Pats seems to inhibit the formation of adjacent
CC heterocysts.
CC -1- SUBCELLULAR LOCATION: Periplasmic (Probable). Seems to diffuse
CC to adjacent cells.
CC -1- DEVELOPMENTAL STAGE: Expressed in proheterocysts.
CC -1- DATABASE: NAME=Protein Spotlight;
CC NOTE=Issue 23 of June 2002;
CC WWW="http://www.expasy.org/spotlight/articles/sptlt023.html".
CC -----
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CC -----
CC EMBL; AF046871; AAC03103.1; -.
DR EMBL; AP003589; BAB74000.1; -.
DR PIR; AF2093; AF2093.
KW Heterocyst; Periplasmic; Complete proteome.
SQ SEQUENCE 17 AA; 1927 MW; 192BE168476867F3 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
Db 8 NF 9

RESULT 72
PSBL SYNNU STANDARD; PRT; 17 AA.
AC P12241;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem II reaction center L protein (PSII 5 kDa protein)
DE (Fragment).
GN PSBL.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
SEQUENCE.
RP Ikeuchi M., Koike H., Inoue Y.;
RA "Identification of psbi and psbl gene products in cyanobacterial
RT photosystem II reaction center preparation.";
RL FEBS Lett. 251:155-160 (1989).
CC -1- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
CC B559.
CC -1- SIMILARITY: BELONGS TO THE PSBL FAMILY.
DR PIR; S05033; S05033.
DR InterPro; IPR003372; PSII_PsBL.
DR Pfam; PF02419; Psbl; 1.

```

KW Photosynthesis; Photosystem II.
 FT NON TER 17
 SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 12 LN 13

RESULT 73
 A2M OCTVU STANDARD; PRT; 18 AA.
 AC P30800;
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alpha-2-macroglobulin homolog (Alpha-2-M) (Fragment).
 OS Octopus vulgaris (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=66645;
 RN [1]
 RP SEQUENCE

RX MEDLINE=92344633; PubMed=1379044;
 RA Theegersen I.B., Salvesen G., Brucato F.H., Pizzo S.V., Enghild J.J.;
 RT "Purification and characterization of an alpha-macroglobulin
 proteinase inhibitor from the mollusc Octopus vulgaris";
 RL Biochem. J. 285:521-527(1992).
 CC -!- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A
 CC UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,
 CC CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES
 CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT
 CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH
 CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST
 CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR
 CC WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE
 CC BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE
 CC COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
 DR PIR: S23971; S23971.
 DR GO: GO:0016975; F:alpha-2 macroglobulin; NAS.
 DR InterPro: IPR001599; MacroglublnA2.
 DR Pfam: PF00207; A2M; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 KW Serine protease inhibitor; Glycoprotein; Plasma; Bait region;
 KW Thioester bond.
 FT NON TER 1 1
 FT CROSSLNK 5 8
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 2011 MW; D8D61C473D901C9D CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 12 NF 13

RESULT 74
 AHD2 TETPY STANDARD; PRT; 18 AA.
 ID P35430;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE 20-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) (20-alpha-HSD
 (Fragment)).
 DE Tetrahymena pyriformis.
 OS Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
 OC Tetrahymenina; Tetrahymena.
 OX NCBI_TaxID=5908;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=W;
 RX MEDLINE=94107273; PubMed=8280099;
 RA Inazu A., Sato K., Nakayama Y., Hara A., Nozawa Y.;
 RT "Purification and characterization of a novel dimeric 20 alpha-
 RT hydroxysteroid dehydrogenase from Tetrahymena pyriformis";
 RL Biochem. J. 297:195-200(1994).
 CC -!- FUNCTION: SPECIFIC FOR THE OXIDATION OF THE 20-ALPHA HYDROXY
 CC GROUP OF 17-ALPHA-HYDROXYPROGESTERONE AND 17-ALPHA-
 CC HYDROXYPREGNENOLONE.
 CC -!- CATALYTIC ACTIVITY: 17-alpha,20-alpha-dihydroxypregn-4-en-3-one +
 CC NAD(P)(+) = 17-alpha-hydroxyprogesterone + NAD(P)H.
 CC -!- SUBUNIT: Homodimer.
 DR PIR: S40502; S40502.
 KW Oxidoreductase; NADP.
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 1861 MW; 16DF6B287E3B0A0D CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 7 LN 8

RESULT 75
 ALL2 CYDPO STANDARD; PRT; 18 AA.
 ID P82153;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiaastatin 2.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricodea; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 18 18
 SQ SEQUENCE 18 AA; 2169 MW; 8E66679C0CDF175C CRC64;
 Query Match 66.7%; Score 2; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 15 NF 16

Search completed: November 25, 2003, 19:28:28
 Job time : 2.13538 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 5.63372 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3

Sequence: 1 LNF 3

Scoring table: OLIGO
Gapop 60.0 ; Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: SPTREMBL 23.*

2: sp_archaea.*

3: sp_bacteria.*

4: sp_fungi.*

5: sp_human.*

6: sp_invertebrate.*

7: sp_mammal.*

8: sp_mbc.*

9: sp_organelle.*

10: sp_phage.*

11: sp_plant.*

12: sp_rhodent.*

13: sp_virus.*

14: sp_vertebrate.*

15: sp_unclassified.*

16: sp_rvirus.*

17: sp_bacteria.*

18: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3	100.0	11	8 Q95E14	Q95E14 dendrochilu
2	3	100.0	12	8 Q95EJ8	Q95EJ8 dendrochilu
3	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
4	3	100.0	12	8 Q95EJ5	Q95EJ5 dendrochilu
5	3	100.0	12	8 Q95E10	Q95E10 dendrochilu
6	3	100.0	12	8 Q95E10	Q95E10 dendrochilu
7	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
8	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
9	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
10	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
11	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
12	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
13	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
14	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
15	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
16	3	100.0	12	8 Q95E16	Q95E16 dendrochilu

17	3	100.0	12	8 Q95E12	Q95E12 dendrochilu
18	3	100.0	12	8 Q95E18	Q95E18 dendrochilu
19	3	100.0	12	8 Q95E18	Q95E18 dendrochilu
20	3	100.0	15	4 Q16297	Q16297 homo sapien
21	3	100.0	15	6 Q9TRA6	Q9TRA6 bos taurus
22	3	100.0	17	6 Q9TR96	Q9TR96 ovis aries
23	3	100.0	18	2 Q56610	Q56610 vibrio chol
24	3	100.0	18	8 Q9ZYW4	Q9ZYW4 habrobraccon
25	3	100.0	18	9 Q9ZX80	Q9ZX80 lactococcus
26	3	100.0	19	8 Q9ZYW3	Q9ZYW3 gnaptodon
27	3	100.0	19	10 Q9S816	Q9S816 gryza sativ
28	3	100.0	20	2 Q9R4D9	Q9R4D9 escherichia
29	3	100.0	20	8 Q9ZY72	Q9ZY72 sathon sp.
30	3	100.0	20	12 Q84858	Q84858 unidentified
31	3	100.0	20	13 Q9PS15	Q9PS15 oncornynchu
32	2	66.7	7	8 Q98866	Q98866 spinacia ol
33	2	66.7	8	2 Q93SR0	Q93SR0 staphylococ
34	2	66.7	8	2 P77556	P77556 escherichia
35	2	66.7	8	2 Q9R5R0	Q9R5R0 shigella dy
36	2	66.7	8	3 P87225	P87225 saccharomyc
37	2	66.7	8	4 Q15889	Q15889 homo sapien
38	2	66.7	8	6 Q8WNS1	Q8WNS1 bos taurus
39	2	66.7	8	8 Q8WGC7	Q8WGC7 petrolisthe
40	2	66.7	8	10 Q40659	Q40659 gryza sativ
41	2	66.7	8	11 Q9QVFE4	Q9QVFE4 rattus sp.
42	2	66.7	9	2 Q57328	Q57328 aeromonas s
43	2	66.7	9	2 Q9RSR1	Q9RSR1 shigella dy
44	2	66.7	9	2 Q44377	Q44377 aeromonas t
45	2	66.7	9	2 Q44468	Q44468 aeromonas v
46	2	66.7	9	2 Q43928	Q43928 aeromonas p
47	2	66.7	9	2 Q44001	Q44001 aeromonas e
48	2	66.7	9	4 Q14715	Q14715 homo sapien
49	2	66.7	9	4 Q9UCN5	Q9UCN5 homo sapien
50	2	66.7	9	5 Q96417	Q96417 drosophila
51	2	66.7	9	6 Q9TRSO	Q9TRSO oryctolagus
52	2	66.7	9	8 Q31653	Q31653 anser caeru
53	2	66.7	9	12 P90359	P90359 barley wild
54	2	66.7	9	12 Q84333	Q84333 simian viru
55	2	66.7	10	2 Q9RSN4	Q9RSN4 clostridium
56	2	66.7	10	2 Q9RSN6	Q9RSN6 clostridium
57	2	66.7	10	2 Q9F5W1	Q9F5W1 vibrio chol
58	2	66.7	10	2 Q47091	Q47091 escherichia
59	2	66.7	10	2 Q8DCC0	Q8DCC0 escherichia
60	2	66.7	10	3 Q8UC02	Q8UC02 encephalito
61	2	66.7	10	4 Q9UJ48	Q9UJ48 homo sapien
62	2	66.7	10	5 Q8WPE7	Q8WPE7 skogsbergia
63	2	66.7	10	6 Q9TR49	Q9TR49 bos taurus
64	2	66.7	10	6 Q8SPN8	Q8SPN8 macaca mula
65	2	66.7	10	8 Q8WB87	Q8WB87 chaetophoru
66	2	66.7	10	8 Q8W8Q2	Q8W8Q2 anolis punc
67	2	66.7	10	8 Q8WD18	Q8WD18 anolis tran
68	2	66.7	10	8 Q8W8Q3	Q8W8Q3 anolis nite
69	2	66.7	10	8 Q8W8Q4	Q8W8Q4 anolis punc
70	2	66.7	10	11 Q9QVK8	Q9QVK8 mus sp. mep
71	2	66.7	10	13 Q73588	Q73588 gallus gall
72	2	66.7	10	13 P82080	P82080 limnodynast
73	2	66.7	11	2 Q9A1Z7	Q9A1Z7 carsonella
74	2	66.7	11	2 Q9R4B1	Q9R4B1 streptococc
75	2	66.7	11	2 Q47604	Q47604 escherichia
76	2	66.7	11	2 Q47345	Q47345 escherichia
77	2	66.7	11	2 Q9A1Z8	Q9A1Z8 carsonella
78	2	66.7	11	2 Q47059	Q47059 escherichia
79	2	66.7	11	4 Q9UCF2	Q9UCF2 homo sapien
80	2	66.7	11	5 Q23876	Q23876 dictyosteli
81	2	66.7	11	8 Q35374	Q35374 paramescium
82	2	66.7	11	8 Q9G682	Q9G682 chelosania
83	2	66.7	11	10 Q9T0L9	Q9T0L9 brassica ol
84	2	66.7	11	10 Q941R5	Q941R5 pinus radia
85	2	66.7	11	12 Q86866	Q86866 lymphocytic
86	2	66.7	11	12 Q86864	Q86864 lymphocytic
87	2	66.7	11	12 Q86868	Q86868 lymphocytic
88	2	66.7	11	15 Q83410	Q83410 mouse mamma
89	2	66.7	12	2 Q9X645	Q9X645 unidentified

90 Q9x638 unidentified
 91 Q9x628 unidentified
 92 Q9wv6 leclercia a
 93 Q9wv5 escherichia
 94 Q9x640 citrobacter
 95 Q9x643 klebsiella
 96 Q9x633 serratia ma
 97 Q9x631 pseudomonas
 98 Q9ntr7 homo sapien
 99 Q8my01 drosophila
 100 Q9twv4 lymanaea sta

KW Chloroplast.
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 4 LNF 6

ALIGNMENTS

RESULT 3

Q95E16 PRELIMINARY; PRT; 12 AA.
 AC Q95E16; 2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Psal (Fragment).
 OS Dendrochilum glumaceum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
 OX NCBI_TaxID=71597;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barkman T.J., Simpson B.B.;
 RT "Hybridization and parentage of Dendrochilum aciferum (Orchidaceae)
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA
 RT sequence data.";
 RL Syst. Bot. 0:0-0(2001).
 DR EMBL; AF389215; AAK82407.1; -.
 KW Chloroplast.
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 4

Q95EJ5 PRELIMINARY; PRT; 12 AA.
 AC Q95EJ5; 2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Psal (Fragment).
 OS Dendrochilum gibbsiae.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
 OX NCBI_TaxID=79421;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barkman T.J., Simpson B.B.;
 RT "Hybridization and parentage of Dendrochilum aciferum (Orchidaceae)
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA
 RT sequence data.";
 RL Syst. Bot. 0:0-0(2001).
 DR EMBL; AF389210; AAK82398.1; -.
 KW Chloroplast.
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

RESULT 1

Q95E14 PRELIMINARY; PRT; 11 AA.
 AC Q95E14; 2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Psal (Fragment).
 OS Dendrochilum arachnites.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
 OX NCBI_TaxID=79412;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barkman T.J., Simpson B.B.;
 RT "Hybridization and parentage of Dendrochilum aciferum (Orchidaceae)
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA
 RT sequence data.";
 RL Syst. Bot. 0:0-0(2001).
 DR EMBL; AF389216; AAK82409.1; -.
 KW Chloroplast.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1296 MW; 4ACTB27CA769C447 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 2

Q95EJ8 PRELIMINARY; PRT; 12 AA.
 AC Q95EJ8; 2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Psal (Fragment).
 OS Dendrochilum grandiflorum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
 OX NCBI_TaxID=79424;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barkman T.J., Simpson B.B.;
 RT "Hybridization and parentage of Dendrochilum aciferum (Orchidaceae)
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA
 RT sequence data.";
 RL Syst. Bot. 0:0-0(2001).
 DR EMBL; AF389208; AAK82395.1; -.

Query Match 100.0%; Score 3; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 5

Q95EL0 PRELIMINARY; PRT; 12 AA.
 AC Q95EL0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Psal (Fragment).
 OS Dendrochilum corrugatum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
 OX NCBI_TaxID=79415;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barkman T.J., Simpson B.B.;
 RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA
 RT sequence data."
 RL Syst. Bot. 0:0-0(2001).
 DR EMBL; AF389202; AAK82383.1; -.
 KW Chloroplast.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 6

Q95EK0 PRELIMINARY; PRT; 12 AA.
 AC Q95EK0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Psal (Fragment).
 OS Dendrochilum jociemensii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
 OX NCBI_TaxID=79427;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barkman T.J., Simpson B.B.;
 RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA
 RT sequence data."
 RL Syst. Bot. 0:0-0(2001).
 DR EMBL; AF389207; AAK82393.1; -.
 KW Chloroplast.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 7

Q95BL6 PRELIMINARY; PRT; 12 AA.
 AC Q95BL6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Psal (Fragment).
 OS Dendrochilum muluense.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
 OX NCBI_TaxID=79434;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barkman T.J., Simpson B.B.;
 RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA
 RT sequence data."
 RL Syst. Bot. 0:0-0(2001).
 DR EMBL; AF389199; AAK82377.1; -.
 KW Chloroplast.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 8

Q95EM2 PRELIMINARY; PRT; 12 AA.
 AC Q95EM2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Psal (Fragment).
 OS Dendrochilum haslamii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
 OX NCBI_TaxID=79425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barkman T.J., Simpson B.B.;
 RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA
 RT sequence data."
 RL Syst. Bot. 0:0-0(2001).
 DR EMBL; AF389196; AAK82371.1; -.
 KW Chloroplast.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

```

Db          |||
            4 LNF 6

RESULT 9
Q95EK8      PRELIMINARY;      PRT;      12 AA.
AC Q95EK8;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum pseudoscriptum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyminae; Dendrochilum.
OX NCBI_TaxID=150393;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389203; AAK82385.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match      100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      |||
            4 LNF 6

RESULT 10
Q95EL2      PRELIMINARY;      PRT;      12 AA.
AC Q95EL2;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum alatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyminae; Dendrochilum.
OX NCBI_TaxID=79410;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389201; AAK82381.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match      100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      |||
            4 LNF 6

RESULT 11
Q95EM0      PRELIMINARY;      PRT;      12 AA.
AC Q95EM0;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum stachyodes.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyminae; Dendrochilum.
OX NCBI_TaxID=79441;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389197; AAK82373.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match      100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      |||
            4 LNF 6

RESULT 12
Q95EJ3      PRELIMINARY;      PRT;      12 AA.
AC Q95EJ3;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum dewindtianum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyminae; Dendrochilum.
OX NCBI_TaxID=79419;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389211; AAK82400.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match      100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      |||
            4 LNF 6

RESULT 13
Q95EL8

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ID Q95EL8 PRELIMINARY; PRT; 12 AA.
AC Q95EL8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum dewildei.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79418;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389198; AAK82375.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 14
Q95EK6 PRELIMINARY; PRT; 12 AA.
ID Q95EK6;
AC Q95EK6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum pterogyne.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79438;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389204; AAK82387.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 15
Q95EK2 PRELIMINARY; PRT; 12 AA.
ID Q95EK2;
AC Q95EK2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum trusmadiense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79444;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389206; AAK82391.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 16
Q95EI1 PRELIMINARY; PRT; 12 AA.
ID Q95EI1;
AC Q95EI1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum tenopokense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79442;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389212; AAK82402.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1393 MW; 1F5AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 17
Q95EI2 PRELIMINARY; PRT; 12 AA.
ID Q95EI2;
AC Q95EI2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Psai (Fragment).

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OS Dendrochilum cupulatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79417;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389217; AAK82411.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

RESULT 18
Q95E18 PRELIMINARY; PRT; 12 AA.
AC Q95E18
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum exasperatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79420;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389214; AAK82405.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

RESULT 19
Q95EK4 PRELIMINARY; PRT; 12 AA.
AC Q95EK4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum alpinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79411;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389205; AAK82389.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

RESULT 20
Q16297 PRELIMINARY; PRT; 15 AA.
AC Q16297
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
DE Kell immunogen (Fragment).
GN KEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95152088; PubMed=7849312;
RX Lee S., Wu X., Reid M., Zelinski T., Redman C.;
RT "Molecular basis of the Kell (K1) phenotype.";
RL Blood 85:912-916(1995).
DR EMBL; S76770; AAB33389.1; -.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1882 MW; 7316158F0E98614F CRC64;

Query Match 100.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

RESULT 21
Q9TRA6 PRELIMINARY; PRT; 15 AA.
AC Q9TRA6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PA700 subunit F31-ATP-dependent 20 S proteasome activator
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=94342244; PubMed=8063704;

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RA DeMartino G.N., Moomaw C.R., Zagnitko O.P., Proske R.J., Chu-Ping M.,
 RA Afendis S.J., Swaffield J.C., Slaughter C.A.;
 RT "PA700, an ATP-dependent activator of the 20 S proteasome, is an
 RT ATPase containing multiple members of a nucleotide-binding protein
 RT family";
 RL J. Biol. Chem. 269:20878-20884(1994).
 FT NON TER 1 1
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1659 MW; D189812E9389B755 CRC64;
 Query Match 100.0%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 Db 6 LNF 8
 RESULT 22
 Q9TR96 PRELIMINARY; PRT; 17 AA.
 AC Q9TR96; 17 AA.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE MEGAPOIETIN=MEGAKARVOCYTE growth and platelet production regulator
 DE (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 CX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95062214; PubMed=7972018;
 RA Kuter D.J., Beeler D.L., Rosenberg R.D.;
 RT "The purification of megapoietin: a physiological regulator of
 RT megakaryocyte growth and platelet production.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11104-11108(1994).
 FT NON TER 1 1
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1975 MW; DA3A5E835A755C9D CRC64;
 Query Match 100.0%; Score 3; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 Db 8 LNF 10
 RESULT 23
 Q56610 PRELIMINARY; PRT; 18 AA.
 AC Q56610; 18 AA.
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Acca (Fragment).
 GN ACCA.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 CX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C6706;
 RX MEDLINE=97074686; PubMed=8917113;
 RA Franco A., Peir-En Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
 RA Morris J.G.;
 RT "Cloning and characterization of dnaE, encoding the catalytic subunit

RT of replicative DNA polymerase III, from Vibrio cholerae strain
 RT C6706";
 RL Gene 175:281-283(1996).
 DR EMBL; U30472; AAC44579.1; --
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 2153 MW; 18EBCDAD212842EF CRC64;
 Query Match 100.0%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 Db 3 LNF 5
 RESULT 24
 Q9ZYW4 PRELIMINARY; PRT; 18 AA.
 AC Q9ZYW4; 18 AA.
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE Cytochrome oxidase II (Fragment).
 OS Habrobracon hebetor.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;
 OC Braconidae; Braconinae; Habrobracon.
 CX NCBI_TaxID=69819;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99152621; PubMed=10028295;
 RA Downton M., Austin A.D.;
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
 RT the hymenoptera.";
 RL Mol. Biol. Evol. 16:298-309(1999).
 DR EMBL; AF034597; AAC79745.1; --
 KW Mitochondrion.
 FT NON TER 1 1
 SQ SEQUENCE 18 AA; 2282 MW; 79721C93C8D5F1D4 CRC64;
 Query Match 100.0%; Score 3; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 Db 8 LNF 10
 RESULT 25
 Q9ZX80 PRELIMINARY; PRT; 18 AA.
 AC Q9ZX80; 18 AA.
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Phage antigenic determinant (Fragment).
 OS Lactococcus lactis phage phi 197.
 OC Viruses.
 CX NCBI_TaxID=12427;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92384563; PubMed=1514794;
 RA Schouler C., Bouet C., Ritzenhaler P., Drouet X., Mata M.;
 RT "Characterization of Lactococcus lactis phage antigens.";
 RL Appl. Environ. Microbiol. 58:2479-2484(1992).
 DR EMBL; S44895; AAB49317.2; --
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 2155 MW; 85601530E6E9DFDA CRC64;
 Query Match 100.0%; Score 3; DB 9; Length 18;

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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
5 LNF 7

RESULT 26
Q92YW3 PRELIMINARY; PRT; 19 AA.
ID Q92YW3
AC Q92YW3 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Cytochrome oxidase II (Fragment).
OS Gnemptonodon pumilio.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Braconidae; Gnemptonotinae; Gnemptonotinae; Gnemptonotinae;
OC NCBI_TaxID=64833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Downton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera.";
RL Mol. Biol. Evol. 16:298-309 (1999).
DR EMBL; AF034598; AAC79746.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 19 AA; 2290 MW; 77F1EE77E787BCA CRC64;

Query Match 100.0%; Score 3; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
17 LNF 19

RESULT 27
Q9S816 PRELIMINARY; PRT; 19 AA.
ID Q9S816
AC Q9S816 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 40 kDa PI 8.5 ABCG11 acid-induced protein (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95175599; PubMed=7870812;
RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;
RT "Molecular and physiological responses to abscisic acid and salts in
RT roots of salt-sensitive and salt-tolerant indica rice varieties.";
RL Plant Physiol. 107:177-186 (1995).
DR Gramene; Q9S816; -.
SQ SEQUENCE 19 AA; 2039 MW; FE1F0A6872F6F620 CRC64;

Query Match 100.0%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
1 LNF 3
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RESULT 28
Q9R4D9 PRELIMINARY; PRT; 20 AA.
ID Q9R4D9
AC Q9R4D9 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Fimbrial protein CS20 (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
RX MEDLINE=96294774; PubMed=8698489;
RA Valvatne H., Sommerfelt H., Gaastera W., Bhan M.K., Grewal H.M.;
RT "Identification and characterization of CS20, a new putative
RT colonization factor of enterotoxigenic Escherichia coli.";
RL Infect. Immun. 64:2635-2642 (1996).
SQ SEQUENCE 20 AA; 1895 MW; F64DFAE56C8C32CC CRC64;

Query Match 100.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
12 LNF 14

RESULT 29
Q9ZY72 PRELIMINARY; PRT; 20 AA.
ID Q9ZY72
AC Q9ZY72 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Cytochrome oxidase II (Fragment).
OS Sathon sp.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Braconidae; Microgastrinae; Sathon.
OX NCBI_TaxID=81091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Downton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera.";
RL Mol. Biol. Evol. 16:298-309 (1999).
DR EMBL; AF082929; AAD17789.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 20 AA; 2436 MW; DAE6F367B8E4A6BC CRC64;

Query Match 100.0%; Score 3; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
17 LNF 19

RESULT 30
Q84858 PRELIMINARY; PRT; 20 AA.
ID Q84858
AC Q84858 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 2.1 kDa protein (Fragment).
OS Unidentified human poliovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
CX NCBI_TaxID=40278;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87169734; PubMed=3031313;
RA Kuge S., Saito I., Nomoto A.;
RT "Primary structure of poliovirus defective-interfering particle
RT genomes and possible generation mechanisms of the particles.";
RL J. Mol. Biol. 192:473-487(1986).
RL EMBL; M30215; AAA66824.1; -.
DR EMBL; M30215; AAA66824.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2105 MW; CED4BCA72BF73D77 CRC64;

Query Match 100.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 1 LNF 3

RESULT 31
Q9PSI5 PRELIMINARY; PRT; 20 AA.
AC Q9PSI5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Creatine kinase (EC 2.7.3.2) (Fragment).
OS Oncorhynchus kisutch (Coho salmon)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
CX NCBI_TaxID=8019;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93080727; PubMed=1449598;
RA White K.C., Babbitt P.C., Buechter D.D., Kenyon G.L.;
RT "The principal islet of the Coho salmon (Oncorhynchus kisutch) contains
RT the BB isoenzyme of creatine kinase.";
RL J. Protein Chem. 11:489-494(1992).
SQ SEQUENCE 20 AA; 2425 MW; BFBCT71D6D2A86E11 CRC64;

Query Match 100.0%; Score 3; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 11 LNF 13

RESULT 32
Q98866 PRELIMINARY; PRT; 7 AA.
AC Q98866;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Cytochrome b/f subunit IV (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
CX NCBI_TaxID=3562;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120353; PubMed=3003688;
RA Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
RT protein s11 and RNA polymerase alpha-subunit.";
RL Nucleic Acids Res. 14:1029-1044(1986).
DR EMBL; X03496; CAA27215.1; -.
KW Chloroplast.
FT NON_TER 1
FT NON_TER 6
SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 6 LN 7

RESULT 33
Q93SR0 PRELIMINARY; PRT; 8 AA.
AC Q93SR0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-lactamase repressor Blai (Fragment).
GN BLAI.
OS Staphylococcus epidermidis.
OG Plasmid pST6.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6;
RA Sidhu M.S., Heir E., Sorum H., Holck A.L.;
RT "Genetic linkage between quaternary ammonium compound and beta-lactam
RT resistance in Staphylococci isolated from food.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY028779; AAK38453.1; -.
KW Plasmid.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 930 MW; 4E3325B05AA44720 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 2 LN 3

RESULT 34
P77556 PRELIMINARY; PRT; 8 AA.
AC P77556;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE TRAY (Fragment).
GN TRAY.
OS Escherichia coli.
OG Plasmid IncFII R1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ECOR11;
MEDLINE=96400908; PubMed=8807284;

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RA Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;
RT "Mosaic structure of plasmids from natural populations of Escherichia
RL coli.";
RL Genetics 143:1091-1100(1996).
DR EMBL; U50661; AAC44245.1; -
DR EMBL; U50650; AAC44234.1; -
DR EMBL; U50651; AAC44235.1; -
DR EMBL; U50652; AAC44236.1; -
DR EMBL; U50653; AAC44237.1; -
DR EMBL; U50654; AAC44238.1; -
DR EMBL; U50655; AAC44239.1; -
DR EMBL; U50656; AAC44240.1; -
DR EMBL; U50657; AAC44241.1; -
DR EMBL; U50658; AAC44242.1; -
DR EMBL; U50659; AAC44243.1; -
DR EMBL; U50660; AAC44244.1; -
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 8 AA; 834 MW; D335A5B0544735A1 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
   ||
Db 3 LN 4

RESULT 35
Q9RSR0 PRELIMINARY; PRT; 8 AA.
ID Q9RSR0
AC Q9RSR0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 11,500 DA product of ORFA (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
RN [1]
RP SEQUENCE.
RX MEDLINE=92085268; PubMed=1660923;
RA Polard P., Prete M.F., Chandler M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an AUU codon
RL in gene expression of bacterial insertion sequence IS911.";
FT J. Mol. Biol. 222:465-477(1991).
FT NON_TER 8
SQ SEQUENCE 8 AA; 935 MW; F4C5B9C45AE33336 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
   ||
Db 5 NF 6

RESULT 36
P87225 PRELIMINARY; PRT; 8 AA.
ID P87225
AC P87225
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GIN11 protein (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]

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RP SEQUENCE FROM N.A.
RA Wedler H., Wedler E., Scharfe M., Wambutt R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z73169; CAA97518.2; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1019 MW; 4E21A9C449D5B73B CRC64;

Query Match 66.7%; Score 2; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
   ||
Db 5 NF 6

RESULT 37
Q15889 PRELIMINARY; PRT; 8 AA.
ID Q15889
AC Q15889
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP15H8B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32070; AAA73879.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 865 MW; 0474472325A761E7 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
   ||
Db 6 LN 7

RESULT 38
Q8WNS1 PRELIMINARY; PRT; 8 AA.
ID Q8WNS1
AC Q8WNS1
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE X-linked zinc finger protein (Fragment).
GN ZFX.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Poloumienko A., Blecher S.;
RT "Comparison between intron-exon structures in ZFX and ZFY genes.";

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RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF045782; AAL58190.1; -.
FT NON_TER 1 8

SQ SEQUENCE 8 AA; 904 MW; DF1DC2C4472AAB1A CRC64;
Query Match 66.7%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 4 LN 5

RESULT 39

Q8WGC7 Q8WGC7 PRELIMINARY; PRT; 8 AA.
AC Q8WGC7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
OS Petrolisthes armatus (green porcelain crab).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Plecocyemata; Anomura;
OC Galatheoidea; Porcellanidae; Petrolisthes.
OX NCBI_TaxID=84662;
RN [1]
RP SEQUENCE FROM N.A.
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA Cunningham C.W.;
RT "Mitochondrial gene rearrangements support a hypothesis of parallel
evolution to the crab-like form."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF436049; AAL31623.1; -.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1010 MW; FE20504B54472696 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 3 LN 4

RESULT 40

Q40659 Q40659 PRELIMINARY; PRT; 8 AA.
AC Q40659;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alpha-amylase (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078641; PubMed=2258052;
RA Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA Rodriguez R.L.;
RT "Expression and secretion of rice alpha-amylase by saccharomyces
cerevisiae."
RL Gene 94:209-216(1990).
DR EMBL: M62916; AAA33892.1; -.
DR Gramene; Q40659; -.

FT NON_TER 8
SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 66.7%; Score 2; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 4 LN 5

RESULT 41

Q9QVF4 Q9QVF4 PRELIMINARY; PRT; 8 AA.
AC Q9QVF4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TRANSFERRIN-PEPTIDE 60 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92165927; PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-
metastasizing tumor cells: identification as transferrin."
RL J. Cell. Biochem. 47:261-271(1991).
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 778 MW; 9D744735B69DDAAD CRC64;

Query Match 66.7%; Score 2; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 6 LN 7

RESULT 42

Q57328 Q57328 PRELIMINARY; PRT; 9 AA.
AC Q57328;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein (Fragment).
GN EXEF.
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=132;
RX MEDLINE=97089747; PubMed=8935655;
RA Karlyshev A.V., Macintyre S.;
RT "Study of the intergenic exef-exeG region and its application as a
simple preliminary test for Aeromonas spp."
RL FEMS Microbiol. Lett. 137:37-44(1996).
DR EMBL: X89466; CAA61647.1; -.
DR EMBL: X89465; CAA61645.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1077 MW; 79E852C69444472B CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LN 2
      ||
Db      3 LN 4

RESULT 43
Q9RSR1 ID Q9RSR1 PRELIMINARY; PRT; 9 AA.
AC Q9RSR1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative transposase (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
RN [1]
RP SEQUENCE.
RX MEDLINE=92085268; PubMed=1660923;
RA Pollard P., Preere M.F., Chandler M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an AUU codon
RL in gene expression of bacterial insertion sequence IS911.";
RL J. Mol. Biol. 222:465-477(1991).
FT NON TER 9
SQ SEQUENCE 9 AA; 1063 MW; 5EE4C5B9C45AE333 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NF 3
      ||
Db      5 NF 6

RESULT 44
Q44377 ID Q44377 PRELIMINARY; PRT; 9 AA.
AC Q44377;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ExeF' protein (Fragment).
GN EXEFP.
OS Aeromonas trota.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29489;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 49659;
RX MEDLINE=97089747; PubMed=8935655;
RA Karlyshev A.V., Macintyre S.;
RT "Study of the intergenic exeF-exeG region and its application as a
RL simple preliminary test for Aeromonas spp.";
RL FEMS Microbiol. Lett. 137:37-44(1996).
DR EMBL; X89468; CAA61651.1; -.
FT NON TER 1
SQ SEQUENCE 9 AA; 1059 MW; 785852C69444472B CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
      ||
Db      3 LN 4

RESULT 45
Q44468 ID Q44468 PRELIMINARY; PRT; 9 AA.
AC Q44468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ExeF' protein (Fragment).
GN EXEFP.
OS Aeromonas veronii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=654;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CDC 1306-83;
RX MEDLINE=97089747; PubMed=8935655;
RA Karlyshev A.V., Macintyre S.;
RT "Study of the intergenic exeF-exeG region and its application as a
RL simple preliminary test for Aeromonas spp.";
RL FEMS Microbiol. Lett. 137:37-44(1996).
DR EMBL; X89457; CAA61629.1; -.
FT NON TER 1
SQ SEQUENCE 9 AA; 1059 MW; 785852C69444472B CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
      ||
Db      3 LN 4

RESULT 46
Q43928 ID Q43928 PRELIMINARY; PRT; 9 AA.
AC Q43928; Q43918; Q43920; Q43921;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DNA for EXEF-EXEG intergenic region (Fragment).
GN EXEFP.
OS Aeromonas punctata (Aeromonas caviae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=648;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VARIOUS STRAINS;
RX MEDLINE=97089747; PubMed=8935655;
RA Karlyshev A.V., Macintyre S.;
RT "Study of the intergenic exeF-exeG region and its application as a
RL simple preliminary test for Aeromonas spp.";
RL FEMS Microbiol. Lett. 137:37-44(1996).
DR EMBL; X89464; CAA61643.1; -.
DR EMBL; X89462; CAA61639.1; -.
DR EMBL; X89460; CAA61635.1; -.
DR EMBL; X89463; CAA61641.1; -.
FT NON TER 1
SQ SEQUENCE 9 AA; 1059 MW; 785852C69444472B CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
      ||
Db      3 LN 4

RESULT 47
Q44001 ID Q44001 PRELIMINARY; PRT; 9 AA.
AC Q44001;

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DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Exer' protein (Fragment).
 GN EXER'.
 OS Aeromonas eucrotophila.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; Aeromonas.
 OX NCBI_TaxID=649;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 9179-79;
 RA MEDLINE=97089747; PubMed=8935655;
 RA Karlyshev A.V., MacIntyre S.;
 RT "Study of the intergenic exef-exeG region and its application as a
 RT simple preliminary test for Aeromonas spp.";
 RL FEMS Microbiol. Lett. 137:37-44(1996).
 DR EMBL; X89461; CAA61637.1; -.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1059 MW; 785852C6944472B CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 3 LN 4

RESULT 48
 Q14715
 ID Q14715 PRELIMINARY; PRT; 9 AA.
 AC Q14715;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Keratin 14 (Fragment).
 GN KRT14.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Coulombe P., Hutton M., Letai A., Hebert A., Paller A., Fuchs E.;
 RT "Point mutations in human keratin 14 genes of epidermolysis bullosa
 RT simplex patients: Genetic and functional analyses.";
 RL Cell 66:1301-1311(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95072587; PubMed=7526926;
 RA Yamaniishi K., Matsuki M., Konishi K., Yasuno H.;
 RT "A novel mutation of Leri22 to phe at a highly conserved hydrophobic
 RT residue in the helix initiation motif of keratin 14 in epidermolysis
 RT bullosa simplex.";
 RL Hum. Mol. Genet. 3:1171-1172(1994).
 DR EMBL; D28807; BAA05967.1; -.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1138 MW; BE300AA449C456D6 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 4 NF 5

RESULT 49
 Q9UCN5

ID Q9UCN5 PRELIMINARY; PRT; 9 AA.
 AC Q9UCN5;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE Cell-surface heparin/HEPARANSULFATE-binding protein peptide 2
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92291065; PubMed=1601862;
 RA Raboudi N., Julian J., Rohde L.H., Carson D.D.;
 RT "Identification of cell-surface heparin/heparan sulfate-binding
 RT proteins of a human uterine epithelial cell line (RL95).";
 RL J. Biol. Chem. 267:11930-11939(1992).
 SQ SEQUENCE 9 AA; 1008 MW; CB56D0544732C732 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 5 LN 6

RESULT 50
 Q96417
 ID Q96417 PRELIMINARY; PRT; 9 AA.
 AC Q96417;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE SXL E1 form (Fragment).
 GN SXL.
 OS Drosophila virilis (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337843; PubMed=9671597;
 RA Erickson J.W., Cline T.W.;
 RT "Key aspects of the primary sex determination mechanism are conserved
 RT across the genus Drosophila.";
 RL Development 125:3259-3268(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Bell M., Cline T.W.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF046045; AAC97605.1; -.
 DR FlyBase; FBgn0016470; Dvir\Sxl.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1089 MW; 9A8BD1AA9C449CA CRC64;

Query Match 66.7%; Score 2; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 4 NF 5

RESULT 51
 Q9TRSO
 ID Q9TRSO PRELIMINARY; PRT; 9 AA.
 AC Q9TRSO;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calyculin-associated protein, CAP50=CA2+/phospholipid-binding protein
DE L-7 fragment (Fragment)
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN SEQUENCE.
RP MEDLINE=92250478; PubMed=1533622;
RA Tokumitsu H., Mitutani A., Minami H., Kobayashi R., Hidaka H.;
RT "A calyculin-associated protein is a newly identified member of the
RT Ca2+/phospholipid-binding proteins, annexin family.";
RL J. Biol. Chem. 267:8919-8924(1992).
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1010 MW; 64E419C44865B72B CRC64;

Query Match 66.7%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
Db 6 NF 7

RESULT 52
Q31653 PRELIMINARY; PRT; 9 AA.
ID Q31653
AC Q31653;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Cytochrome b (Fragment).
GN CYTOCHROME B.
OS Anser caerulescens (Snow goose).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8849;
RN SEQUENCE FROM N.A.
RP MEDLINE=94141942; PubMed=8308909;
RA Quinn T.W., Wilson A.C.;
RT "Sequence evolution in and around the mitochondrial control region in
RT birds";
RL J. Mol. Evol. 37:417-425(1993).
DR EMBL; X77190; CAA54411.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 9 AA; 1095 MW; 4751472693344B17 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 7 LN 8

RESULT 53
P90359 PRELIMINARY; PRT; 9 AA.
ID P90359
AC P90359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Polyprotein (Fragment).
OS Barley mild mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Bymovirus.
OX NCBI_TaxID=12466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UK-M(R);
RA Peerboom E., Jacobi V., Cartwright E.J., Adams M.J., Steinbiss H.H.,
RA Antoniw J.F.;
RT "A large duplication in the 3'-untranslated region of a sub-population
RT of RNA2 of the UK-M isolate of barley mild mosaic bymovirus.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X96970; CAA63658.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 9 AA; 1177 MW; C40404473401F1B6 CRC64;

Query Match 66.7%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 6 LN 7

RESULT 54
Q84333 PRELIMINARY; PRT; 9 AA.
ID Q84333
AC Q84333;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Defective variant in 1449) with monkey alu-type insert
DE (Fragment).
OS Simian virus 40 (SV40).
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10633;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81054804; PubMed=6254029;
RA Dhruva B.R., Shenk T., Subramanian K.N.;
RT "Integration in vivo into Simian virus 40 DNA of a sequence that
RT resembles a certain family of genomic interspersed repeated
RT sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4514-4518(1980).
DR EMBL; K01001; AAA47875.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1133 MW; 802204044732C33A CRC64;

Query Match 66.7%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 5 LN 6

RESULT 55
Q9R5N4 PRELIMINARY; PRT; 10 AA.
ID Q9R5N4
AC Q9R5N4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neurotoxin type A HN+ 35 kDa subunit (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., Dasgupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or

RT without hemagglutinating activity: do they share common amino acid
 RT sequences and genes?;
 RL J. Protein Chem. 10:415-425(1991).
 FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1143 MW; CF3CB4A44735B456 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 6 LN 7

RESULT 56

ID Q9RSN6 PRELIMINARY; PRT; 10 AA.
 AC Q9RSN6;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Neurotoxin type B HN+ 35 kDa SUBUNIT-BAND 3A (Fragment).
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=92143938; PubMed=1781887;
 RA Somers E., DasGupta B.R.;
 RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
 RT without hemagglutinating activity: do they share common amino acid
 RT sequences and genes?";
 RL J. Protein Chem. 10:415-425(1991).
 FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1169 MW; 00CF7E3AA4472054 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 5 LN 6

RESULT 57

ID Q9F5W1 PRELIMINARY; PRT; 10 AA.
 AC Q9F5W1;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE Cep (Fragment).
 GN CEP.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9803;

RA Rui Y.Y., Kan B., Gao S.Y., Liu Y.Q., Qi G.M.;
 RT "RS region of Vibrio cholerae O139 nct-CTXphi, includes rstr (Rstr),
 RT rsta (Rsta) and rstB (rstB) genes."; ;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF302794; AAG27711.1;
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1181 MW; 9DC61A34433735A5 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 9 LN 10

RESULT 58

ID Q47091 PRELIMINARY; PRT; 10 AA.
 AC Q47091;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Colicin E1 (Fragment).
 OS Escherichia coli.
 OG Plasmid ColE1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86094231; PubMed=3936034;
 RA Waleh N.S., Johnson P.H.;
 RT "Structural and functional organization of the colicin E1 operon."; ;
 RL Proc. Natl. Acad. Sci. U.S.A. 82:8389-8393(1985).
 DR EMBL; M12543; AAA23065.1;
 KW Plasmid.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1085 MW; 88F00B32CB144041 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 1 LN 2

RESULT 59

ID Q8GDC0 PRELIMINARY; PRT; 10 AA.
 AC Q8GDC0;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Sulfonamide resistance protein (Fragment).
 GN SULI.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Neonakis I.K., Scoulica E.V., Tselentis Y.J.;
 RT "First detection of blaVIM-1 in an Escherichia coli clinical
 RT isolate."; ;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY152821; AAN77716.1;
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1106 MW; 91F57E205879D2D1 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 8 LN 9

RESULT 60
Q8J0C2 PRELIMINARY; PRT; 10 AA.
AC Q8J0C2; 2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hsp70 (Fragment).
OS Encephalitozoon hellem.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=27973;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PV6/95, and PV7/95;
RA Haro M., del Aguila C., Fenoy S., Henriques-Gil N.;
RT "Genotype variability in the microsporidian Encephalitozoon hellem.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY171238; AAN73415.1; -;
DR EMBL; AY171239; AAN73417.1; -;
FT NON TER 10
SQ SEQUENCE 10 AA; 1100 MW; 107C0D472DD44DD4 CRC64;
Query Match 66.7%; Score 2; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LN 2
Db 7 LN 8

RESULT 61
Q9UJ48 PRELIMINARY; PRT; 10 AA.
AC Q9UJ48;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Latrophilin-2 (Fragment).
GN LPHH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99153747; PubMed=10030676;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Isolation and characterisation of a human homologue of the
latrophilin gene from a region of lp31.1 implicated in breast
cancer.";
RL Oncogene 17:3513-3519 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20225451; PubMed=10760572;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Genomic structure and expression profile of LPHH1, a 7TM gene
variably expressed in breast cancer cell lines.";
RL Biochim. Biophys. Acta 1491:75-92 (2000).
DR EMBL; AJ244514; CAB60206.1; -;
FT NON TER 1
SQ SEQUENCE 10 AA; 1112 MW; 06CC4C2720544724 CRC64;
Query Match 66.7%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LN 2
Db 4 LN 5

RESULT 62
Q8WPE7 PRELIMINARY; PRT; 10 AA.
AC Q8WPE7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Opsin (Fragment).
OS Skogsbergia leneri.
OC Sukaryota; Metazoa; Arthropoda; Crustacea; Ostracoda; Myodocopa;
OC Myodocopida; Cypridinoida; Cypridinidae; Skogsbergia.
OX NCBI_TaxID=176979;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Entire organism;
RA Oakley T.H., Huber D.R.;
RT "Eye-specific expression of multiple opsin loci in ostracod
crustaceans.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF353372; AAL37547.1; -;
FT NON TER 1
SQ SEQUENCE 10 AA; 1035 MW; 1F4B3117672DDDD4 CRC64;
Query Match 66.7%; Score 2; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LN 2
Db 2 LN 3

RESULT 63
Q9TR49 PRELIMINARY; PRT; 10 AA.
AC Q9TR49;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Amphoterin homologue (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96029671; PubMed=7592757;
RA Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,
RA Nagashima M., Lundh E.R., Vijay S., Nitecki D.;
RT "The receptor for advanced glycation end products (RAGE) is a cellular
binding site for amphoterin. Mediation of neurite outgrowth and co-
expression of rage and amphoterin in the developing nervous system.";
RL J. Biol. Chem. 270:25752-25761 (1995).
SQ SEQUENCE 10 AA; 1106 MW; 88BED1C452DAEDDA CRC64;
Query Match 66.7%; Score 2; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NF 3
Db 7 NF 8

RESULT 64
Q8SPN8 PRELIMINARY; PRT; 10 AA.
AC Q8SPN8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Solute carrier family 6 member 4 (Fragment).

GN SLC6A4.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 ON NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nergren R.B. Jr., Zink M.A., Jia Y., Ojeda S.R., Spindel E.R.;
 RT "Construction of a targeted rhesus macaque microarray."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY083583; AAM11998.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1043 MW; 3B07C4473412CAA8 CRC64;

Query Match 66.7%; Score 2; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 7 LN 8

RESULT 65
 Q8WB7
 ID Q8WB7 PRELIMINARY; PRT; 10 AA.
 AC Q8WB7
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cytochrome oxidase subunit I (Fragment).
 GN COI.
 OS Chaitophorus leucomelas.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 OC Aphidoidea; Drepanosiphidae; Chaitophorus.
 ON NCBI_TaxID=136351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shingleton A.W., Stern D.L.;
 RT "Molecular phylogenetic evidence for multiple origins of ant mutualism
 within the aphid genus Chaitophorus."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF444288; AAL38565.1; -.
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;

Query Match 66.7%; Score 2; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
 ||
 Db 9 NF 10

RESULT 66
 Q8WBQ2
 ID Q8WBQ2 PRELIMINARY; PRT; 10 AA.
 AC Q8WBQ2
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cytochrome oxidase subunit 1 (Fragment).
 GN COI.
 OS Anolis punctatus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 ON NCBI_TaxID=174263;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Glor R.E., Vitt L.J., Larson A.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF337775; AAL72033.1; -.
 DR EMBL; AF337776; AAL72035.1; -.
 DR EMBL; AF337777; AAL72037.1; -.
 KW Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 3 LN 4

RESULT 67
 Q8WDI8
 ID Q8WDI8 PRELIMINARY; PRT; 10 AA.
 AC Q8WDI8
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cytochrome oxidase subunit 1 (Fragment).
 GN COI.
 OS Anolis transversalis.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 ON NCBI_TaxID=174264;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Glor R.E., Vitt L.J., Larson A.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF337769; AAL72021.1; -.
 KW Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 ||
 Db 3 LN 4

RESULT 68
 Q8W8Q3
 ID Q8W8Q3 PRELIMINARY; PRT; 10 AA.
 AC Q8W8Q3
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cytochrome oxidase subunit 1 (Fragment).
 GN COI.
 OS Anolis nitens.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 ON NCBI_TaxID=174262;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Glor R.E., Vitt L.J., Larson A.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF337802; AAL72087.1; -.
 DR EMBL; AF337803; AAL72089.1; -.
 DR EMBL; AF337804; AAL72091.1; -.

KW Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 Db 3 LN 4

RESULT 69
 Q8W8Q4 PRELIMINARY; PRT; 10 AA.
 ID Q8W8Q4
 AC Q8W8Q4;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Cytochrome oxidase subunit 1 (Fragment).
 GN C01.
 OS Anolis punctatus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Polychrotinae; Anolis.
 NCBI_TaxId=174263;
 [1]
 RN SEQUENCE FROM N.A.
 RP
 RA Glor R.E., Vitt L.J., Larson A.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF337770; AAL72023.1; -
 DR EMBL; AF337771; AAL72025.1; -
 DR EMBL; AF337772; AAL72027.1; -
 DR EMBL; AF337773; AAL72029.1; -
 DR EMBL; AF337774; AAL72031.1; -
 KW Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1315 MW; 4B3480C733640447 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
 Db 3 LN 4

RESULT 70
 Q9QVK8 PRELIMINARY; PRT; 10 AA.
 ID Q9QVK8
 AC Q9QVK8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE MEPRIN=METALLOENDOPEPTIDASE (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10095;
 [1]
 RN SEQUENCE.
 RP
 RA MEDLINE=91363409; PubMed=1888759;
 RX Flannery A.V., Macadam G.C., Beynon R.J.;
 RT "Immunological characterisation of different meprin species in mice."
 RL Biochim. Biophys. Acta 1079:119-122(1991).
 FT NON TER 1
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1163 MW; DD6436144731B2C9 CRC64;

Query Match 66.7%; Score 2; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;

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Db          8 LN 9
||
RESULT 73
Q9AIZ7      PRELIMINARY;      PRT;      11 AA.
AC Q9AIZ7;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
RA Baumann P.;
RT "Cospeciation of psyllids and their primary prokaryotic
RT endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861(2001).
DR EMBL; AF211132; AAK15377.1; -.
KW Aminoacyl-tRNA synthetase.
FT NON TER 1
SQ SEQUENCE 11 AA; 1333 MW; A28C67D6533059C6 CRC64;

Query Match      66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
||
Db 2 LN 3

RESULT 74
Q9R4B1      PRELIMINARY;      PRT;      11 AA.
AC Q9R4B1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE BX protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE.
RX MEDLINE=95252678; PubMed=7734831;
RA Gerlach D., Gunther E., Kohler W., Vettermann S., Fleischer B.,
RA Schmidt K.H.;
RT "Isolation and characterization of a mitogen characteristic of group A
RT streptococci (Streptococcus pyogenes).";
RL Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis. 282:67-
RL 82(1995).
SQ SEQUENCE 11 AA; 1216 MW; CE527287CAA455A2 CRC64;

Query Match      66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
||
Db 1 LN 2

RESULT 75
Q47604      PRELIMINARY;      PRT;      11 AA.
ID Q47604;
AC Q47604;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE REase protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63621; AAA24560.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match      66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
||
Db 6 LN 7

Search completed: November 25, 2003, 19:34:16
Job time : 7.63372 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 7.65698 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3

Sequence: 1 LNF 3

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq_19Jun03.*

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	100.0	3	22	Colostrin derixe
2	3	100.0	4	11	Peptidase substrat
3	3	100.0	4	12	Peptide component
4	3	100.0	4	12	Peptide component
5	3	100.0	4	12	Ketone analogue pr
6	3	100.0	4	14	HIV-1 inhibiting p
7	3	100.0	4	19	Oxirane compound w
8	3	100.0	4	20	Peptide used to ma
9	3	100.0	4	20	Peptide used to ma

10	3	100.0	4	21	AAV80828	Fluorophore-label
11	3	100.0	4	21	AAV80856	Fluorophore-label
12	3	100.0	5	14	AAE85691	HIV-1 inhibiting p
13	3	100.0	5	19	AAW80256	Oxirane compound w
14	3	100.0	5	19	AAW80257	Peptide used to ma
15	3	100.0	5	20	AAV15749	Peptide used to ma
16	3	100.0	5	20	AAV15699	Peptide used to ma
17	3	100.0	5	20	AAV15701	Peptide used to ma
18	3	100.0	5	21	AAV80853	Fluorophore-label
19	3	100.0	5	21	AAV80855	Fluorophore-label
20	3	100.0	5	21	AAV80903	Fluorophore-label
21	3	100.0	5	23	AAO15547	Australian taipan
22	3	100.0	5	23	AAU85424	Human colon specif
23	3	100.0	6	11	AAU85424	Human colon specif
24	3	100.0	6	13	AAU85424	Protease chromogen
25	3	100.0	6	13	AAU85424	Protease chromogen
26	3	100.0	6	18	AAW42234	Biotinylated S-pro
27	3	100.0	6	19	AAW54253	Acylated peptide c
28	3	100.0	6	20	AAV15740	Peptide used to ma
29	3	100.0	6	20	AAV15698	Peptide used to ma
30	3	100.0	6	20	AAV15700	Peptide used to ma
31	3	100.0	6	21	AAV80852	Fluorophore-label
32	3	100.0	6	21	AAV80854	Fluorophore-label
33	3	100.0	6	21	AAV80894	Fluorophore-label
34	3	100.0	7	11	AAU85415	Retroviral proteas
35	3	100.0	7	12	AAU85415	Retroviral proteas
36	3	100.0	7	14	AAU85415	HIV-1 inhibiting p
37	3	100.0	7	19	AAW80253	Oxirane compound w
38	3	100.0	7	20	AAV15697	Peptide used to ma
39	3	100.0	7	20	AAV15651	Peptide used to ma
40	3	100.0	7	21	AAV85416	Protophila bag pro
41	3	100.0	7	21	AAV85416	Blk protein fragme
42	3	100.0	7	21	AAV80815	Fluorophore-label
43	3	100.0	7	21	AAV80881	Fluorophore-label
44	3	100.0	7	22	ABO1089	Core polypeptide f
45	3	100.0	7	22	ABO2538	Viral core polypep
46	3	100.0	7	22	AAU13635	Dp178-like/Dp107-1
47	3	100.0	7	22	AAU44074	H11 binding site c
48	3	100.0	7	22	AAU44079	H11 binding site c
49	3	100.0	7	22	AAU44124	H11 binding site c
50	3	100.0	7	22	AAU44129	H11 binding site c
51	3	100.0	7	22	AAU44134	H11 binding site c
52	3	100.0	7	22	AAU44139	H11 binding site c
53	3	100.0	7	22	AAU44144	H11 binding site c
54	3	100.0	7	22	AAU44154	H11 binding site c
55	3	100.0	7	22	AAU44560	H11 binding site c
56	3	100.0	7	22	AAU44565	H11 binding site c
57	3	100.0	7	22	AAU44570	H11 binding site c
58	3	100.0	7	22	AAU44575	H11 binding site c
59	3	100.0	7	22	AAU44661	H11 binding site c
60	3	100.0	7	22	AAU45665	H11 binding site c
61	3	100.0	7	22	AAU45884	H11 binding site c
62	3	100.0	7	22	AAU45974	H11 binding site c
63	3	100.0	7	22	AAU46173	H11 binding site c
64	3	100.0	7	22	AAU46416	H11 binding site c
65	3	100.0	7	22	AAU46609	H11 binding site c
66	3	100.0	7	22	AAU46895	H11 binding site c
67	3	100.0	7	22	AAU46895	H11 binding site c
68	3	100.0	7	24	ABJ37364	G-protein coupled
69	3	100.0	7	24	ABJ37444	Protease chromogen
70	3	100.0	8	13	AAU28732	PR/RT HIV protease
71	3	100.0	8	15	AAU63662	Synthetic pMEL17 p
72	3	100.0	8	18	AAU38400	Molecular mimetic
73	3	100.0	8	19	AAU75337	Mammalian tub prot
74	3	100.0	8	20	AAU75463	Human immunodefici
75	3	100.0	8	21	AAV70353	HIV A01 super moti
76	3	100.0	8	22	ABP11732	HIV A01 super moti
77	3	100.0	8	22	ABP11733	HIV A24 super moti
78	3	100.0	8	22	ABP15843	HIV A24 super moti
79	3	100.0	8	22	ABP15844	HIV B62 super moti
80	3	100.0	8	22	ABP19130	HIV B62 super moti
81	3	100.0	8	22	ABP19336	HIV A03 motif pol
82	3	100.0	8	22	ABP21231	HIV A03 motif pol

83 HIV A03 motif pol
84 Peptide #42 for il
85 Murine Ob receptor
86 HIV peptide SEQ ID
87 HIV peptide SEQ ID
88 HIV peptide SEQ ID
89 Hepatitis C virus
90 Hepatitis B virus
91 Hepatitis B virus
92 Hepatitis B virus
93 Hepatitis B virus
94 Hepatitis B virus
95 Hepatitis B virus
96 Hepatitis B virus
97 Hepatitis B virus
98 Hepatitis B virus
99 Hepatitis B virus
100 Hepatitis B virus

3 100.0 8 22 ABP21574
3 100.0 8 22 ABM47412
3 100.0 8 22 AAE12614
3 100.0 8 22 AAM22971
3 100.0 8 22 AAM22972
3 100.0 8 22 AAM23292
3 100.0 8 22 AAJ02053
3 100.0 8 22 AAB76323
3 100.0 8 22 ABJ05965
3 100.0 8 23 ABJ06309
3 100.0 8 23 ABJ06816
3 100.0 8 23 ABJ06848
3 100.0 8 23 ABJ06909
3 100.0 8 23 ABJ07208
3 100.0 8 23 ABJ07476
3 100.0 8 23 ABJ07868
3 100.0 8 23 ABJ08346
3 100.0 8 23 ABJ08613

ALIGNMENTS

RESULT 1
AAB72278
ID AAB72278 standard; peptide; 3 AA.
XX
AC AAB72278;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrin derived cytokine inducing peptide SEQ ID 33.
XX
KW Colostrin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
FN WO200111937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22818.
XX
PR 17-AUG-1999; 99US-0149311.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GV, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2001-202804/20.
XX
DR Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrin as an immunological
PT regulator -
XX
PS Claim 1; Page 34; 50pp; English.
XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX
SQ Sequence 3 AA;
Query Match 100.0%; Score 3; DB 22; Length 3;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
DB 1 LNF 3
RESULT 2
AAR04018
ID AAR04018 standard; Protein; 4 AA.
XX
AC AAR04018;
XX
DT 25-MAR-2003 (updated)
DT 19-NOV-1991 (first entry)
XX
DE Peptidase substrate analogues having peptidase inhibition activity.
XX
KW Elastase; plasminogen activator; cathepsin; calpain; enkephalinase;
KW Angiotensin converting enzyme.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /label= Terminal modified from -COOH to -COCOR
FT /note= "R = alkyl group or -H"
XX
FN EF363284-A.
XX
PD 11-APR-1990.
XX
PF 06-OCT-1989; 89EP-0402762.
XX
PR 07-OCT-1988; 88US-0254762.
PR 06-OCT-1989; 89EP-0402763.
XX
PA (RICH) MERRELL DOW PHARM INC.
PA (RICH) MERRELL PHARM INC.
PI Bey P, Angelastro M, Mehdi S;
XX
DR WPI; 1990-109579/15.
XX
PT New peptidase substrate analogue cpds. - useful as protease
PT inhibitors in treatment of disease states.
XX
PS Claim 45; Page 31; 33pp; English.
XX
CC The analogues may be useful in treatment of a variety of disease
CC states. The scissile amide group is replaced with H or a substituted
CC Carbon moiety effectively inhibiting the activity of peptidases such
CC as elastase, plasmin thrombin, urokinase etc.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 3; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
DB 2 LNF 4
RESULT 3
AAR10879


```
ID XX AAR10879 standard; Protein; 4 AA.
AC XX AAR10879;
DT XX 10-APR-1991 (first entry)
DE XX Peptide component of pentafluoroethylcarbonyl analogue.
KW XX Protease inhibitor; rheumatoid arthritis; thrombosis; psoriasis;
KW XX male contraceptive.
XX XX Synthetic.
OS XX
XX XX EP410411-A.
XX XX
XX XX 30-JAN-1991.
XX XX
XX XX 25-JUL-1990; 90EP-0114250.
XX XX
XX XX 26-JUL-1989; 89US-0385624.
XX XX (RICH ) MERRELL DOW PHARM INC.
XX XX
XX XX Bey P, Peet NP, Angelastro MR, Mehdi S;
XX XX WPI; 1991-030811/05.
XX XX Novel serine-, carboxylic acid- and metallo-proteinase-inhibitors
XX XX - inhibit range of proteinase(s) in treating rheumatoid
XX XX arthritis, thrombosis and psoriasis, also is a male contraceptive
XX XX Claim 44; page 28; 40pp; English.
XX XX
XX XX This peptide is the R1 gp. of the cpd. of formula: RINHCH(R2)-
XX XX COCF2CF3. This cpd. is a peptidase substrate analogue and is a
XX XX specific enzyme inhibitor for a range of proteases, e.g. serine-,
XX XX carboxylic acid-, and metallo-proteases. It is useful in the
XX XX treatment of rheumatoid arthritis, thrombosis and psoriasis and is
XX XX also used as a male contraceptive. See also AAR10876-82 and AAR10886-
XX XX 88.
XX XX
XX XX SQ Sequence 4 AA;
XX XX
XX XX Query Match 100.0%; Score 3; DB 12; Length 4;
XX XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX Qy 1 LNF 3
XX XX |||
XX XX 2 LNF 4
XX XX
XX XX RESULT 5
XX XX AAR11232
XX XX ID AAR11232 standard; Protein; 4 AA.
XX XX
XX XX AAR11232;
XX XX
XX XX 24-MAY-1991 (first entry)
XX XX
XX XX Ketone analogue protease inhibitor #11.
XX XX
XX XX protease inhibitor; antiinflammatory agent; hypotensive; analgesic;
XX XX antiproliferative agent; antidemyelinating agent; antithrombotic.
XX XX
XX XX Synthetic.
XX XX
XX XX Key Location/Qualifiers
XX XX Modified-site 4 /label= carboxyloxalyl-Phe
XX XX
XX XX EP417721-A.
XX XX
XX XX 20-MAR-1991.
XX XX
XX XX 11-SEP-1990; 90EP-0117461.
XX XX
XX XX 11-SEP-1989; 89US-0405491.
XX XX
XX XX (RICH ) MERRELL DOW PHARM INC.
XX XX
XX XX Flynn GA, Bey P;
XX XX
XX XX WPI; 1991-081980/12.
XX XX
XX XX New ketone analogue peptidase and isomerase inhibitors - for
XX XX inhibition of leukocyte elastase, cathepsin G, thrombin,
XX XX chymotrypsin, plasmin etc.
XX XX
XX XX Claim 44; Page 30; 50pp; English.
XX XX
XX XX This peptide is a specific example of a highly generic protease
XX XX
```

```
ID XX AAR10879 standard; Protein; 4 AA.
AC XX AAR10879;
DT XX 10-APR-1991 (first entry)
DE XX Peptide component of pentafluoroethylcarbonyl analogue.
KW XX Protease inhibitor; rheumatoid arthritis; thrombosis; psoriasis;
KW XX male contraceptive.
XX XX Synthetic.
OS XX
XX XX EP410411-A.
XX XX
XX XX 30-JAN-1991.
XX XX
XX XX 25-JUL-1990; 90EP-0114250.
XX XX
XX XX 26-JUL-1989; 89US-0385624.
XX XX (RICH ) MERRELL DOW PHARM INC.
XX XX
XX XX Bey P, Peet NP, Angelastro MR, Mehdi S;
XX XX WPI; 1991-030811/05.
XX XX Novel serine-, carboxylic acid- and metallo-proteinase-inhibitors
XX XX - inhibit range of proteinase(s) in treating rheumatoid
XX XX arthritis, thrombosis and psoriasis, also is a male contraceptive
XX XX Claim 44; page 28; 40pp; English.
XX XX
XX XX This peptide is the R1 gp. of the cpd. of formula: RINHCH(R2)-
XX XX COCF2CF3. This cpd. is a peptidase substrate analogue and is a
XX XX specific enzyme inhibitor for a range of proteases, e.g. serine-,
XX XX carboxylic acid-, and metallo-proteases. It is useful in the
XX XX treatment of rheumatoid arthritis, thrombosis and psoriasis and is
XX XX also used as a male contraceptive. See also AAR10876-78, AAR10880-83
XX XX and AAR10886-88.
XX XX
XX XX SQ Sequence 4 AA;
XX XX
XX XX Query Match 100.0%; Score 3; DB 12; Length 4;
XX XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX Qy 1 LNF 3
XX XX |||
XX XX 2 LNF 4
XX XX
XX XX RESULT 4
XX XX AAR10883
XX XX ID AAR10883 standard; Protein; 4 AA.
XX XX
XX XX AAR10883;
XX XX
XX XX 10-APR-1991 (first entry)
XX XX
XX XX Peptide component of pentafluoroethylcarbonyl analogue.
XX XX
XX XX Protease inhibitor; rheumatoid arthritis; thrombosis; psoriasis;
XX XX male contraceptive.
XX XX
XX XX Synthetic.
XX XX
XX XX EP410411-A.
XX XX
XX XX 30-JAN-1991.
XX XX
XX XX 25-JUL-1990; 90EP-0114250.
XX XX
```

CC inhibitor useful for medical purposes. The peptide analogues include
 CC inhibitors of urokinase, renin, cathepsin D, etc. which can be used
 CC as anti-proliferative agents and abortifacients, hypotensives,
 CC antiinflammatory and antidiemvelinating agents, respectively.
 CC See also AAR11222-R11230 and AAR11231-R11238.

XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 3; DB 12; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 6
 AAR65692
 ID AAR65692 standard; peptide; 4 AA.
 XX
 AC AAR65692;

XX 25-MAR-2003 (updated)
 DT 08-JAN-1995 (first entry)

XX HIV-1 inhibiting pseudopeptide.

XX Aspartic proteinase; reversible inhibitor; pseudopeptide;
 KW phosphinate methylene ammonium group; exploding transition analogue;
 HIV-1.

XX Synthetic.

FT Key Location/Qualifiers
 FT Modified-site 1 /note= "Acetyl-Leu"
 FT Modified-site 3..4
 FT Modified-site 4 /note= "CONH linkage replaced by P(O) (OH) CH2NH"
 FT /label= OTHER
 FT /note= "piperidine-2(S)-carbonyl tert. butylamide
 FT or (4aS, 8aS)-decahydro-3(S)-isoquinoline
 FT carbonyl tert. butylamide"

XX WO9314114-A1.

XX 22-JUL-1993.

XX 11-JAN-1993; 93WO-US00228.

XX 09-JAN-1992; 92US-0819356.

XX (SCRI) SCRIPPS RES INST.

XX Ikeda S, Janda KD, Wirsching P;

XX WPI; 1993-243142/30.

XX New peptide linkage unit - comprising phosphinate methylene
 PT ammonium gp., esp. for pseudo-peptide aspartic proteinase
 PT inhibitors

XX Claims 37,38; Page 71; 76pp; English.

XX The invention relates to a phosphinic acid methylene amine linkage
 CC PO(OH)CH2NH to be used in place of a peptide linkage CONH at the
 CC cleavage site in an aspartic proteinase substrate. The linkage is
 CC resistant to cleavage and serves as an exploding transition state
 CC analogue of the cleavage site, thus the peptide containing it can
 CC bind or interfere with the active site of the aspartic proteinase
 CC enzyme and inhibit its activity.

CC The present sequence is a specifically claimed example of a

CC HIV-1 inhibiting peptide containing the linkage.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 3; DB 14; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 7
 AAW80261
 ID AAW80261 standard; peptide; 4 AA.
 XX
 AC AAW80261;

XX 06-JAN-1999 (first entry)

XX Oxirane compound which is an inhibitor of HIV-1 protease.

XX Oxirane compound; human immunodeficiency virus; HIV protease inhibitor;
 KW gag; pol; HIV-1 protease.

XX Synthetic.

XX US5827827-A.

XX 27-OCT-1998.

XX 20-JUN-1996; 96US-0667001.

XX 20-JUN-1996; 96US-0667001.

XX 16-FEB-1995; 95US-0335039.

XX (SCRI) SCRIPPS RES INST.

XX Janda KD, Wirsching P;

XX WPI; 1998-594033/50.

XX Oxirane compounds e.g. oxirane-substituted oligo-peptide(s) - used
 PT as human immunodeficiency virus protease inhibitors

XX Disclosure; Column 10; 29pp; English.

XX The present sequence is part of an oxirane compound which acts as a
 CC human immunodeficiency virus (HIV) protease inhibitor. The compounds
 CC have a terminal epoxide moiety. The compounds inhibit HIV protease
 CC and the cleavage of gag and gag pol polyproteins of HIV by HIV-1
 CC protease.

XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 3; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 8
 AAY15702
 ID AAY15702 standard; Peptide; 4 AA.
 XX
 AC AAY15702;

XX 27-JUL-1999 (first entry)
 DT

XX DE Peptide used to make fluorescent reporter molecules.

XX KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;

XX KW apoptosis; protease; peptidase; apoptosis cascade; cancer;

XX KW chemotherapeutic agent; cell death; viral protease activity.

XX OS Synthetic.

XX PN WO9918856-A1.

XX PD 22-APR-1999.

XX PF 09-OCT-1998; 98WO-US21231.

XX PR 03-MAR-1998; 98US-0033661.

XX PR 10-OCT-1997; 97US-0061582.

XX PA (CYTO-) CYTOVIA INC.

XX PI Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;

XX PD WPI; 1999-312448/26.

XX PF New fluorogenic or fluorescent reporter molecules

XX PT Disclosure; Page 183; 202pp; English.

XX CC AAY15618-Y15759 represent peptides used to make the fluorogenic or

XX CC fluorescent reporter molecules of the invention. These molecules

XX CC contain a peptide moiety (e.g. present sequence) which acts as a

XX CC substrate for enzymes involved in apoptosis or protease or peptidase

XX CC enzymes. The compounds can be used as fluorogenic or fluorescent

XX CC substrates for enzymes. Depending on the peptide moiety used, the

XX CC fluorescent molecules can be used for detecting or measuring the

XX CC activity of an enzyme involved in the apoptosis cascade in cells; to

XX CC determine whether a test compound has an effect on an enzyme involved

XX CC in the apoptosis cascade in cells; for determining the sensitivity of

XX CC an animal with cancer to treatment with chemotherapeutic agents or

XX CC enhances cell death of test cells; for detecting or measuring the

XX CC activity of a viral protease in cells; for determining whether a test

XX CC compound has an effect on the activity of a viral protease in cells;

XX CC and for measuring the activity or determining whether a test substance

XX CC has an effect on the activity of a protease or peptidase in cells.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 20; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db 1 LNF 3

RESULT 9

AAY15671

ID AAY15671 standard; Peptide; 4 AA.

AC AAY15671;

XX 27-JUL-1999 (first entry)

XX DE Peptide used to make fluorescent reporter molecules.

XX KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;

XX KW apoptosis; protease; peptidase; apoptosis cascade; cancer;

XX KW chemotherapeutic agent; cell death; viral protease activity.

XX OS Synthetic.

PN WO9918856-A1.

XX 22-APR-1999.

XX PF 09-OCT-1998; 98WO-US21231.

XX PR 03-MAR-1998; 98US-0033661.

XX PR 10-OCT-1997; 97US-0061582.

XX PA (CYTO-) CYTOVIA INC.

XX PI Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;

XX PD WPI; 1999-312448/26.

XX PF New fluorogenic or fluorescent reporter molecules

XX PS Disclosure; Page 174; 202pp; English.

XX CC AAY15618-Y15759 represent peptides used to make the fluorogenic or

XX CC fluorescent reporter molecules of the invention. These molecules

XX CC contain a peptide moiety (e.g. present sequence) which acts as a

XX CC substrate for enzymes involved in apoptosis or protease or peptidase

XX CC enzymes. The compounds can be used as fluorogenic or fluorescent

XX CC substrates for enzymes. Depending on the peptide moiety used, the

XX CC fluorescent molecules can be used for detecting or measuring the

XX CC activity of an enzyme involved in the apoptosis cascade in cells; to

XX CC determine whether a test compound has an effect on an enzyme involved

XX CC in the apoptosis cascade in cells; for determining the sensitivity of

XX CC an animal with cancer to treatment with chemotherapeutic agents or

XX CC enhances cell death of test cells; for detecting or measuring the

XX CC activity of a viral protease in cells; for determining whether a test

XX CC compound has an effect on the activity of a viral protease in cells;

XX CC and for measuring the activity or determining whether a test substance

XX CC has an effect on the activity of a protease or peptidase in cells.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 20; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db 2 LNF 4

RESULT 10

AAY80828

ID AAY80828 standard; peptide; 4 AA.

XX AC AAY80828;

XX 22-MAY-2000 (first entry)

XX DE Fluorophore-labelled HIV protease substrate peptide, SEQ ID NO:54.

XX KW Protease substrate; fluorescent label; fluorophore; rhodamine;

XX KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;

XX KW methionine aminopeptidase type 2; MetAP-2; drug screening.

XX OS Synthetic.

XX PN WO200004914-A1.

XX PD 03-FEB-2000.

XX PF 21-JUL-1999; 99WO-US16423.

XX PR 21-JUL-1998; 98US-0093642.

XX PA (CYTO-) CYTOVIA INC.

PA (ZHAN/) ZHANG H.
 PA (CAIS/) CAI S. X.
 PA (DREW/) DREW J. A.
 PA (YANG/) YANG W.
 XX
 FI Zhang H, Cai SX, Drewe JA, Yang W;
 XX WPI; 2000-195079/17.
 DR
 XX
 XX
 PT New fluorescently labeled amino acids or peptides, used as substrates
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
 PT agents, contains a halobenzoyl N-blocking group -
 XX
 XX
 PS Disclosure; Page 36; 174pp; English.
 CC
 CC The invention relates to fluorescently labelled peptides containing
 CC a halobenzoyl group on the fluorophore. They are of the structure
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being
 CC assayed. The labelled peptides are reporters for detecting intracellular
 CC proteolytic enzymes, particularly caspases and other enzymes involved in
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
 CC cytomegalovirus and hepatitis C virus proteases); and methionine
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly useful to
 CC identify modulators of these enzymes which may be potentially useful as
 CC agents for treating conditions such as cancer, neurodegeneration,
 CC autoimmune diseases, myocardial infarction and viral infection.
 CC Modulators identified may also be used to prolong the life of cells being
 CC cultured for recombinant protein production, or to monitor the treatment
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
 CC potential anti- angiogenic or anticancer agents. Sequences
 CC AAY80782-Y80910 represent peptides, some of which are specifically
 CC claimed, which may be used in assay methods according to the invention.
 XX
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 11
 AAY80856
 ID AAY80856 standard; peptide; 4 AA.
 XX
 AC AAY80856;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:85.
 XX
 KW Protease substrate; fluorescent label; fluorophore; rhodamine;
 KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;
 KW methionine aminopeptidase type 2; MetAP-2; drug screening.
 XX
 OS Synthetic.
 XX
 XX WO200004914-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-US16423.
 XX
 XX 21-JUL-1998; 98US-0093642.
 XX
 XX (CYTO-) CYTOVIA INC.
 PA (ZHAN/) ZHANG H.
 FA (CAIS/) CAI S. X.

PA (DREW/) DREW J. A.
 PA (YANG/) YANG W.
 XX
 FI Zhang H, Cai SX, Drewe JA, Yang W;
 XX WPI; 2000-195079/17.
 DR
 XX
 XX
 PT New fluorescently labeled amino acids or peptides, used as substrates
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
 PT agents, contains a halobenzoyl N-blocking group -
 XX
 XX
 PS Claim 30; Page 109; 174pp; English.
 CC
 CC The invention relates to fluorescently labelled peptides containing
 CC a halobenzoyl group on the fluorophore. They are of the structure
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being
 CC assayed. The labelled peptides are reporters for detecting intracellular
 CC proteolytic enzymes, particularly caspases and other enzymes involved in
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
 CC cytomegalovirus and hepatitis C virus proteases); and methionine
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly useful to
 CC identify modulators of these enzymes which may be potentially useful as
 CC agents for treating conditions such as cancer, neurodegeneration,
 CC autoimmune diseases, myocardial infarction and viral infection.
 CC Modulators identified may also be used to prolong the life of cells being
 CC cultured for recombinant protein production, or to monitor the treatment
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
 CC potential anti- angiogenic or anticancer agents. Sequences
 CC AAY80782-Y80910 represent peptides, some of which are specifically
 CC claimed, which may be used in assay methods according to the invention.
 XX
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 12
 AAR65691
 ID AAR65691 standard; peptide; 5 AA.
 XX
 AC AAR65691;
 XX
 DT 25-MAR-2003 (updated)
 DT 08-JAN-1995 (first entry)
 XX
 DE HIV-1 inhibiting pseudopeptide.
 XX
 KW Aspartic proteinase; reversible inhibitor; pseudopeptide;
 KW phosphate methylene ammonium group; exploding transition analogue;
 KW HIV-1.
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "Acetyl-Ser"
 FT Modified-site 4..5 /note= "CONH linkage replaced by P(O) (OH) CH2NH"
 FT Modified-site 5 /label= OTHER
 FT 21-JUL-1998; 98US-0093642. /note= "piperidine-2(S)-carbonyl tert. butylamide
 FT or (4aS, 8aS)-decahydro-3(S)-isoquinoline
 FT carbonyl tert. butylamide"
 XX
 XX WO9314114-A1.

```

XX PD 22-JUL-1993.
XX XX
XX PF 11-JAN-1993; 93WO-US00228.
XX XX
XX PR 09-JAN-1992; 92US-0819356.
XX XX
XX PA (SCRI ) SCRIPPS RES INST.
XX XX
XX PI Ikeda S, Janda KD, Wirsching P;
XX DR WPI; 1993-243142/30.
XX XX
XX PT New peptide linkage unit - comprising phosphinate methylene
XX PT ammonium gp., esp. for pseudo-peptide aspartic proteinase
XX PT inhibitors
XX XX
XX PS Claim 35; Page 70; 76pp; English.
XX XX
XX CC The invention relates to a phosphinic acid methylene amine linkage
XX CC PO(OH)CH2NH2 to be used in place of a peptide linkage CONH at the
XX CC cleavage site in an aspartic proteinase substrate. The linkage is
XX CC resistant to cleavage and serves as an exploding transition state
XX CC analogue of the cleavage site. Thus the peptide containing it can
XX CC bind or interfere with the active site of the aspartic proteinase
XX CC enzyme and inhibit its activity.
XX CC The present sequence is a specifically claimed example of a
XX CC HIV-1 inhibiting peptide containing the linkage.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX XX
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LNF 3
Db 2 LNF 4

RESULT 13
AAW80256
ID AAW80256 standard; peptide; 5 AA.
XX XX
XX AC AAW80256;
XX XX
XX DT 06-JAN-1999 (first entry)
XX DE Oxirane compound which is an inhibitor of HIV-1 protease.
XX KW Oxirane compound; human immunodeficiency virus; HIV protease inhibitor;
XX KW gag; pol; HIV-1 protease.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Ser is linked to CH3C(O) "
XX FT Modified-site 4..5 /note= "these residues are linked by a pseudo
XX FT Modified-site 5 peptide linkage comprising 1-epoxy-ethylene"
XX FT /note= "PIC-NH-tBu, where
XX FT PIC=piperidine-2-(S)-carboxyl (proline
XX FT analogue), and tBu=tert-butyl"
XX PN US5827827-A.
XX PD 27-OCT-1998.
XX PF 20-JUN-1996; 96US-0667001.
XX XX
XX PR 20-JUN-1996; 96US-0667001.
XX PR 16-FEB-1995; 95US-0335039.
XX XX
XX PA (SCRI ) SCRIPPS RES INST.
XX XX
XX PI Janda KD, Wirsching P;
XX DR WPI; 1998-594033/50.
XX XX

Query Match 100.0%; Score 3; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LNF 3
Db 2 LNF 4

RESULT 14
AAW80257
ID AAW80257 standard; peptide; 5 AA.
XX XX
XX AC AAW80257;
XX XX
XX DT 06-JAN-1999 (first entry)
XX DE Oxirane compound which is an inhibitor of HIV-1 protease.
XX KW Oxirane compound; human immunodeficiency virus; HIV protease inhibitor;
XX KW gag; pol; HIV-1 protease.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Ser is linked to CH3C(O) "
XX FT Modified-site 4..5 /note= "these residues are linked by a pseudo
XX FT Modified-site 5 peptide linkage comprising 1-epoxy-ethylene"
XX FT /note= "PIC-NH-tBu, where
XX FT PIC=(4aS,8aS)-decahydro-3(S)-isoquinoline
XX FT carbonyl (proline analogue),
XX FT and tBu=tert-butyl"
XX PN US5827827-A.
XX PD 27-OCT-1998.
XX PF 20-JUN-1996; 96US-0667001.
XX XX
XX PR 20-JUN-1996; 96US-0667001.
XX PR 16-FEB-1995; 95US-0335039.
XX XX
XX PA (SCRI ) SCRIPPS RES INST.
XX XX
XX PI Janda KD, Wirsching P;
XX DR WPI; 1998-594033/50.
XX XX

```

PT Oxirane compounds e.g. oxirane-substituted oligo-peptide(s) - used
PT as human immunodeficiency virus protease inhibitors
XX
XX Disclosure; Column 9; 29pp; English.

XX The present sequence is part of an oxirane compound which acts as a
CC human immunodeficiency virus (HIV) protease inhibitor. The compounds
CC have a terminal epoxide moiety. The compounds inhibit HIV protease
CC and the cleavage of gag and gag pol polyproteins of HIV by HIV-1
CC protease.
XX
XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db |||
2 LNF 4

RESULT 15

AAV15749
ID AAY15749 standard; Peptide; 5 AA.

XX AAY15749;

XX 27-JUL-1999 (first entry)

XX Peptide used to make fluorescent reporter molecules.

XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;
KW apoptosis; protease; peptidase; apoptosis cascade; cancer;
KW chemotherapeutic agent; cell death; viral protease activity.

XX Synthetic.

XX WO9918856-A1.

XX 22-APR-1999.

XX 09-OCT-1998; 98WO-US21231.

XX 03-MAR-1998; 98US-0033661.

XX 10-OCT-1997; 97US-0061582.

XX (CYTO-) CYTOVIA INC.

XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;

XX WPI; 1999-312448/26.

XX New fluorogenic or fluorescent reporter molecules

XX Claim 39; Page 196; 202pp; English.

XX AAY15618-Y15759 represent peptides used to make the fluorogenic or
CC fluorescent reporter molecules of the invention. These molecules
CC contain a peptide moiety (e.g. present sequence) which acts as a
CC substrate for enzymes involved in apoptosis or protease or peptidase
CC enzymes. The compounds can be used as fluorogenic or fluorescent
CC substrates for enzymes. Depending on the peptide moiety used, the
CC fluorescent molecules can be used for detecting or measuring the
CC activity of an enzyme involved in the apoptosis cascade in cells; to
CC determine whether a test compound has an effect on an enzyme involved
CC in the apoptosis cascade in cells; for determining the sensitivity of
CC an animal with cancer to treatment with chemotherapeutic agents or
CC determining whether a test substance inhibits, prevents, causes or
CC enhances cell death of test cells; for detecting or measuring the
CC activity of a viral protease in cells; for determining whether a test
CC compound has an effect on the activity of a viral protease in cells;
CC and for measuring the activity or determining whether a test substance

CC has an effect on the activity of a protease or peptidase in cells.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db |||
2 LNF 4

RESULT 16

AAV15699
ID AAY15699 standard; Peptide; 5 AA.

XX AAY15699;

XX 27-JUL-1999 (first entry)

XX Peptide used to make fluorescent reporter molecules.

XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;
KW apoptosis; protease; peptidase; apoptosis cascade; cancer;
KW chemotherapeutic agent; cell death; viral protease activity.

XX Synthetic.

XX WO9918856-A1.

XX 22-APR-1999.

XX 09-OCT-1998; 98WO-US21231.

XX 03-MAR-1998; 98US-0033661.

XX 10-OCT-1997; 97US-0061582.

XX (CYTO-) CYTOVIA INC.

XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;

XX WPI; 1999-312448/26.

XX New fluorogenic or fluorescent reporter molecules

XX Disclosure; Page 182; 202pp; English.

XX AAY15618-Y15759 represent peptides used to make the fluorogenic or
CC fluorescent reporter molecules of the invention. These molecules
CC contain a peptide moiety (e.g. present sequence) which acts as a
CC substrate for enzymes involved in apoptosis or protease or peptidase
CC enzymes. The compounds can be used as fluorogenic or fluorescent
CC substrates for enzymes. Depending on the peptide moiety used, the
CC fluorescent molecules can be used for detecting or measuring the
CC activity of an enzyme involved in the apoptosis cascade in cells; to
CC determine whether a test compound has an effect on an enzyme involved
CC in the apoptosis cascade in cells; for determining the sensitivity of
CC an animal with cancer to treatment with chemotherapeutic agents or
CC determining whether a test substance inhibits, prevents, causes or
CC enhances cell death of test cells; for detecting or measuring the
CC activity of a viral protease in cells; for determining whether a test
CC compound has an effect on the activity of a viral protease in cells;
CC and for measuring the activity or determining whether a test substance
CC has an effect on the activity of a protease or peptidase in cells.

XX Sequence 5 AA;

Query Match 100.0%; Score 3; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

```

Db      |||
        2 LNF 4

RESULT 17
AAV15701
ID  AAV15701 standard; Peptide; 5 AA.
XX
XX  AAV15701;
AC
XX
XX  27-JUL-1999 (first entry)
DT
XX
XX  Peptide used to make fluorescent reporter molecules.
DE
XX
XX  Fluorogenic; fluorescent reporter molecule; enzyme substrate;
KW  apoptosis; protease; peptidase; apoptosis cascade; cancer;
KW  chemotherapeutic agent; cell death; viral protease activity.
XX
XX  Synthetic.
OS
XX  WO9918856-A1.
PN
XX
XX  22-APR-1999.
PD
XX
XX  09-OCT-1998; 98WO-US21231.
PF
XX
XX  03-MAR-1998; 98US-0033661.
PR
XX  10-OCT-1997; 97US-0061582.
XX
XX  (CYTO-) CYTOVIA INC.
PA
XX
XX  Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;
PI
XX  WPI; 1999-312448/26.
DR
XX
XX  New fluorogenic or fluorescent reporter molecules
PT
XX
XX  Disclosure; Page 182; 202pp; English.
PS
XX
XX  AAV15618-Y1579 represent peptides used to make the fluorogenic or
CC  fluorescent reporter molecules of the invention. These molecules
CC  contain a peptide moiety (e.g. present sequence) which acts as a
CC  substrate for enzymes involved in apoptosis or protease or peptidase
CC  enzymes. The compounds can be used as fluorogenic or fluorescent
CC  substrates for enzymes. Depending on the peptide moiety used, the
CC  fluorescent molecules can be used for detecting or measuring the
CC  activity of an enzyme involved in the apoptosis cascade in cells; to
CC  determine whether a test compound has an effect on an enzyme involved
CC  in the apoptosis cascade in cells; for determining the sensitivity of
CC  an animal with cancer to treatment with chemotherapeutic agents or
CC  determining whether a test substance inhibits, prevents, causes or
CC  enhances cell death of test cells; for detecting or measuring the
CC  activity of a viral protease in cells; for determining whether a test
CC  compound has an effect on the activity of a viral protease in cells;
CC  and for measuring the activity or determining whether a test substance
CC  has an effect on the activity of a protease or peptidase in cells.
XX
SQ  Sequence 5 AA;

Query Match 100.0%; Score 3; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 1 LNF 3

RESULT 18
AAV80853
ID  AAV80853 standard; peptide; 5 AA.
XX
XX  AAV80853;
AC
XX
XX  22-MAY-2000 (first entry)
DT
XX
XX  22-MAY-2000 (first entry)
DT
XX
XX  Fluorophore-labelled protease substrate peptide, SEQ ID NO:82.
DE
XX
XX  Protease substrate; fluorescent label; fluorophore; rhodamine;
KW  blocking group; halobenzoyl group; cleavage; caspase; viral protease;
KW  methionine aminopeptidase type 2; MetAP-2; drug screening.
XX
XX  Synthetic.
OS
XX  WO200004914-A1.
PN
XX
XX  03-FEB-2000.
PD
XX
XX  21-JUL-1999; 99WO-US16423.
PF
XX
XX  21-JUL-1998; 98US-0093642.
PR
XX
XX  (CYTO-) CYTOVIA INC.
PA  (ZHAN/) ZHANG H.
PA  (CAIS/) CAI S X.
PA  (DREW/) DREWE J A.
PA  (YANG/) YANG W.
XX
XX  Zhang H, Cai SX, Drewe JA, Yang W;
PI
XX  WPI; 2000-195079/17.
DR
XX
XX  New fluorescently labeled amino acids or peptides, used as substrates
PT  for detecting enzymes or their modulators, e.g. anticancer or antiviral
PT  agents, contains a halobenzoyl N-blocking group -
XX
XX  Claim 30; Page 109; 174pp; English.
PS
XX
XX  The invention relates to fluorescently labelled peptides containing
CC  a halobenzoyl group on the fluorophore. They are of the structure
CC  peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking
CC  group, Y is a fluorescent or fluorogenic moiety (preferably a
CC  rhodamine), and the peptide-Y bond is cleavable by the enzyme being
CC  assayed. The labelled peptides are reporters for detecting intracellular
CC  proteolytic enzymes, particularly caspases and other enzymes involved in
CC  apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
CC  cytomegalovirus and hepatitis C virus proteases); and methionine
CC  aminopeptidase type 2 (MetAP-2). The peptides are particularly useful to
CC  identify modulators of these enzymes which may be potentially useful as
CC  agents for treating conditions such as cancer, neurodegeneration,
CC  autoimmune diseases, myocardial infarction and viral infection.
CC  Modulators identified may also be used to prolong the life of cells being
CC  cultured for recombinant protein production, or to monitor the treatment
CC  of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
CC  potential anti- angiogenic or anticancer agents. Sequences
CC  AAY80782-Y80910 represent peptides, some of which are specifically
CC  claimed, which may be used in assay methods according to the invention.
XX
SQ  Sequence 5 AA;

Query Match 100.0%; Score 3; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 2 LNF 4

RESULT 19
AAV80855
ID  AAV80855 standard; peptide; 5 AA.
XX
XX  AAV80855;
AC
XX
XX  22-MAY-2000 (first entry)
DT

```

XX DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:84.
 XX KW Protease substrate; fluorescent label; fluorophore; rhodamine;
 XX KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;
 XX KW methionine aminopeptidase type 2; MetAP-2; drug screening.
 XX OS Synthetic.
 XX PN WO200004914-A1.
 XX PD 03-FEB-2000.
 XX PF 21-JUL-1999; 99WO-US16423.
 XX PR 21-JUL-1998; 98US-0093642.
 XX PA (CYTO-) CYTOVIA INC.
 XX PA (ZHAN/) ZHANG H.
 XX PA (CAIS/) CAI S X.
 XX PA (DREW/) DREWE J A.
 XX PA (YANG/) YANG W.
 XX PI Zhang H, Cai SX, Drewe JA, Yang W;
 XX DR WPI; 2000-195079/17.
 XX PT New fluorescently labeled amino acids or peptides, used as substrates
 XX PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
 XX PT agents, contains a halobenzoyl N-blocking group -
 XX PS Claim 30; Page 109; 174pp; English.
 XX CC The invention relates to fluorescently labelled peptides containing
 XX CC a halobenzoyl group on the fluorophore. They are of the structure
 XX CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking
 XX CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 XX CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being
 XX CC assayed. The labelled peptides are reporters for detecting intracellular
 XX CC proteolytic enzymes, particularly caspases and other enzymes involved in
 XX CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
 XX CC cytomegalovirus and hepatitis C virus proteases); and methionine
 XX CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to
 XX CC identify modulators of these enzymes which may be potentially useful as
 XX CC agents for treating conditions such as cancer, neurodegeneration,
 XX CC autoimmune diseases, myocardial infarction and viral infection.
 XX CC Modulators identified may also be used to prolong the life of cells being
 XX CC cultured for recombinant protein production, or to monitor the treatment
 XX CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
 XX CC potential anti- angiogenic or anticancer agents. Sequences
 XX CC AAY80782-Y80910 represent peptides, some of which are specifically
 XX CC claimed, which may be used in assay methods according to the invention.
 XX SQ Sequence 5 AA;
 XX Query Match 100.0%; Score 3; DB 21; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 LNF 3
 XX Db 1 LNF 3
 XX RESULT 20
 XX AAY80903
 XX ID AAY80903 standard; peptide; 5 AA.
 XX AC AAY80903;
 XX DT 22-MAY-2000 (first entry)
 XX DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:132.

XX KW Protease substrate; fluorescent label; fluorophore; rhodamine;
 XX KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;
 XX KW methionine aminopeptidase type 2; MetAP-2; drug screening.
 XX OS Synthetic.
 XX PN WO200004914-A1.
 XX PD 03-FEB-2000.
 XX PF 21-JUL-1999; 99WO-US16423.
 XX PR 21-JUL-1998; 98US-0093642.
 XX PA (CYTO-) CYTOVIA INC.
 XX PA (ZHAN/) ZHANG H.
 XX PA (CAIS/) CAI S X.
 XX PA (DREW/) DREWE J A.
 XX PA (YANG/) YANG W.
 XX PI Zhang H, Cai SX, Drewe JA, Yang W;
 XX DR WPI; 2000-195079/17.
 XX PT New fluorescently labeled amino acids or peptides, used as substrates
 XX PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
 XX PT agents, contains a halobenzoyl N-blocking group -
 XX PS Claim 29; Page 109; 174pp; English.
 XX CC The invention relates to fluorescently labelled peptides containing
 XX CC a halobenzoyl group on the fluorophore. They are of the structure
 XX CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking
 XX CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 XX CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being
 XX CC assayed. The labelled peptides are reporters for detecting intracellular
 XX CC proteolytic enzymes, particularly caspases and other enzymes involved in
 XX CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
 XX CC cytomegalovirus and hepatitis C virus proteases); and methionine
 XX CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to
 XX CC identify modulators of these enzymes which may be potentially useful as
 XX CC agents for treating conditions such as cancer, neurodegeneration,
 XX CC autoimmune diseases, myocardial infarction and viral infection.
 XX CC Modulators identified may also be used to prolong the life of cells being
 XX CC cultured for recombinant protein production, or to monitor the treatment
 XX CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
 XX CC potential anti- angiogenic or anticancer agents. Sequences
 XX CC AAY80782-Y80910 represent peptides, some of which are specifically
 XX CC claimed, which may be used in assay methods according to the invention.
 XX SQ Sequence 5 AA;
 XX Query Match 100.0%; Score 3; DB 21; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 LNF 3
 XX Db 2 LNF 4
 XX RESULT 21
 XX AAO15547
 XX ID AAO15547 standard; protein; 5 AA.
 XX AC AAO15547;
 XX DT 24-OCT-2002 (first entry)
 XX DE Australian taipan snake venom Beta-taipoxin derived peptide #3.
 XX KW Australian taipan; snake venom; peptide therapy; Beta-taipoxin; wound;

KW burn; cellular growth medium; beautifying agent; mitogenic peptide;
 KW oxynor peptide-10.
 OS Oxyuranus scutellatus scutellatus.
 XX

XX WO200261044-A2.
 PN

XX 08-AUG-2002.
 PD

XX 30-JAN-2002; 2002WO-US02633.
 PF

XX 30-JAN-2001; 2001US-264984P.
 PR

XX (LIPP/) LIPPS B V.
 PA

XX Lipps BV;
 PI

XX WPI; 2002-627476/67.
 DR

XX New synthetic peptides with mitogenic properties, useful as a
 PT medication for treating wounds or burns, as a component of a cellular
 PT growth medium, or as a beautifying agent -

XX Claim 3; Page 8; 12pp; English.
 PS

XX The invention comprises mitogenic peptides derived from the Australian
 CC taipan (Oxyuranus scutellatus scutellatus) snake venom Beta-taipoxin
 CC protein. The Beta-taipoxin derived peptides of the invention are useful
 CC as a medication for treating wounds (e.g. burns), as a component of a
 CC cellular growth medium, or as a beautifying agent. The present amino acid
 CC sequence represents an Australian taipan snake venom Beta-taipoxin
 CC derived peptide of the invention.
 XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 3 LNF 5

RESULT 22
 AAU85424

ID AAU85424 standard; Peptide; 5 AA.

XX AAU85424;
 AC

XX 21-MAY-2002 (first entry)
 DT

XX Human colon specific polypeptide antibody binding site #1.
 DE

XX Human; colon specific gene; CSG; cytostatic; metastasis;
 KW colon cancer staging; antibody binding site.
 KW

XX Homo sapiens.
 OS

XX WO200206515-A2.
 PN

XX 24-JAN-2002.
 PD

XX 17-JUL-2001; 2001WO-US22454.
 PF

XX 17-JUL-2000; 2000US-0618596.
 PR

XX (DIAD-) DIADEXUS INC.
 PA

XX Macina RA, Sun Y;
 PI

XX WPI; 2002-171815/22.
 DR

XX

PT Diagnosing, staging or monitoring colon cancer involves determining a
 PT colon specific gene in cells, tissues or body fluids in patient, and
 PT comparing it with levels of the gene from a normal human control -
 XX
 PS Disclosure; Page 20; 52pp; English.
 XX

XX The invention relates to diagnosing the presence of colon cancer,
 CC metastases of colon cancer, staging colon cancer, monitoring colon cancer
 CC for the onset of metastasis or monitoring a change in stage of colon
 CC cancer in a patient. The method involves determining a colon specific
 CC gene (CSG) in cells, tissues or bodily fluids and comparing it with
 CC levels of CSG in cells, tissues or bodily fluids from a normal human
 CC control. Colon cancer can be treated by administering a molecule which
 CC down regulates the expression or activity of CSG. An immune response
 CC against a target cell expressing CSG can be induced by delivering an
 CC immunologically stimulatory amount of a CSG protein to a patient, so that
 CC an immune response is mounted. Therapeutic agents are useful for imaging
 CC colon cancer in a patient by administering an agent labelled with
 CC paramagnetic ions or a radioisotope to the patient. They are also useful
 CC for preventing the onset of colon cancer, and in diagnosis and treatment
 CC of the disease. Sequences AAU85424-AAU85502 represent human colon
 CC specific protein antibody binding sites used in the method of the
 CC invention.
 XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 3 LNF 5

RESULT 23

AAU85673

ID AAR06673 standard; protein; 6 AA.

XX AAR06673;
 AC

XX 25-MAR-2003 (updated)
 DT

XX 08-JAN-1991 (first entry)
 DT

XX Retroviral protease inhibitor.
 DE

XX AIDS; HIV; ARC; antiviral therapy.
 KW

XX HIV.
 OS

XX Key Location/Qualifiers
 FH Modified-site 3..4
 FT /note="CH2-N isostere links these residues"

XX EP387231-A.
 PN

XX 12-SEP-1990.
 PD

XX 07-MAR-1990; 90EP-0870034.
 PF

XX 08-MAR-1989; 89US-0320742.
 PR

XX (UNIV) UNIV WASHINGTON.
 PA

XX Marshall GR, Toth MV;
 PI

XX WPI; 1990-277234/37.
 DR

XX Novel inhibitors of retroviral protease, partic. HIV protease -
 PT used in the treatment of AIDS.
 PT

XX Claim 4; Page 8; 9pp; English.
 PS

XX

CC Inhibitors are based on substrates for HIV protease derived from
 CC HIV-1 and HIV-2 known cleavage sites. Inhibitors are potentially
 CC useful in treatment of AIDS and AIDS related complex.
 CC The peptides carry an internal CH2-N bond isostere.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 3; DB 11; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 24
 AAR28733
 ID AAR28733 standard; peptide; 6 AA.

XX AC AAR28733;

XX DT 25-MAR-2003 (updated)
 XX DT 02-APR-1993 (first entry)

XX DE Protease chromogenic substrate #4 - to assay retroviral protease.
 XX AIDS; HIV; acquired immunodeficiency syndrome; protease; peptidase;
 XX human immunodeficiency virus; proteinase.
 XX Synthetic.

XX FH Key Location/Qualifiers
 XX FT Modified-site 3
 XX FT Modified-site /note= "p-NO2 Phe"
 XX FT Modified-site 1
 XX FT Modified-site /note= "Acetylated"

XX FN US5164300-A.

XX PD 17-NOV-1992.

XX PP 11-DEC-1990; 90US-0625395.

XX PR 28-DEC-1989; 89US-0458060.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Marshall GR, Toth MV;

XX DR WPI; 1992-407144/49.

XX PT Fluorimetric determ. of activity of retroviral protease - e.g.
 PT to isolate protease inhibitors for use as anti-AIDS agents

XX PS Disclosure; Column 6; 8pp; English.

XX CC This peptide represents a novel fluorimetric substrate for the
 CC assay of retroviral proteases (esp. that of HIV). It can be used to
 CC screen for retroviral protease inhibitors which are therapeutic
 CC possibilities in the search for AIDS drugs.
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 3; DB 13; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 25

AAW42234
 ID AAW42234 standard; Peptide; 6 AA.

XX AC AAW42234;

XX DT 08-APR-1998 (first entry)

XX DE Biotinylated S-protein 6-mer peptide ligand 12.

XX KW Bacteriophage peptide library; peptide epitope; therapeutic target;
 XX variegated compound library.

XX OS Synthetic.

XX FN WO9735194-A2.

XX PD 25-SEP-1997.

XX PP 21-MAR-1997; 97WO-US04176.

XX PR 21-MAR-1996; 96US-0622338.

XX PA (HARD) HARVARD COLLEGE.

XX PI Forster AC;

XX DR WPI; 1997-480355/44.

XX PT Identifying compounds which interact with target molecules - using
 PT enantiomers of the target molecules and testing of enantiomers of
 PT selected compounds.

XX PS Disclosure; Fig 3; 89pp; English.

XX CC 6-mer peptides AAW42223-38 are part of a peptide library. They were
 CC identified as ligands of the control target, a biotinylated S-protein,
 CC using the method of the invention. This novel method identifies
 CC compounds which interact with a target molecule, and comprises contacting
 CC a screening molecule with a variegated compound library, where the
 CC the target molecule is chiral. Compounds which have a desired
 CC interaction with the target molecule are selected, and the ability of
 CC their enantiomer to interact with the target molecule is tested. Ligands
 CC for a target protein can be identified by combining a D-enantiomer of a
 CC target protein (a D-target protein), and a variegated compound library,
 CC and then selecting one or more compounds from the library which have a
 CC desired binding interaction with the D-target protein. The methods can
 CC be used for identifying agonists or antagonists of targets such as
 CC receptors, enzymes, DNA binding proteins or signal transduction
 CC proteins. The methods can provide a structurally selective
 CC approach in addition to scoring for interaction of functional groups.
 CC They provide a powerful selection method that allows for the production
 CC of ligands with the same diversity as peptides but with the greatly
 CC improved pharmacokinetic profiles needed for drug activity.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 3; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 26
 AAW54253
 ID AAW54253 standard; peptide; 6 AA.
 XX

AC AAW54253;
 XX
 DT 30-JUL-1998 (first entry)
 XX
 DE Acylated peptide cytolytic peptide inhibitor (b).
 XX
 KW Inhibition; melittin; dimeric; melittin-induced haemolysis; lysis;
 KW CEM T cell lymphoma.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site /note= "N-terminal acetyl"
 FT Modified-site 6
 FT Modified-site /note= "C-terminal amide"
 XX
 PN WO9806743-A1.
 XX
 XX 19-FEB-1998.
 XX
 XX 13-AUG-1997; 97WO-AU00511.
 XX
 XX 13-AUG-1996; 96AU-0001611.
 XX
 XX (BIOM-) BIOMOLECULAR RES INST.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 XX Baell J, Curtain CC, Hewish DR, Matthews BR, Rivett DE;
 PI Werkmeister J;
 XX
 XX WPI; 1998-168791/15.
 XX
 XX New acylated peptide compounds - are capable of inhibiting cytolytic
 PT compounds, and may thus be used in inhibiting melittin-induced
 PT haemolysis
 XX
 PS Claim 16; Page 22; 34pp; English.
 XX
 XX Acylated peptides (AAW54242-W54260) inhibit cytolytic peptides such as
 CC melittin. They may be incorporated into, or conjugated to, larger
 CC molecules which retain the activity of the above compounds/peptides.
 CC They may, for example, be in dimeric form and may be used, e.g. to
 CC inhibit melittin-induced haemolysis and melittin-induced lysis of CEM T
 CC cell lymphoma cells.
 XX
 SQ Sequence 6 AA;
 XX
 Query Match 100.0%; Score 3; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 Db 3 LNF 5
 XX
 RESULT 27
 AAY15740
 ID AAY15740 standard; Peptide; 6 AA.
 XX
 AC AAY15740;
 XX
 XX 27-JUL-1999 (first entry)
 DT
 XX
 DE Peptide used to make fluorescent reporter molecules.
 XX
 KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;
 KW chemotherapeutic agent; cell death; viral protease activity.
 XX
 OS Synthetic.
 XX

PN WO9918856-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 09-OCT-1998; 98WO-US21231.
 XX
 PR 03-MAR-1998; 98US-0033661.
 PR 10-OCT-1997; 97US-0061582.
 XX
 PA (CYTO-) CYTOVIA INC.
 XX
 PI Cai SX, Drewe JA, Keana JFW, Weber B, Zhang H;
 DR WPI; 1999-312448/26.
 XX
 PT New fluorogenic or fluorescent reporter molecules
 XX
 PS Claim 39; Page 193; 202pp; English.
 XX
 XX AAY15618-V15759 represent peptides used to make the fluorogenic or
 CC fluorescent reporter molecules of the invention. These molecules
 CC contain a peptide moiety (e.g. present sequence) which acts as a
 CC substrate for enzymes involved in apoptosis or protease or peptidase
 CC enzymes. The compounds can be used as fluorogenic or fluorescent
 CC substrates for enzymes. Depending on the peptide moiety used, the
 CC fluorescent molecules can be used for detecting or measuring the
 CC activity of an enzyme involved in the apoptosis cascade in cells; to
 CC determine whether a test compound has an effect on an enzyme involved
 CC in the apoptosis cascade in cells; for determining the sensitivity of
 CC an animal with cancer to treatment with chemotherapeutic agents or
 CC determining whether a test substance inhibits, prevents, causes or
 CC enhances cell death of test cells; for detecting or measuring the
 CC activity of a viral protease in cells; for determining whether a test
 CC compound has an effect on the activity of a viral protease in cells;
 CC and for measuring the activity or determining whether a test substance
 CC has an effect on the activity of a protease or peptidase in cells.
 XX
 SQ Sequence 6 AA;
 XX
 Query Match 100.0%; Score 3; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 Db 2 LNF 4
 XX
 RESULT 28
 AAY15698
 ID AAY15698 standard; Peptide; 6 AA.
 XX
 AC AAY15698;
 XX
 XX 27-JUL-1999 (first entry)
 DT
 XX
 DE Peptide used to make fluorescent reporter molecules.
 XX
 KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;
 KW chemotherapeutic agent; cell death; viral protease activity.
 XX
 OS Synthetic.
 XX
 PN WO9918856-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 09-OCT-1998; 98WO-US21231.
 XX
 PR 03-MAR-1998; 98US-0033661.
 PR 10-OCT-1997; 97US-0061582.
 XX

PA (CYTO-) CYTOVIA INC.
XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;
XX WPI; 1999-312448/26.
DR
XX New fluorogenic or fluorescent reporter molecules
PT
XX Disclosure; Page 181; 202pp; English.
PS
XX
CC AAY15618-Y15759 represent peptides used to make the fluorogenic or
CC fluorescent reporter molecules of the invention. These molecules
CC contain a peptide moiety (e.g. present sequence) which acts as a
CC substrate for enzymes involved in apoptosis or protease or peptidase
CC enzymes. The compounds can be used as fluorogenic or fluorescent
CC substrates for enzymes. Depending on the peptide moiety used, the
CC fluorescent molecules can be used for detecting or measuring the
CC activity of an enzyme involved in the apoptosis cascade in cells; to
CC determine whether a test compound has an effect on an enzyme involved
CC in the apoptosis cascade in cells; for determining the sensitivity of
CC an animal with cancer to treatment with chemotherapeutic agents or
CC determining whether a test substance inhibits, prevents, causes or
CC enhances cell death of test cells; for detecting or measuring the
CC activity of a viral protease in cells; for determining whether a test
CC compound has an effect on the activity of a viral protease in cells;
CC and for measuring the activity or determining whether a test substance
CC has an effect on the activity of a protease or peptidase in cells.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 3; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db |||
2 LNF 4
RESULT 29
AAY15700
ID AAY15700 standard; Peptide; 6 AA.
XX
AC AAY15700;
XX
DT 27-JUL-1999 (first entry)
DE Peptide used to make fluorescent reporter molecules.
XX
KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;
KW apoptosis; protease; peptidase; apoptosis cascade; cancer;
KW chemotherapeutic agent; cell death; viral protease activity.
XX
OS Synthetic.
XX
PN WO9918856-A1.
XX
XX 22-APR-1999.
XX
XX 09-OCT-1998; 98WO-US21231.
PF
XX 03-MAR-1998; 98US-0033661.
PR
XX 10-OCT-1997; 97US-0061582.
XX
PA (CYTO-) CYTOVIA INC.
XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;
XX WPI; 1999-312448/26.
DR
XX New fluorogenic or fluorescent reporter molecules
PT
XX Disclosure; Page 182; 202pp; English.

XX
CC AAY15618-Y15759 represent peptides used to make the fluorogenic or
CC fluorescent reporter molecules of the invention. These molecules
CC contain a peptide moiety (e.g. present sequence) which acts as a
CC substrate for enzymes involved in apoptosis or protease or peptidase
CC enzymes. The compounds can be used as fluorogenic or fluorescent
CC substrates for enzymes. Depending on the peptide moiety used, the
CC fluorescent molecules can be used for detecting or measuring the
CC activity of an enzyme involved in the apoptosis cascade in cells; to
CC determine whether a test compound has an effect on an enzyme involved
CC in the apoptosis cascade in cells; for determining the sensitivity of
CC an animal with cancer to treatment with chemotherapeutic agents or
CC determining whether a test substance inhibits, prevents, causes or
CC enhances cell death of test cells; for detecting or measuring the
CC activity of a viral protease in cells; for determining whether a test
CC compound has an effect on the activity of a viral protease in cells;
CC and for measuring the activity or determining whether a test substance
CC has an effect on the activity of a protease or peptidase in cells.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 3; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db |||
1 LNF 3
RESULT 30
AAY80852
ID AAY80852 standard; peptide; 6 AA.
XX
AC AAY80852;
XX
DT 22-MAY-2000 (first entry)
DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:81.
XX
KW Protease substrate; fluorescent label; fluorophore; rhodamine;
KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;
KW methionine aminopeptidase type 2; MetAP-2; drug screening.
XX
OS Synthetic.
XX
PN WO200004914-A1.
XX
PD 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-US16423.
XX
PR 21-JUL-1998; 98US-0093642.
XX
PA (CYTO-) CYTOVIA INC.
PA (ZHAN/) ZHANG H.
PA (CAIS/) CAI S X.
PA (DREW/) DREWE J A.
PA (YANG/) YANG W.
XX
PI Zhang H, Cai SX, Drewe JA, Yang W;
XX WPI; 2000-195079/17.
DR
XX New fluorescently labeled amino acids or peptides, used as substrates
PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
PT agents, contains a halobenzoyl N-blocking group -
XX
PS Claim 30; Page 109; 174pp; English.
XX
CC The invention relates to fluorescently labelled peptides containing
CC a halobenzoyl group on the fluorophore. They are of the structure
CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking

CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being
 CC assayed. The labelled peptides are reporters for detecting intracellular
 CC proteolytic enzymes, particularly caspases and other enzymes involved in
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
 CC cytomegalovirus and hepatitis C virus proteases); and methionine
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly useful as
 CC identify modulators of these enzymes which may be potentially useful as
 CC agents for treating conditions such as cancer, neurodegeneration,
 CC autoimmune diseases, myocardial infarction and viria infection.
 CC Modulators identified may also be used to prolong the life of cells being
 CC cultured for recombinant protein production, or to monitor the treatment
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
 CC potential anti- angiogenic or anticancer agents. Sequences
 CC AAY80782-Y80910 represent peptides, some of which are specifically
 CC claimed, which may be used in assay methods according to the invention.

XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 3; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db 2 LNF 4

RESULT 31
 AAY80854
 ID AAY80854 standard; peptide; 6 AA.
 XX
 AC AAY80854;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:83.
 XX
 KW Protease substrate; fluorescent label; fluorophore; rhodamine;
 KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;
 KW methionine aminopeptidase type 2; MetAP-2; drug screening.

XX Synthetic.
 OS
 PN WO200004914-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-US16423.
 XX
 PR 21-JUL-1998; 98US-0093642.
 XX
 PA (CYTO-) CYTOVIA INC.
 PA (ZHAN/) ZHANG H.
 PA (CAIS/) CAI S X.
 PA (DREW/) DREWE J A.
 PA (YANG/) YANG W.
 XX
 PI Zhang H, Cai SX, Drewe JA, Yang W;
 XX
 DR WPI; 2000-195079/17.
 XX

XX New fluorescently labeled amino acids or peptides, used as substrates
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
 PT agents, contains a halobenzoyl N-blocking group -
 XX
 PS Claim 30; Page 109; 174pp; English.

XX The invention relates to fluorescently labelled peptides containing
 CC a halobenzoyl group on the fluorophore. They are of the structure
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being
 CC assayed. The labelled peptides are reporters for detecting intracellular
 CC proteolytic enzymes, particularly caspases and other enzymes involved in

CC assayed. The labelled peptides are reporters for detecting intracellular
 CC proteolytic enzymes, particularly caspases and other enzymes involved in
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
 CC cytomegalovirus and hepatitis C virus proteases); and methionine
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly useful as
 CC identify modulators of these enzymes which may be potentially useful as
 CC agents for treating conditions such as cancer, neurodegeneration,
 CC autoimmune diseases, myocardial infarction and viria infection.
 CC Modulators identified may also be used to prolong the life of cells being
 CC cultured for recombinant protein production, or to monitor the treatment
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
 CC potential anti- angiogenic or anticancer agents. Sequences
 CC AAY80782-Y80910 represent peptides, some of which are specifically
 CC claimed, which may be used in assay methods according to the invention.

XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 3; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db 1 LNF 3

RESULT 32
 AAY80894
 ID AAY80894 standard; peptide; 6 AA.
 XX
 AC AAY80894;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:123.
 XX
 KW Protease substrate; fluorescent label; fluorophore; rhodamine;
 KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;
 KW methionine aminopeptidase type 2; MetAP-2; drug screening.

XX Synthetic.
 OS
 PN WO200004914-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-US16423.
 XX
 PR 21-JUL-1998; 98US-0093642.
 XX
 PA (CYTO-) CYTOVIA INC.
 PA (ZHAN/) ZHANG H.
 PA (CAIS/) CAI S X.
 PA (DREW/) DREWE J A.
 PA (YANG/) YANG W.
 XX
 PI Zhang H, Cai SX, Drewe JA, Yang W;
 XX
 DR WPI; 2000-195079/17.
 XX
 PT New fluorescently labeled amino acids or peptides, used as substrates
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
 PT agents, contains a halobenzoyl N-blocking group -
 XX
 PS Claim 29; Page 109; 174pp; English.

XX The invention relates to fluorescently labelled peptides containing
 CC a halobenzoyl group on the fluorophore. They are of the structure
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being
 CC assayed. The labelled peptides are reporters for detecting intracellular
 CC proteolytic enzymes, particularly caspases and other enzymes involved in

CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
 CC cytomegalovirus and hepatitis C virus proteases); and methionine
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to
 CC identify modulators of these enzymes which may be potentially useful as
 CC agents for treating conditions such as cancer, neurodegeneration,
 CC autoimmune diseases, myocardial infarction and viral infection.
 CC Modulators identified may also be used to prolong the life of cells being
 CC cultured for recombinant protein production, or to monitor the treatment
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
 CC potential anti-angiogenic or anticancer agents. Sequences
 CC RAY80782-Y80910 represent peptides, some of which are specifically
 CC claimed, which may be used in assay methods according to the invention.

XX Sequence 6 AA;

SQ Query Match 100.0%; Score 3; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 Db 2 LNF 4

RESULT 33

AAR06674
 ID AAR06674 standard; protein; 7 AA.

XX AAR06674;

XX 25-MAR-2003 (updated)
 DT 08-JAN-1991 (first entry)

XX Retroviral protease inhibitor.

XX AIDS; HIV; ARC; antiviral therapy.

XX HIV.

XX Key Location/Qualifiers
 FT Modified-site 4..5
 FT /note="CH2-N isostere links these residues"

XX EP387231-A.

XX 12-SEP-1990.

XX 07-MAR-1990; 90EP-0870034.

XX 08-MAR-1989; 89US-0320742.

XX (UNIW) UNIV WASHINGTON.

XX Marshall GR, Toth MV;

XX WPI; 1990-277234/37.

XX Novel inhibitors of retroviral protease, partic. HIV protease -
 PT used in the treatment of AIDS.

XX Claim 4; Page 8; 9pp; English.

XX Inhibitors are based on substrates for HIV protease derived from
 CC HIV-1 and HIV-2 known cleavage sites. Inhibitors are potentially
 CC useful in treatment of AIDS and AIDS related complex.
 CC The peptides carry an internal CH2-N bond isostere.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 3; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 Db 2 LNF 4

RESULT 34

AAR12883
 ID AAR12883 standard; Protein; 7 AA.

XX AAR12883;

XX 25-MAR-2003 (updated)
 DT 17-SEP-1991 (first entry)

XX HIV protease inhibiting variant (2).

XX HIV; protease; inhibition.

XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 1
 FT /label= N-acetyl-O-benzylSer
 FT Modified-site 7
 FT /label= Val methyl ester
 FT Modified-site 4
 FT /label= amino-2-hydroxy-4-Phe
 FT Modified-site 4..5
 FT /label= Phe(CHOCH2N) Pro

XX WO9108221-A.

XX 13-JUN-1991.

XX 03-DEC-1990; 90NO-US07059.

XX 04-DEC-1989; 89US-0445070.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Rich DH, Green J, Sun C;

XX WPI; 1991-193150/26.

XX New HIV protease inhibiting variant peptide(s) - are potential
 PT drugs for human immune deficiency virus infected patient(s)

XX Example 5.2; Page 12; 30 pp; English.

XX The peptide variant preferentially binds to HIV protease so as to
 CC inhibit its activity. The amino-alcohol variants of the protease's
 CC pref. binding site are incorporated in the peptide backbone to
 CC preferentially bind and occupy the protease.
 CC The peptides are built out from a core which is the ketone precursor
 CC of the amino-alcohol. The leucine variant or phenyl variant are pref.
 CC A series of amino acids are linked on one side of the core to build
 CC half the peptide. Separately the other half of the peptide is
 CC built up. Then the two halves are coupled together and the alcohol
 CC formed. See also AAR12882-86.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 3; DB 12; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 Db 2 LNF 4

```
RESULT 35
AAW80253
ID AAR65689 standard; peptide; 7 AA.
XX
AC AAR65689;
XX
XX 25-MAR-2003 (updated)
DT 08-JAN-1995 (first entry)
XX
DE HIV-1 inhibiting pseudopeptide.
XX
KW Aspartic proteinase; reversible inhibitor; pseudopeptide;
KW phosphinate methylene ammonium group; exploding transition analogue;
KW HIV-1.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Misc-difference 2 /note= "Acetyl-Ser or hexanoyl-Ser"
FT FT
FT /note= "can also be D-Leu when Ser(1) is acetyl-Ser"
FT Modified-site 4..5
FT /note= "CONH linkage replaced by P(O) (OH)CH2NH"
FT Modified-site 7
FT /note= "Val-OCH3"
FT FT
XX WO9314114-A1.
PN
XX
XX 22-JUL-1993.
PD
XX
XX 11-JAN-1993; 93WO-US00228.
PF
XX
XX 09-JAN-1992; 92US-0819356.
PR
XX
XX (SCRI ) SCRIPPS RES INST.
PA
XX Ikeda S, Janda KD, Wirsching P;
PI
XX WPI; 1993-243142/30.
DR
XX
XX New peptide linkage unit - comprising phosphinate methylene
PT ammonium gp., esp. for pseudo-peptide aspartic proteinase
PT inhibitors
PT
XX
XX Claims 31-33; Pages 69,70; 76pp; English.
PS
XX
XX The invention relates to a phosphinic acid methylene amine linkage
CC PO(OH)CH2NH to be used in place of a peptide linkage CONH at the
CC cleavage site in an aspartic proteinase substrate. The linkage is
CC resistant to cleavage and serves as an exploding transition state
CC analogue of the cleavage site. Thus the peptide containing it can
CC bind or interfere with the active site of the aspartic proteinase
CC enzyme and inhibit its activity.
CC The present sequence is a specifically claimed example of a
CC HIV-1 inhibiting peptide containing the linkage.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 14; Length 7;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db |||
2 LNF 4
RESULT 36
AAW80253
ID AAW80253 standard; peptide; 7 AA.
XX
```

```
AC AAW80253;
XX
XX 06-JAN-1999 (first entry)
DT
XX
DE Oxirane compound which is an inhibitor of HIV-1 protease.
XX
XX Oxirane compound; human immunodeficiency virus; HIV protease inhibitor;
KW gag; pol; HIV-1 protease.
KW
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Ser is linked to CH3C(O) or C5H11C(O) "
FT Modified-site 4..5
FT /note= "these residues are linked by a pseudo
FT peptide linkage comprising 1-epoxy-ethylene"
FT Modified-site 7
FT /note= "Val is linked to OCH3"
FT FT
XX US5827827-A.
PN
XX 27-OCT-1998.
PD
XX 20-JUN-1996; 96US-0667001.
PF
XX 20-JUN-1996; 96US-0667001.
PR 16-FEB-1995; 95US-0335039.
PR
XX (SCRI ) SCRIPPS RES INST.
PA
XX Janda KD, Wirsching P;
PI
XX WPI; 1998-594033/50.
DR
XX
XX Oxirane compounds e.g. oxirane-substituted oligo-peptide(s) - used
PT as human immunodeficiency virus protease inhibitors
PT
XX Disclosure; Column 9; 29pp; English.
PS
XX
XX The present sequence is part of an oxirane compound which acts as a
CC human immunodeficiency virus (HIV) protease inhibitor. The compounds
CC have a terminal epoxide moiety. The compounds inhibit HIV protease
CC and the cleavage of gag and gag pol polyproteins of HIV by HIV-1
CC protease.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 19; Length 7;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db |||
2 LNF 4
RESULT 37
AAV15697
ID AAV15697 standard; Peptide; 7 AA.
XX
XX AAV15697;
AC
XX 27-JUL-1999 (first entry)
DT
XX
XX Peptide used to make fluorescent reporter molecules.
XX
XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;
KW apoptosis; protease; peptidase; apoptosis cascade; cancer;
KW chemotherapeutic agent; cell death; viral protease activity.
XX
XX Synthetic.
OS
XX
```

PN WO9918856-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 09-OCT-1998; 98WO-US21231.
 XX
 PR 03-MAR-1998; 98US-0033661.
 PR 10-OCT-1997; 97US-0061582.
 XX
 PA (CYTO-) CYTOVIA INC.
 XX
 PI Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;
 XX WPI; 1999-312448/26.
 XX
 PT New fluorogenic or fluorescent reporter molecules
 XX
 PS Disclosure; Page 181; 202pp; English.
 XX
 CC AAY15618-Y15759 represent peptides used to make the fluorogenic or
 CC fluorescent reporter molecules of the invention. These molecules
 CC contain a peptide moiety (e.g. present sequence) which acts as a
 CC substrate for enzymes involved in apoptosis or protease or peptidase
 CC enzymes. The compounds can be used as fluorogenic or fluorescent
 CC substrates for enzymes. Depending on the peptide moiety used, the
 CC fluorescent molecules can be used for detecting or measuring the
 CC activity of an enzyme involved in the apoptosis cascade in cells; to
 CC determine whether a test compound has an effect on an enzyme involved
 CC in the apoptosis cascade in cells; for determining the sensitivity of
 CC an animal with cancer to treatment with chemotherapeutic agents or
 CC determining whether a test substance inhibits, prevents, causes or
 CC enhances cell death of test cells; for detecting or measuring the
 CC activity of a viral protease in cells; for determining whether a test
 CC compound has an effect on the activity of a viral protease in cells;
 CC and for measuring the activity or determining whether a test substance
 CC has an effect on the activity of a protease or peptidase in cells.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 3; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db |||
 2 LNF 4
 RESULT 38
 AAY15651
 ID AAY15651 standard; Peptide; 7 AA.
 XX
 AC AAY15651;
 XX
 DT 27-JUL-1999 (first entry)
 XX
 DE Peptide used to make fluorescent reporter molecules.
 XX
 KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;
 KW chemotherapeutic agent; cell death; viral protease activity.
 XX
 OS Synthetic.
 XX
 PN WO9918856-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 09-OCT-1998; 98WO-US21231.
 XX
 PR 03-MAR-1998; 98US-0033661.
 PR 10-OCT-1997; 97US-0061582.
 XX

PA (CYTO-) CYTOVIA INC.
 XX
 PI Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;
 XX WPI; 1999-312448/26.
 XX
 PT New fluorogenic or fluorescent reporter molecules
 XX
 PS Claim 39; Page 169; 202pp; English.
 XX
 CC AAY15618-Y15759 represent peptides used to make the fluorogenic or
 CC fluorescent reporter molecules of the invention. These molecules
 CC contain a peptide moiety (e.g. present sequence) which acts as a
 CC substrate for enzymes involved in apoptosis or protease or peptidase
 CC enzymes. The compounds can be used as fluorogenic or fluorescent
 CC substrates for enzymes. Depending on the peptide moiety used, the
 CC fluorescent molecules can be used for detecting or measuring the
 CC activity of an enzyme involved in the apoptosis cascade in cells; to
 CC determine whether a test compound has an effect on an enzyme involved
 CC in the apoptosis cascade in cells; for determining the sensitivity of
 CC an animal with cancer to treatment with chemotherapeutic agents or
 CC determining whether a test substance inhibits, prevents, causes or
 CC enhances cell death of test cells; for detecting or measuring the
 CC activity of a viral protease in cells; for determining whether a test
 CC compound has an effect on the activity of a viral protease in cells;
 CC and for measuring the activity or determining whether a test substance
 CC has an effect on the activity of a protease or peptidase in cells.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 3; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db |||
 2 LNF 4
 RESULT 39
 AAY85415
 ID AAY85415 standard; peptide; 7 AA.
 XX
 AC AAY85415;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Drosophila Rag protein fragment.
 XX
 KW HERG; mutation; long QT syndrome; LQT syndrome; gene therapy; eag.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200006772-A1.
 XX
 PD 10-FEB-2000.
 XX
 PF 20-JUL-1999; 99WO-US16337.
 XX
 PR 27-JUL-1998; 98US-0122847.
 PR 06-JAN-1999; 99US-0226012.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Keating MT, Splawski I;
 XX WPI; 2000-195319/17.
 XX
 PT New isolated mutant HERG nucleic acids, useful for developing products
 XX for the diagnosis, prevention and treatment of long QT syndrome -
 PS Disclosure; Fig 12H; 163pp; English.
 XX

CC The invention relates to a HERG protein having a mutation compared to
 CC wild-type HERG, and is useful for developing products for the diagnosis,
 CC prevention and treatment of long QT (LQT) syndrome. The products and
 CC methods can be used for the diagnosis of subjects with LQT syndrome.
 CC They can also be used to screen for drugs for treating or preventing LQT
 CC syndrome. The HERG nucleic acids can also be used for gene therapy and
 CC HERG peptides can be used for peptide therapy. Sequences AAY85407-421
 CC represents regions of HERG from humans, mouse, rat and drosophila.
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 40
 AAY85416
 ID AAY85416 standard; peptide; 7 AA.
 XX
 AC AAY85416;

XX 19-JUN-2000 (first entry)
 DT
 XX Elk protein fragment.
 DE
 XX
 XX

KW HERG; mutation; long QT syndrome; LQT syndrome; gene therapy; elk.
 XX

OS Unidentified.
 XX
 PN WO200006772-A1.
 XX

PD 10-FEB-2000.

XX 20-JUL-1999; 99WO-US16337.

PR 27-JUL-1998; 98US-0122847.

PR 06-JAN-1999; 99US-0226012.

XX (UTAH) UNIV UTAH RES FOUND.

XX Keating MT, Splawski I;

XX WPI; 2000-195319/17.

XX New isolated mutant HERG nucleic acids, useful for developing products
 PT for the diagnosis, prevention and treatment of long QT syndrome -
 PT

PS Disclosure; Fig 12H; 163pp; English.

XX The invention relates to a HERG protein having a mutation compared to
 CC wild-type HERG, and is useful for developing products for the diagnosis,
 CC prevention and treatment of long QT (LQT) syndrome. The products and
 CC methods can be used for the diagnosis of subjects with LQT syndrome.
 CC They can also be used to screen for drugs for treating or preventing LQT
 CC syndrome. The HERG nucleic acids can also be used for gene therapy and
 CC HERG peptides can be used for peptide therapy. Sequences AAY85407-421
 CC represents regions of HERG from humans, mouse, rat and drosophila.
 XX

SQ Sequence 7 AA;
 Query Match 100.0%; Score 3; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 41

AAY80815
 ID AAY80815 standard; peptide; 7 AA.

XX AAY80815;

XX 22-MAY-2000 (first entry)

DE Fluorophore-labelled HIV protease substrate peptide, SEQ ID NO:34.

XX Protease substrate; fluorescent label; fluorophore; rhodamine;

KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;

XX methionine aminopeptidase type 2; MetAP-2; drug screening.

XX Synthetic.

XX WO200004914-A1.

XX 03-FEB-2000.

XX 21-JUL-1999; 99WO-US16423.

XX 21-JUL-1998; 98US-0093642.

XX (CYTO-) CYTOVIA INC.

XX (ZHAN/) ZHANG H.

XX (CAIS/) CAI S X.

XX (DREW/) DREW J A.

XX (YANG/) YANG W.

XX Zhang H, Cai SX, Drewe JA, Yang W;

XX WPI; 2000-195079/17.

XX New fluorescently labeled amino acids or peptides, used as substrates
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
 PT agents, contains a halobenzoyl N-blocking group -

PS Claim 29; Page 108; 174pp; English.

XX The invention relates to fluorescently labelled peptides containing
 CC a halobenzoyl group on the fluorophore. They are of the structure
 CC peptide-V-Z, where Z represents a halo-substituted benzoyl blocking
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being
 CC assayed. The labelled peptides are reporters for detecting intracellular
 CC proteolytic enzymes, particularly caspases and other enzymes involved in
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
 CC cytomegalovirus and hepatitis C virus proteases); and methionine
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to
 CC identify modulators of these enzymes which may be potentially useful as
 CC agents for treating conditions such as cancer, neurodegeneration,
 CC autoimmune diseases, myocardial infarction and viral infection.
 CC Modulators identified may also be used to prolong the life of cells being
 CC cultured for recombinant protein production, or to monitor the treatment
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
 CC potential anti- angiogenic or anticancer agents. Sequences
 CC AAY80782-Y80910 represent peptides, some of which are specifically
 CC claimed, which may be used in assay methods according to the invention.

XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 3; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

|||

Db 2 LNF 4

RESULT 42

KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 XX infection.
 OS Viridiae.
 XX
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 7 /note= "N-terminal is substituted by Ac"
 FT Modified-site 7 /note= "C-terminal amide"
 XX
 XX WO200164013-A2.
 PN
 XX
 XX 07-SEP-2001.
 PD
 XX
 XX 07-FEB-2001; 2001WO-US03988.
 PF
 XX 29-FEB-2000; 2000US-0515965.
 PR
 XX (TRIM-) TRIMERIS INC.
 PA
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
 PI WPI; 2001-514829/56.
 XX
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus
 PT infection -
 XX
 XX Disclosure; Page 55; 587pp; English.
 PS
 XX The invention relates to isolated analogues of the heptad repeat region
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1
 CC and HR2 regions of proteins interact non-covalently with each other
 CC and/or with peptides derived from them. This interaction is required for
 CC normal infectivity of viruses such as RSV and HIV. The heptad
 CC repeat region peptide analogues may be used to inhibit respiratory
 CC repeat region peptide analogues may be used to inhibit respiratory
 CC syncytial virus (RSV) infection in a cell. They may also be used to
 CC inhibit HIV infection. The present sequence is a peptide provided in
 CC the specification.
 XX
 XX SQ Sequence 7 AA;
 PS
 XX Query Match 100.0%; Score 3; DB 22; Length 7;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 LNF 3
 DB |||
 DB 1 LNF 3
 XX
 XX RESULT 45
 ABB02538
 ID ABB02538 standard; Peptide; 7 AA.
 AC
 XX ABB02538;
 XX
 XX 03-JAN-2002 (first entry)
 DT
 XX
 XX Viral core polypeptide, SEQ ID NO: 1065.
 DE
 XX
 XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 KW infection.
 XX
 XX Viridiae.
 OS
 XX WO200164013-A2.
 PN
 XX 07-SEP-2001.
 PD

XX 07-FEB-2001; 2001WO-US03988.
 PF
 XX 29-FEB-2000; 2000US-0515965.
 PR
 XX (TRIM-) TRIMERIS INC.
 PA
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
 PI WPI; 2001-514829/56.
 XX
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus
 PT infection -
 XX
 XX Disclosure; Page 448; 587pp; English.
 PS
 XX The invention relates to isolated analogues of the heptad repeat region
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1
 CC and HR2 regions of proteins interact non-covalently with each other
 CC and/or with peptides derived from them. This interaction is required for
 CC normal infectivity of viruses such as RSV and HIV. The heptad
 CC repeat region peptide analogues may be used to inhibit respiratory
 CC syncytial virus (RSV) infection in a cell. They may also be used to
 CC inhibit HIV infection. The present sequence is a peptide provided in
 CC the specification.
 XX
 XX SQ Sequence 7 AA;
 PS
 XX Query Match 100.0%; Score 3; DB 22; Length 7;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 LNF 3
 DB |||
 DB 1 LNF 3
 XX
 XX RESULT 46
 AAU13635
 ID AAU13635 standard; Peptide; 7 AA.
 AC
 XX AAU13635;
 XX
 XX 21-NOV-2001 (first entry)
 DT
 XX
 XX DP178-like/DP107-like peptide T-1243.
 DE
 XX
 XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
 KW antitumor; antiviral; HIV transmission; mutant; mutein.
 KW
 XX Human immunodeficiency virus 1 isolate LAI.
 OS
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal is substituted by Ac"
 FT Modified-site 7 /note= "C-terminal amide"
 FT
 XX
 XX WO200151673-A2.
 PN
 XX
 XX 19-JUL-2001.
 PD
 XX
 XX 05-JUL-2000; 2000WO-US35727.
 PF
 XX
 XX 09-JUL-1999; 99US-0350841.
 PR
 XX (TRIM-) TRIMERIS INC.
 PA
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
 PI

XX WPI; 2001-442157/47.
 XX Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antitumor, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex -
 XX Disclosure; Page 74; 259pp; English.
 XX The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds
 CC to amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence
 CC and absence of a test compound, in a reaction mixture containing DP107
 CC and DP178 peptides. The method is useful for identifying compounds,
 CC including small molecule compounds, which may themselves exhibit
 CC antitumor, antiviral or intracellular modulatory activity. The
 CC DP178-like/DP107-like peptides are useful to inhibit human and non-human
 CC retroviral, particularly HIV, transmission to uninfected cells. The
 CC present sequence represents one of the DP178-like/DP107-like peptides
 CC of the invention.
 XX Sequence 7 AA;
 SQ Query Match 100.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db |||
 1 LNF 3
 RESULT 47
 AAM44074
 ID AAM44074 standard; Peptide; 7 AA.
 XX AAM44074;
 AC AAM44074;
 XX 25-OCT-2001 (first entry)
 DT H11 binding site consensus conforming peptide (CCP) #345.
 DE Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX Homo sapiens.
 OS Synthetic.
 XX CA2290722-A1.
 PN 08-JUN-2001.
 XX 08-DEC-1999; 99CA-2290722.
 PF 08-DEC-1999; 99CA-2290722.
 PR (NOVO-) NOVOPHARM BIOTECH INC.
 PA Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 XX Entwistle JM, MacDonald GC;
 PI WPI; 2001-425937/46.
 DR Composition useful for treating and diagnosing cancer, comprises stress
 XX protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -

PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 XX complex -
 PS Example 4; Page 102; 154pp; English.
 XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural,
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.
 XX Sequence 7 AA;
 SQ Query Match 100.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db |||
 4 LNF 6
 RESULT 48
 AAM44079
 ID AAM44079 standard; Peptide; 7 AA.
 XX AAM44079;
 AC AAM44079;
 XX 25-OCT-2001 (first entry)
 DT H11 binding site consensus conforming peptide (CCP) #350.
 DE Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX Homo sapiens.
 OS Synthetic.
 XX CA2290722-A1.
 PN 08-JUN-2001.
 XX 08-DEC-1999; 99CA-2290722.
 PF 08-DEC-1999; 99CA-2290722.
 PR (NOVO-) NOVOPHARM BIOTECH INC.
 PA Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 XX Entwistle JM, MacDonald GC;
 PI WPI; 2001-425937/46.
 DR Composition useful for treating and diagnosing cancer, comprises stress
 XX protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -

XX PS Example 4; Page 102; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress

XX CC protein-peptide complexes (SPPC) associated with tumours that is

XX CC specifically immunogenically cross-reactive with cell surface-associated

XX CC SPSCs specific to target cancer (TC). Also described is an isolated

XX CC antigen-binding fragment of an antibody that binds specifically to SPSCs

XX CC or a population of different SPSCs consisting of immunogenic cancer cell

XX CC surface-associated SPSC of TC. (I) has cytostatic activity and can be

XX CC used in vaccine production and as a tumour-specific immunogenic response

XX CC inducer. (I) is useful for treating 71 types of cancers or tumours in a

XX CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,

XX CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural

XX CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including

XX CC vaccines. (I) is useful for diagnostic and palliative use, for detecting

XX CC or imaging cancer cells, and to monitor the course of amelioration of

XX CC malignancy in an individual. AAM43707 to AAM47109 represent peptides

XX CC which are used in the exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 22; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

DB 4 LNF 6

RESULT 49

AAM44124

ID AAM44124 standard; Peptide; 7 AA.

XX AC AAM44124;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #395.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPSC;

XX KW immunogenically cross-reactive; cancer; immunogenic cancer cell;

XX KW cytostatic; vaccine; tumour-specific immunogenic response inducer;

XX KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;

XX KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.

XX OS Synthetic.

XX CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

XX PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX PT Composition useful for treating and diagnosing cancer, comprises stress

XX PT protein-peptide complexes associated with tumor, and isolated

XX PT antigen-binding fragments of an antibody that binds specifically to the

XX PT complex -

XX PS Example 4; Page 102; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress

XX CC protein-peptide complexes (SPPC) associated with tumours that is

XX CC specifically immunogenically cross-reactive with cell surface-associated

XX CC SPSCs specific to target cancer (TC). Also described is an isolated

XX CC antigen-binding fragment of an antibody that binds specifically to SPSCs

XX CC or a population of different SPSCs consisting of immunogenic cancer cell

XX CC surface-associated SPSC of TC. (I) has cytostatic activity and can be

XX CC used in vaccine production and as a tumour-specific immunogenic response

XX CC inducer. (I) is useful for treating 71 types of cancers or tumours in a

XX CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,

XX CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural

XX CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including

XX CC vaccines. (I) is useful for diagnostic and palliative use, for detecting

XX CC or imaging cancer cells, and to monitor the course of amelioration of

XX CC malignancy in an individual. AAM43707 to AAM47109 represent peptides

XX CC which are used in the exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 22; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

DB 4 LNF 6

RESULT 50

AAM44129

ID AAM44129 standard; Peptide; 7 AA.

XX AC AAM44129;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #400.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPSC;

XX KW immunogenically cross-reactive; cancer; immunogenic cancer cell;

XX KW cytostatic; vaccine; tumour-specific immunogenic response inducer;

XX KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;

XX KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.

XX OS Synthetic.

XX CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

XX PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX PT Composition useful for treating and diagnosing cancer, comprises stress

XX PT protein-peptide complexes associated with tumor, and isolated

XX PT antigen-binding fragments of an antibody that binds specifically to the

XX PT complex -

XX PS Example 4; Page 102; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress

XX CC protein-peptide complexes (SPPC) associated with tumours that is

XX CC specifically immunogenically cross-reactive with cell surface-associated

XX CC SPSCs specific to target cancer (TC). Also described is an isolated

XX CC antigen-binding fragment of an antibody that binds specifically to SPSCs

CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;
 Query Match 100.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 51
 AAM44134
 ID AAM44134 standard; Peptide; 7 AA.

XX AC AAM44134;
 XX DT 25-OCT-2001 (first entry)
 XX DE H11 binding site consensus conforming peptide (CCP) #405.
 XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.
 OS Synthetic.

XX CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -

XX Example 4; Page 102; 154pp; English.

XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a

CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 52
 AAM44139
 ID AAM44139 standard; Peptide; 7 AA.

XX AC AAM44139;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #410.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.

OS Synthetic.

XX CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -

XX Example 4; Page 102; 154pp; English.

XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting

CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.

XX SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 4 LNF 6

RESULT 53
AAM44144
ID AAM44144 standard; Peptide; 7 AA.
XX AC AAM44144;
XX DT 25-OCT-2001 (first entry)
XX DE H11 binding site consensus conforming peptide (CCP) #415.
XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendrogloma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.
XX PD 08-JUN-2001.
XX PF 08-DEC-1999; 99CA-2290722.
XX PR 08-DEC-1999; 99CA-2290722.
XX PA (NOVO-) NOVOPHARM BIOTECH INC.
XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX PI Entwistle JM, MacDonald GC;
XX DR WPI; 2001-425937/46.
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX Example 4; Page 102; 154pp; English.

XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendrogloma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.

XX SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 4 LNF 6

RESULT 54
AAM44194
ID AAM44194 standard; Peptide; 7 AA.
XX AC AAM44194;
XX DT 25-OCT-2001 (first entry)
XX DE H11 binding site consensus conforming peptide (CCP) #465.
XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendrogloma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.
XX PD 08-JUN-2001.
XX PF 08-DEC-1999; 99CA-2290722.
XX PR 08-DEC-1999; 99CA-2290722.
XX PA (NOVO-) NOVOPHARM BIOTECH INC.
XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX PI Entwistle JM, MacDonald GC;
XX DR WPI; 2001-425937/46.
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX Example 4; Page 102; 154pp; English.

XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendrogloma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 DB 4 LNF 6

RESULT 55
 AAM44560
 ID AAM44560 standard; Peptide; 7 AA.
 XX
 AC AAM44560;
 DT 25-OCT-2001 (first entry)
 DE H11 binding site consensus conforming peptide (CCP) #831.
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN CH2290722-A1.
 XX
 PD 08-JUN-2001.
 XX
 PF 08-DEC-1999; 99CA-2290722.
 XX
 PR 08-DEC-1999; 99CA-2290722.
 XX
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;
 XX
 DR WPI; 2001-425937/46.
 XX
 PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -
 XX
 PS Example 4; Page 104; 154pp; English.
 XX
 CC The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 DB 4 LNF 6

Db 4 LNF 6

RESULT 56
 AAM44565
 ID AAM44565 standard; Peptide; 7 AA.
 XX
 AC AAM44565;
 DT 25-OCT-2001 (first entry)
 DE H11 binding site consensus conforming peptide (CCP) #836.
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN CH2290722-A1.
 XX
 PD 08-JUN-2001.
 XX
 PF 08-DEC-1999; 99CA-2290722.
 XX
 PR 08-DEC-1999; 99CA-2290722.
 XX
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;
 XX
 DR WPI; 2001-425937/46.
 XX
 PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -
 XX
 PS Example 4; Page 104; 154pp; English.
 XX
 CC The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 DB 4 LNF 6

RESULT 57


```

AAM44570
ID AAM44570 standard; Peptide; 7 AA.
AC AAM44570;
XX
XX
DT 25-OCT-2001 (first entry)
DE H11 binding site consensus conforming peptide (CCP) #841.
XX
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-Al.
XX
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-2290722.
XX
PR 08-DEC-1999; 99CA-2290722.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex -
XX
XX Example 4; Page 104; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db 4 LNF 6
RESULT 58
AAM44575
ID AAM44575 standard; Peptide; 7 AA.
XX
XX AAM44575;

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XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #846.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-Al.
XX
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-2290722.
XX
PR 08-DEC-1999; 99CA-2290722.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex -
XX
XX Example 4; Page 104; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db 4 LNF 6
RESULT 59
AAM44661
ID AAM44661 standard; Peptide; 7 AA.
XX
XX AAM44661;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #932.

```

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendrogloma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN CA2290722-A1.
 XX
 PD 08-JUN-2001.
 XX
 PF 08-DEC-1999; 99CA-2290722.
 XX
 PR 08-DEC-1999; 99CA-2290722.
 XX
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;
 XX
 DR WPI; 2001-425937/46.
 XX
 PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -
 XX
 PS Example 4; Page 104; 154pp; English.
 XX
 CC The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumors that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendrogloma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db |||
 4 LNF 6
 RESULT 60
 AAM45665
 ID AAM45665 standard; Peptide; 7 AA.
 XX
 AC AAM45665;
 XX
 DT 25-OCT-2001 (first entry)
 XX
 DE H11 binding site consensus conforming peptide (CCP) #1936.
 XX
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendrogloma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX

KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendrogloma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN CA2290722-A1.
 XX
 PD 08-JUN-2001.
 XX
 PF 08-DEC-1999; 99CA-2290722.
 XX
 PR 08-DEC-1999; 99CA-2290722.
 XX
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;
 XX
 DR WPI; 2001-425937/46.
 XX
 PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -
 XX
 PS Example 4; Page 107; 154pp; English.
 XX
 CC The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumors that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendrogloma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db |||
 4 LNF 6
 RESULT 61
 AAM45884
 ID AAM45884 standard; Peptide; 7 AA.
 XX
 AC AAM45884;
 XX
 DT 25-OCT-2001 (first entry)
 XX
 DE H11 binding site consensus conforming peptide (CCP) #2155.
 XX
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendrogloma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX
 OS Homo sapiens.


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PR 08-DEC-1999; 99CA-2290722.
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
FI Entwistle JM, MacDonald GC;
XX
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
XX complex -
XX
XX Example 4; Page 109; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumors that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPCCs
CC or a population of different SPCCs consisting of immunogenic cancer cell
CC surface-associated SPCC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
4 LNF 6

RESULT 64
AAM46416
ID AAM46416 standard; Peptide; 7 AA.
XX
XX AAM46416;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #2687.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX

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PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
XX complex -
XX
XX Example 4; Page 110; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumors that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPCCs
CC or a population of different SPCCs consisting of immunogenic cancer cell
CC surface-associated SPCC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
4 LNF 6

RESULT 65
AAM46609
ID AAM46609 standard; Peptide; 7 AA.
XX
XX AAM46609;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #2880.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX

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XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX Example 4; Page 111; 154pp; English.
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LNF 3
Db 4 LNF 6
RESULT 66
AAM46895
ID AAM46895 standard; Peptide; 7 AA.
XX AC AAM46895;
XX 25-OCT-2001 (first entry)
XX H11 binding site consensus conforming peptide (CCP) #3166.
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX Homo sapiens.
XX Synthetic.
XX CA2290722-A1.
XX 08-JUN-2001.
XX 08-DEC-1999; 99CA-2290722.
XX 08-DEC-1999; 99CA-2290722.
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the

PT complex -
XX Example 4; Page 112; 154pp; English.
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LNF 3
Db 4 LNF 6
RESULT 67
AAB78082
ID AAB78082 standard; Peptide; 7 AA.
XX AC AAB78082;
XX 19-APR-2001 (first entry)
XX Core polypeptide T1243.
XX Core polypeptide; enhancer; antiviral; anti-HIV;
XX virucide; hepatotropic; antiinflammatory; hybrid polypeptide;
XX coiled-coil peptide interaction; fusion-related disorder;
XX bacterial infection; viral infection.
XX Unidentified.
XX W0200103723-A1.
XX 18-JAN-2001.
XX 10-JUL-2000; 2000WO-US18772.
XX 09-JUL-1999; 99US-0350641.
XX (TRIM-) TRIMERIS INC.
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2001-147136/15.
XX New hybrid polypeptides, useful for preventing, treating and diagnosing
XX e.g. viral infections, comprises an enhancer peptide linked to a core
XX polypeptide -
XX Disclosure; Page 55; 151pp; English.
XX The present sequence is a core polypeptide which may be linked to
XX an enhancer peptide to form a novel hybrid polypeptide. The hybrid
XX polypeptide exhibits enhanced pharmacokinetic properties relative to
XX those exhibited by the core polypeptide when introduced into a living

CC system. It is used to increase the in vitro or ex vivo half-life of
 CC the core polypeptide. The hybrid and core polypeptides can be used for
 CC modulating fusogenic events and intracellular processes involving
 CC coiled-coil peptide interactions. Other uses include preventing,
 CC treating and/or diagnosing disorders involving fusion events (e.g.
 CC modulation of neurotransmitter exchange and sperm-egg fusion).
 CC intracellular processes involving coiled-coil peptides (e.g. bacterial
 CC infections) and viral infections that involve cell-cell and/or
 CC virus-cell fusion (e.g. viral infections caused by human
 CC immunodeficiency virus, respiratory syncytial virus, Epstein-Barr
 CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).
 CC The enhancer peptide sequence increases the half-life and reduces the
 CC clearance rate of therapeutic peptides, which increases their efficacy
 CC and minimises the incidence and severity of adverse side effects.
 CC In addition, this increases the sensitivity of the diagnostic procedure
 CC in which they are used.

XX Sequence 7 AA;
 SQ Query Match 100.0%; Score 3; DB 22; Length 7;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3
 DB 1 LNF 3

RESULT 68
 ABJ37364
 ID ABJ37364 standard; Peptide; 7 AA.

XX AC ABJ37364;

XX DT 08-MAY-2003 (first entry)

XX DE G-protein coupled receptor peptide region #76.

XX KW Compound library; microenvironment; G-protein Coupled Receptor; GPCR.

XX OS Unidentified.

XX PN WO2003004147-A2.

XX PD 16-JAN-2003.

XX PF 05-JUL-2002; 2002WO-GB03094.

XX PR 06-JUL-2001; 2001GB-0016570.

XX PA (BIOF-) BIOFOCUS PLC.

XX PI Crossley R, Rose VS, Stevens AP;

XX DR WPI; 2003-221549/21.

XX PT Producing compound library, by generating biological target model using
 CC target sequence information, defining microenvironments interacting
 CC with ligand and motifs interacting with microenvironment, and
 CC assembling motifs -

XX PS Disclosure; Fig 3; 39pp; English.

XX The invention relates to a novel method for producing a compound library.
 CC The novel method involves reducing a biological target into a group of
 CC one or more amino acids required for interaction with a ligand, to
 CC generate a model of the biological target, using the model to define a
 CC microenvironment in the biological target capable of interacting with the
 CC ligand, defining motifs which interact with the microenvironment, and
 CC assembling the motifs to generate a compound library for screening.
 CC The novel method is useful to produce a compound libraries for screening
 CC natural ligands such as peptides and proteins or for producing chemical
 CC compounds based on drug motifs for screening. This sequence represents a

CC peptide of a G-protein Coupled Receptor (GPCR), which relates to the
 CC novel compound library production method of the invention.

XX Sequence 7 AA;

XX Query Match 100.0%; Score 3; DB 24; Length 7;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3
 DB 5 LNF 7

RESULT 69
 ABJ37444
 ID ABJ37444 standard; Peptide; 7 AA.

XX AC ABJ37444;

XX DT 08-MAY-2003 (first entry)

XX DE G-protein coupled receptor endothelin ET-A receptor peptide #76.

XX KW Compound library; microenvironment; G-protein Coupled Receptor; GPCR.

XX OS Unidentified.

XX PN WO2003004147-A2.

XX PD 16-JAN-2003.

XX PF 05-JUL-2002; 2002WO-GB03094.

XX PR 06-JUL-2001; 2001GB-0016570.

XX PA (BIOF-) BIOFOCUS PLC.

XX PI Crossley R, Rose VS, Stevens AP;

XX DR WPI; 2003-221549/21.

XX PT Producing compound library, by generating biological target model using
 CC target sequence information, defining microenvironments interacting
 CC with ligand and motifs interacting with microenvironment, and
 CC assembling motifs -

XX PS Disclosure; Fig 7; 39pp; English.

XX The invention relates to a novel method for producing a compound library.
 CC The novel method involves reducing a biological target into a group of
 CC one or more amino acids required for interaction with a ligand, to
 CC generate a model of the biological target, using the model to define a
 CC microenvironment in the biological target capable of interacting with the
 CC ligand, defining motifs which interact with the microenvironment, and
 CC assembling the motifs to generate a compound library for screening.
 CC The novel method is useful to produce compound libraries for screening
 CC natural ligands such as peptides and proteins or for producing chemical
 CC compounds based on drug motifs for screening. This sequence represents a
 CC peptide of a G-protein Coupled Receptor (GPCR) including Endothelin ET-A
 CC receptor, which relates to the novel compound library production method
 CC of the invention.

XX Sequence 7 AA;

XX Query Match 100.0%; Score 3; DB 24; Length 7;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3
 DB 5 LNF 7

RESULT 70
 AAR28732
 ID AAR28732 standard; peptide; 8 AA.
 AC AAR28732;
 XX
 DT 25-MAR-2003 (updated)
 DT 02-APR-1993 (first entry)
 DE Protease chromogenic substrate #3 - to assay retroviral protease.
 XX
 XX AIDS; HIV; acquired immunodeficiency syndrome; protease; peptidase;
 KW human immunodeficiency virus; proteinase.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "p-NO2 Phe"
 XX
 PN US5164300-A.
 XX
 PD 17-NOV-1992.
 XX
 PF 11-DEC-1990; 90US-0625395.
 XX
 PR 28-DEC-1989; 89US-0458060.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Marshall CR, Toth MV;
 XX
 DR WPI; 1992-407144/49.
 XX
 PT Fluorimetric determ. of activity of retroviral protease - e.g.
 PT to isolate protease inhibitors for use as anti-AIDS agents
 XX
 PS Disclosure; Column 6; 8pp; English.
 XX
 CC This peptide represents a novel fluorimetric substrate for the
 CC assay of retroviral proteases (esp. that of HIV). It can be used to
 CC screen for retroviral protease inhibitors which are therapeutic
 CC possibilities in the search for AIDS drugs.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 3; DB 13; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db |||
 2 LNF 4
 RESULT 71
 AAR63662
 ID AAR63662 standard; Protein; 8 AA.
 AC AAR63662;
 XX
 DT 28-APR-1995 (first entry)
 XX
 DE PR/RT HIV protease substrate amino acid sequence.
 XX
 KW PR/RT HIV protease substrate; HIV protease inhibitors.
 XX
 OS Synthetic.
 XX
 PN GB2276621-A.
 XX

PD 05-OCT-1994.
 XX
 PF 24-MAR-1994; 94GB-0005865.
 XX
 PR 02-APR-1993; 93US-0045264.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Condra JH, Gotlib L, Graham DJ;
 XX
 DR WPI; 1994-296383/37.
 XX
 XX New plasmid pPrBG1, vector for mutated HIV protease sequences -
 PT used to produce a colour screen vector library to detect drug
 PT resistant proteases and new protease inhibitors
 XX
 PS Disclosure; Page 7; 34pp; English.
 XX
 CC AAR71462 and AAR63657 to AAR63667 are HIV protease substrate sequences.
 CC These sequences were used in the process to isolate and detect new
 CC inhibitors of HIV protease, unaffected by HIV drug resistance.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 3; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db |||
 2 LNF 4
 RESULT 72
 AAW38400
 ID AAW38400 standard; peptide; 8 AA.
 AC AAW38400;
 XX
 DT 08-APR-1998 (first entry)
 XX
 DE Synthetic pMEL17 peptide.
 XX
 KW Melanoma; immunogen; cytotoxic T lymphocyte; CTL;
 KW human leukocyte antigen-A1; HLA-A1; human leukocyte antigen-A3;
 KW HLA-A3; epitope; pMEL-17; tyrosinase; vaccine; protection.
 XX
 OS Synthetic.
 OS
 XX WO9734613-A1.
 PN
 XX 25-SEP-1997.
 PD
 XX 17-MAR-1997; 97WO-US04958.
 PF
 XX 04-OCT-1996; 96US-0027627.
 PR
 XX 19-MAR-1996; 96US-0013972.
 PR
 XX (UYVI-) UNIV VIRGINIA PATENT FOUND.
 PA
 XX Cox AL, Engelhard VH, Hendrikson RC, Hunt DF, Kittlesen D;
 PI Shabanowitz J, Skipper J, Slingluff CL;
 XX
 DR WPI; 1997-479982/44.
 XX
 XX Melanoma-specific immunogens of pMel-17 and tyrosinase - useful in
 PT vaccination for producing melanoma-specific cytotoxic T lymphocytes
 PT
 XX Example 9; Page 65; 106pp; English.
 PS
 XX The present peptide was used in the preparation of a novel melanoma
 CC specific immunogen, comprising at least 1 melanoma specific
 CC cytotoxic T lymphocyte (CTL) epitope, where at least 1 of the

CC epitopes is substantially homologous to a human leukocyte
 CC antigen-A1 (HLA-A1) and HLA-A3 restricted epitope of a melanoma
 CC antigen, either pMEL-17 or tyrosinase. The immunogen can be used in
 CC vaccines for protection against melanoma in mammals.

XX Sequence 8 AA;
 Query Match 100.0%; Score 3; DB 18; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 73

AAW57537

ID AAW57537 standard; peptide; 8 AA.

XX AC AAW57537;

XX DT 11-AUG-1998 (first entry)

XX DE Molecular mimetic of unique N. meningitidis epitope, Pep 37.

XX KW Molecular mimetic; epitope; serotype B; MenB; capsular polysaccharide;
 KW immune disease; non-autoreactive antibody; vaccine; passive immunisation;
 KW Escherichia coli K1 disease; bacterial meningitis; sepsis;
 KW oligosaccharide protein conjugate vaccine.

XX OS Synthetic.

XX OS Neisseria meningitidis.

XX PN WO9808874-A1.

XX PD 05-MAR-1998.

XX PF 27-AUG-1997; 97WO-US15167.

XX PR 27-AUG-1996; 96US-0025799.

XX PA (CHIR) CHIRON CORP.

XX PI Granoff D, Moe GR;

XX PS WPI; 1998-216938/19.

XX PT Antibodies to Neisseria meningitidis serotype B - prepared using
 PT capsular polysaccharide derivatives, used to develop products for
 PT treating or preventing infections, e.g. meningitis and sepsis

XX PS Claim 17; Fig 7A; 109pp; English.

XX This sequence represents a molecular mimetic of a unique epitope of
 CC Neisseria meningitidis serotype B (MenB). This sequence was isolated
 CC using the antibodies (Ab) of the invention. The Ab are directed against
 CC a MenB capsular polysaccharide (PS) derivative, and are not autoreactive.
 CC The Ab either do not cross-react or they are minimally cross-reactive
 CC with host tissues and therefore pose minimal risk of evoking immune
 CC disease. The non-autoreactive Ab are particularly useful for identifying
 CC molecular mimetics of unique MenB PS epitopes that can be used in vaccine
 CC compositions. Furthermore, the Ab, humanised versions of the Ab,
 CC fragments and functional equivalents, will also find use in passive
 CC immunisation against, and/or as an adjunct to therapy for, MenB and
 CC Escherichia coli K1 disease. Such disease includes bacterial meningitis
 CC and sepsis in infants, children and adults. The anti-MenB Ab can also be
 CC used to investigate the bactericidal and/or opsonic function of Ab of
 CC different specificities, as well as to identify the molecular nature of
 CC the unique epitopes on the MenB bacterial surface that are not
 CC cross-reactive with host PS. The anti-MenB Ab can be used to isolated
 CC fractions of MenB bacteria or MenB PS derivatives. Once isolated, the
 CC critical epitopes reactive with the anti-MenB Ab can be characterised and

CC employed directly in oligosaccharide protein conjugate vaccines or to
 CC model synthetic saccharides or mimetics for use in vaccines.

XX Sequence 8 AA;

Query Match 100.0%; Score 3; DB 19; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 74

AAW75463

ID AAW75463 standard; peptide; 8 AA.

XX AC AAW75463;

XX DT 27-APR-1999 (first entry)

XX DE Mammalian tub protein tyrosine phosphorylation site.

XX KW Human; wild type; tubby; identification; SH2 domain; mammal; obesity;
 KW body weight disorder; cachexia; anorexia.
 XX OS Homo sapiens.
 XX OS Mus sp.
 XX PN US5861239-A.

XX PD 19-JAN-1999.

XX PF 02-SEP-1997; 97US-0922267.

XX PR 02-SEP-1997; 97US-0922267.

XX PR 12-APR-1996; 96US-0631200.

XX PR 28-MAR-1997; 97US-0829553.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Kapeller R, Kleyn PW, Moore KJ;

XX PS WPI; 1999-130383/11.

XX PT Identifying compounds which modulate tub protein activity - by
 PT detecting compounds which alter the interaction of tub protein with
 PT a SH2 containing peptide, used to develop agents for treating e.g.
 PT obesity, cachexia or anorexia

XX PS Disclosure; Column 13; 95pp; English.

XX This sequence represents a tyrosine phosphorylation site/SH2 docking
 CC domain found in the amino acid sequence of the mouse and human "tub"
 CC proteins (AAW75450 and AAW75451 respectively). The invention relates to
 CC a method for identifying compounds that modulate tub protein activity,
 CC especially its interaction with proteins containing an SH2 domain. The
 CC method can be used for identifying compounds which modulate tub protein
 CC activity for use in the treatment of mammalian body weight disorders
 CC including obesity, cachexia and anorexia.

XX Sequence 8 AA;

Query Match 100.0%; Score 3; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 5 LNF 7

RESULT 75
AAAY70353
ID AAY70353 standard; peptide; 8 AA.
XX
AC AAY70353;
XX 21-JUN-2000 (first entry)
XX
DE Human immunodeficiency virus protease cleavage site-8.
XX
KW Protease cleavage site; PCS; ligand binding domain; DNA binding domain;
expression modulator domain; fusion protein; protease; treatment;
protease inhibitor; Alzheimer's disease; cystic fibrosis; emphysema;
hypertension; tumour; metastasis; viral disease; HIV aspartyl protease;
Human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus.
XX
PN WO200012727-A1.
XX
PD 09-MAR-2000.
XX
PF 31-AUG-1999; 99WO-US19926.
XX
PR 31-AUG-1998; 98US-0144759.
XX
PA (VERT-) VERTEX PHARM INC.
XX
PI Germann U, Hoock T, Kwong A;
XX
DR WPI; 2000-246756/21.
XX
PT Novel fusion protein comprising a protease cleavage site, a ligand
binding domain, and a DNA binding domain useful for characterizing
proteases, detecting viral infection, and screening for protease
inhibitors -
XX
PS Claim 9; Page 62; 80pp; English.
XX
CC The patent discloses fusion proteins comprising a protease cleavage
site (PCS), ligand binding domain, DNA binding domain and an expression
modulator domain that regulates transcription of a reporter gene.
CC Fusion proteins and the DNA encoding them can be used to detect viral,
cellular or microbial proteases, assay protease activity, detect viral
infections, determine substrate specificity of proteases, for
biochemical characterisation of proteases and to screen for potential
protease inhibitors. Protease inhibitors may be useful for treating
Alzheimer's disease, cystic fibrosis, emphysema, hypertension, tumour
invasion and metastasis and viral-associated diseases. The present
peptide sequence is the human immunodeficiency virus (HIV) protease
cleavage site, which is recognised by HIV aspartyl protease.
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 3; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db 2 LNF 4

Search completed: November 25, 2003, 19:27:23
Job time : 8.65698 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 4.81395 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3

Sequence: 1 LNF 3

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3	100.0	3 15	US-10-281-652-33
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3	3	100.0	4 10	US-09-947-387-85
4	3	100.0	4 12	US-10-138-375-54
5	3	100.0	4 12	US-10-138-375-85
6	3	100.0	5 10	US-09-947-387-82
7	3	100.0	5 10	US-09-947-387-84
8	3	100.0	5 10	US-09-947-387-132
9	3	100.0	5 12	US-10-138-375-82
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11	3	100.0	5 12	US-10-138-375-132
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13	3	100.0	6 10	US-09-947-387-83
14	3	100.0	6 10	US-09-947-387-123
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 94 Sequence 482, App
 95 Sequence 495, App
 96 Sequence 508, App
 97 Sequence 520, App
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 US-10-226-629A-541
 US-10-188-445-89

ALIGNMENTS

RESULT 1
 US-10-281-652-33

; Sequence 33, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDGOH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/10/281,652
 ; PRIOR FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/09/641,803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 33
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide

US-10-281-652-33
 Query Match 100.0%; Score 3; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 2

US-09-947-387-54
 ; Sequence 54, Application US/09947387
 ; Patent No. US20020150885A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weber, Eckard
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Keana, John F.W.
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Zhang, Han-Zhong
 ; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecu
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
 ; TITLE OF INVENTION: Use Thereof
 ; FILE REFERENCE: 1735.0290005
 ; CURRENT APPLICATION NUMBER: US/09/947,387
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/061,582
 ; PRIOR FILING DATE: 1997-10-10

; PRIOR APPLICATION NUMBER: US 60/145,746
 ; PRIOR FILING DATE: 1998-03-03
 ; PRIOR APPLICATION NUMBER: US 09/168,888
 ; PRIOR FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 142
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 54
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 ; US-09-947-387-54

Query Match 100.0%; Score 3; DB 10; Length 4;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 3

US-09-947-387-85
 ; Sequence 85, Application US/09947387
 ; Patent No. US20020150885A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weber, Eckard
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Keana, John F.W.
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Zhang, Han-Zhong
 ; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecu
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
 ; TITLE OF INVENTION: Use Thereof
 ; FILE REFERENCE: 1735.0290005
 ; CURRENT APPLICATION NUMBER: US/09/947,387
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/061,582
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: US 60/145,746
 ; PRIOR FILING DATE: 1998-03-03
 ; PRIOR APPLICATION NUMBER: US 09/168,888
 ; PRIOR FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 142
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 85
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide

US-09-947-387-85

Query Match 100.0%; Score 3; DB 10; Length 4;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 4

US-10-138-375-54
 ; Sequence 54, Application US/10138375
 ; Publication No. US20030208037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Han-Zhong

APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for Fluorescence Screening Assays for Caspases, Peptidases, Proteases
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735-0030001
CURRENT APPLICATION NUMBER: US/10/138,375
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-138-375-54

Query Match 100.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 2 LNF 4

RESULT 5
US-10-138-375-85
Sequence 85, Application US/10138375
Publication No. US20030208037A1
GENERAL INFORMATION:
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for Fluorescence Screening Assays for Caspases, Peptidases, Proteases
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735-0030001
CURRENT APPLICATION NUMBER: US/10/138,375
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 85
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-138-375-85

Query Match 100.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 1 LNF 3

RESULT 6

US-09-947-387-82
Sequence 82, Application US/09947387
Patent No. US20020150885A1
GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecu
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735-0290005
CURRENT APPLICATION NUMBER: US/09/947,387
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: US 09/168,888
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-947-387-82

Query Match 100.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 2 LNF 4

RESULT 7
US-09-947-387-84
Sequence 84, Application US/09947387
Patent No. US20020150885A1
GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecu
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735-0290005
CURRENT APPLICATION NUMBER: US/09/947,387
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: US 09/168,888
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 84
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-947-387-84

```
; OTHER INFORMATION: Peptide
US-09-947-387-84
Query Match      100.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      1 LNF 3

RESULT 8
US-09-947-387-132
; Sequence 132, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-132
Query Match      100.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 9
US-10-138-375-82
; Sequence 82, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642

; OTHER INFORMATION: Peptide
US-10-138-375-82
Query Match      100.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      1 LNF 3

RESULT 11
US-10-138-375-132
; Sequence 132, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642

; OTHER INFORMATION: Peptide
US-10-138-375-84
Query Match      100.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      1 LNF 3

RESULT 10
US-10-138-375-84
; Sequence 84, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-10-138-375-84
Query Match      100.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      1 LNF 3

RESULT 11
US-10-138-375-132
; Sequence 132, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
```

; CURRENT APPLICATION NUMBER: US/10/138,375
 ; CURRENT FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
 ; NUMBER OF SEQ ID NOS: 139
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 132
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 ; OTHER INFORMATION: Peptide
 US-10-138-375-132

Query Match 100.0%; Score 3; DB 12; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 12
 US-09-947-387-81
 ; Sequence 81, Application US/09947387
 ; Patent No. US20020150885A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weber, Eckard
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Keana, John F.W.
 ; APPLICANT: Zhang, Han-Zhong
 ; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
 ; TITLE OF INVENTION: Use Thereof
 ; FILE REFERENCE: 1735-0290005
 ; CURRENT APPLICATION NUMBER: US/09/947,387
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/061,582
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: US 60/145,746
 ; PRIOR FILING DATE: 1998-03-03
 ; PRIOR APPLICATION NUMBER: US 09/168,888
 ; PRIOR FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 142
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 81
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 ; OTHER INFORMATION: Peptide
 US-09-947-387-81

Query Match 100.0%; Score 3; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 13
 US-09-947-387-83
 ; Sequence 83, Application US/09947387
 ; Patent No. US20020150885A1

; GENERAL INFORMATION:
 ; APPLICANT: Weber, Eckard
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Keana, John F.W.
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Zhang, Han-Zhong
 ; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
 ; TITLE OF INVENTION: Use Thereof
 ; FILE REFERENCE: 1735-0290005
 ; CURRENT APPLICATION NUMBER: US/09/947,387
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/061,582
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: US 60/145,746
 ; PRIOR FILING DATE: 1998-03-03
 ; PRIOR APPLICATION NUMBER: US 09/168,888
 ; PRIOR FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 142
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 83
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 ; OTHER INFORMATION: Peptide
 US-09-947-387-83

Query Match 100.0%; Score 3; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 14
 US-09-947-387-123
 ; Sequence 123, Application US/09947387
 ; Patent No. US20020150885A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weber, Eckard
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Keana, John F.W.
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Zhang, Han-Zhong
 ; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
 ; TITLE OF INVENTION: Use Thereof
 ; FILE REFERENCE: 1735-0290005
 ; CURRENT APPLICATION NUMBER: US/09/947,387
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/061,582
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: US 60/145,746
 ; PRIOR FILING DATE: 1998-03-03
 ; PRIOR APPLICATION NUMBER: US 09/168,888
 ; PRIOR FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 142
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 123
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 ; OTHER INFORMATION: Peptide
 US-09-947-387-123

Query Match 100.0%; Score 3; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 15
 US-10-138-375-81
 ; Sequence 81, Application US/10138375
 ; Publication No. US20030208037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Han-Zhong
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Yang, Wu
 ; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications fo
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof
 ; FILE REFERENCE: 1735.0030001
 ; CURRENT APPLICATION NUMBER: US/10/138,375
 ; CURRENT FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: US/09/357,952
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
 ; NUMBER OF SEQ ID NOS: 139
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 81
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-10-138-375-81

Query Match 100.0%; Score 3; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 16
 US-10-138-375-83
 ; Sequence 83, Application US/10138375
 ; Publication No. US20030208037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Han-Zhong
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Yang, Wu
 ; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications fo
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof
 ; FILE REFERENCE: 1735.0030001
 ; CURRENT APPLICATION NUMBER: US/10/138,375
 ; CURRENT FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
 ; NUMBER OF SEQ ID NOS: 139
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 83
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-10-138-375-83

Query Match 100.0%; Score 3; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 17
 US-10-138-375-123
 ; Sequence 123, Application US/10138375
 ; Publication No. US20030208037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Han-Zhong
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Yang, Wu
 ; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications f
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteas
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof
 ; FILE REFERENCE: 1735.0030001
 ; CURRENT APPLICATION NUMBER: US/10/138,375
 ; CURRENT FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
 ; NUMBER OF SEQ ID NOS: 139
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 123
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-10-138-375-123

Query Match 100.0%; Score 3; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 18
 US-09-735-995-110
 ; Sequence 110, Application US/09735995
 ; Patent No. US20010034024A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Keating, Mark T.
 ; APPLICANT: Splawski, Igor
 ; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
 ; TITLE OF INVENTION: SYNDROME GENE
 ; FILE REFERENCE: 2323-136
 ; CURRENT APPLICATION NUMBER: US/09/735,995
 ; CURRENT FILING DATE: 2000-12-14
 ; PRIOR APPLICATION NUMBER: 09/226,012
 ; PRIOR FILING DATE: 1999-01-06
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 110
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster

US-09-735-995-110

Query Match 100.0%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 4 LNF 6

RESULT 19

US-09-735-995-111
; Sequence 111, Application US/09735995
; Patent No. US20010034024A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/735,995
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/226,012
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: See Warnke and
; OTHER INFORMATION: Ganetzky, 1994.

US-09-735-995-111

Query Match 100.0%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 4 LNF 6

RESULT 20

US-09-947-387-34
; Sequence 34, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-34

Query Match 100.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 2 LNF 4

RESULT 21

US-09-947-387-80
; Sequence 80, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-80

Query Match 100.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 2 LNF 4

RESULT 22

US-10-351-641-1065
; Sequence 1065, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24

; PRIOR APPLICATION NUMBER: 09/350,641
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/315,304
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/082,279
 ; PRIOR FILING DATE: 1998-05-20
 ; NUMBER OF SEQ ID NOS: 1757
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1065
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Core polypeptide
 ; US-10-351-641-1065

Query Match 100.0%; Score 3; DB 12; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 Db 1 LNF 3

RESULT 23
 US-10-138-375-34
 ; Sequence 34, Application US/10138375
 ; Publication No. US20030208037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Han-Zhong
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Yang, Wu
 ; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
 ; FILE REFERENCE: 1735.0030001
 ; CURRENT APPLICATION NUMBER: US/10/138,375
 ; CURRENT FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-21
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
 ; NUMBER OF SEQ ID NOS: 139
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 34
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 ; US-10-138-375-34

Query Match 100.0%; Score 3; DB 12; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 Db 2 LNF 4

RESULT 24
 US-10-138-375-80
 ; Sequence 80, Application US/10138375
 ; Publication No. US20030208037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Han-Zhong
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Yang, Wu

; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications f
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteas
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof
 ; FILE REFERENCE: 1735.0030001
 ; CURRENT APPLICATION NUMBER: US/10/138,375
 ; CURRENT FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
 ; NUMBER OF SEQ ID NOS: 139
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 80
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 ; US-10-138-375-80

Query Match 100.0%; Score 3; DB 12; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 Db 2 LNF 4

RESULT 25
 US-10-214-932-70
 ; Sequence 70, Application US/10214932
 ; Publication No. US20030100707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HWANG, Inhwan
 ; APPLICANT: KIM, Dae Heon
 ; APPLICANT: LEE, Yong Jik
 ; TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
 ; FILE REFERENCE: APB02/US
 ; CURRENT APPLICATION NUMBER: US/10/214,932
 ; CURRENT FILING DATE: 2002-08-08
 ; NUMBER OF SEQ ID NOS: 133
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 70
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Sequence
 ; US-10-214-932-70

Query Match 100.0%; Score 3; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 Db 2 LNF 4

RESULT 26
 US-09-910-552-37
 ; Sequence 37, Application US/09910552
 ; Publication No. US20020197260A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Granoff, Dan M.
 ; APPLICANT: Moe, Gregory R.
 ; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
 ; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
 ; TITLE OF INVENTION: COMPOSITIONS
 ; FILE REFERENCE: 1238.002
 ; CURRENT APPLICATION NUMBER: US/09/910,552

; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/494,822
; FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence from
; OTHER INFORMATION: a phage display peptide library
US-09-910-552-37

Query Match 100.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 1 LNF 3

RESULT 27

US-10-072-419-4
; Sequence 4, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Schistocerca gregaria
US-10-072-419-4

Query Match 100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 28

US-10-072-419-9
; Sequence 9, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Pyrrhocoris apterus
US-10-072-419-9

Query Match 100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 29

US-10-072-419-10
; Sequence 10, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Locusta migratoria
US-10-072-419-10

Query Match 100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 30

US-10-072-419-11
; Sequence 11, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Locusta migratoria
US-10-072-419-11

Query Match 100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 31

US-10-072-419-15
; Sequence 15, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07

```
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Phymateus leprosus
US-10-072-419-15

Query Match      100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      2 LNF 4

RESULT 32
US-10-072-419-20
; Sequence 20, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Tenebrio molitor
US-10-072-419-20

Query Match      100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      2 LNF 4

US-10-072-419-25
; Sequence 25, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Libanasidus vittatus
US-10-072-419-25

Query Match      100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      2 LNF 4

RESULT 34
US-10-072-419-25
; Sequence 25, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Libanasidus vittatus
US-10-072-419-25

Query Match      100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      2 LNF 4

RESULT 35
US-10-226-629A-451
; Sequence 451, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 451
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-451

Query Match      100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      4 LNF 6

RESULT 36
US-10-226-629A-464
; Sequence 464, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
```

; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 464
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-464

Query Match 100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 5 LNF 7

RESULT 37

US-10-226-629A-477
; Sequence 477, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 477
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-477

Query Match 100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 6 LNF 8

RESULT 38

US-10-231-417-346
; Sequence 346, Application US/10231417
; Publication No. US20030176681A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 148 Human Secreted Proteins
; FILE REFERENCE: P2019P1
; CURRENT APPLICATION NUMBER: US/10/231,417
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/296,622
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 619
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 346
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-417-346

Query Match 100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
|||
Db 5 LNF 7

RESULT 39

US-10-079-625-33
; Sequence 33, Application US/10079625
; Publication No. US20020182676A1
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,625
; FILING DATE: 2002-FEB-19
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-079-625-33

Query Match 100.0%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 4 LNF 6

RESULT 40

US-10-300-757-8

; Sequence 8, Application US/10300757
 ; Publication No. US20030083467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hock, Thomas
 ; APPLICANT: Germann, Ursula
 ; APPLICANT: Kwong, Ann
 ; TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS
 ; FILE REFERENCE: VPI/98-08
 ; CURRENT APPLICATION NUMBER: US/10/300,757
 ; PRIOR FILING DATE: 2002-11-20
 ; PRIOR APPLICATION NUMBER: US/09/570,267
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: 09/144,759
 ; PRIOR FILING DATE: 1998-08-31
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-300-757-8

Query Match 100.0%; Score 3; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 41

US-09-894-018-72

; Sequence 72, Application US/09894018
 ; Patent No. US20020119127A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE, Inc.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Chestnut, Robert
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Baker, Denisw
 ; APPLICANT: Newman, Mark
 ; APPLICANT: Brown, David
 ; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
 ; FILE REFERENCE: 39963-20033.00
 ; CURRENT APPLICATION NUMBER: US/09/894,018
 ; PRIOR FILING DATE: 2001-06-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/35568
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/173,390
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: US 60/284,221
 ; PRIOR FILING DATE: 2001-04-16
 ; NUMBER OF SEQ ID NOS: 368
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 72
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligopeptide
 US-09-894-018-72

Query Match 100.0%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 42

US-09-894-018-152

; Sequence 152, Application US/09894018
 ; Patent No. US20020119127A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE, Inc.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Chestnut, Robert
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Baker, Denisw
 ; APPLICANT: Newman, Mark
 ; APPLICANT: Brown, David
 ; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
 ; FILE REFERENCE: 39963-20033.00
 ; CURRENT APPLICATION NUMBER: US/09/894,018
 ; PRIOR FILING DATE: 2001-06-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/35568
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/173,390
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: US 60/284,221
 ; PRIOR FILING DATE: 2001-04-16
 ; NUMBER OF SEQ ID NOS: 368
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 152
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Transgenic mouse
 US-09-894-018-152

Query Match 100.0%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 43

US-09-897-107-2

; Sequence 2, Application US/09897107
 ; Patent No. US20020137094A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YAMAGISHI, Akihiko
 ; TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAVING
 ; FILE REFERENCE: 210383USO
 ; CURRENT APPLICATION NUMBER: US/09/897,107
 ; PRIOR FILING DATE: 2001-07-03
 ; PRIOR APPLICATION NUMBER: JP2000-201920
 ; PRIOR FILING DATE: 2000-07-04
 ; PRIOR APPLICATION NUMBER: JP2001-164332
 ; PRIOR FILING DATE: 2001-05-31
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Sulfolobus sp.
 US-09-897-107-2

Query Match 100.0%; Score 3; DB 10; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 1 LNF 3
|||
Db 6 LNF 8

RESULT 44

US-09-865-548A-156
; Sequence 156, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-156

Query Match 100.0%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 5 LNF 7

RESULT 45

US-10-226-629A-452
; Sequence 452, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 452
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-452

Query Match 100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 4 LNF 6

RESULT 46
US-10-226-629A-465
; Sequence 465, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 465
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-465

Query Match 100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 5 LNF 7

RESULT 47
US-10-226-629A-478
; Sequence 478, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 478
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-478

Query Match 100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 6 LNF 8

RESULT 48

US-10-226-629A-491
; Sequence 491, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott

```

; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 491
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
; US-10-226-629A-491

Query Match      100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 7 LNF 9

RESULT 49
US-10-371-069-220
; Sequence 220, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV ENV 197 (peptide 20.0137)
US-10-371-069-220

Query Match      100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 6 LNF 8

RESULT 50
US-10-371-069-354
; Sequence 354, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.

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; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 354
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0041)
US-10-371-069-354

Query Match      100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 2 LNF 4

RESULT 51
US-10-371-645-220
; Sequence 220, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV ENV 197 (peptide 20.0137)
US-10-371-645-220

Query Match      100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 6 LNF 8

```

RESULT 52

US-10-371-645-354
 ; Sequence 354, Application US/10371645
 ; Publication No. US20030216343A1
 ; GENERAL INFORMATION:

; APPLICANT: EPIMUNE INC.
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; FILE OF INVENTION: Immune Response and Methods of Using the Same

; FILE REFERENCE: 39963-20022.11

; CURRENT APPLICATION NUMBER: US/10/371,645

; CURRENT FILING DATE: 2003-06-20

; PRIOR FILING DATE: 1998-05-13

; PRIOR APPLICATION NUMBER: US 60/085,751

; NUMBER OF SEQ ID NOS: 463

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 354

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0041)

US-10-371-645-354

Query Match 100.0%; Score 3; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 53

US-10-133-210-18
 ; Sequence 18, Application US/10133210
 ; Publication No. US20030103964A1
 ; GENERAL INFORMATION:

; APPLICANT: Delisi, Charles
 ; APPLICANT: Berzofsky, Jay
 ; APPLICANT: Gulukota, Kamalakara
 ; APPLICANT: Vaccaro, Dennis
 ; APPLICANT: Weng, Zhiping
 ; APPLICANT: Zhang, Chao

; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
 ; FILE OF INVENTION: COMPOSITIONS THEREOF

; FILE REFERENCE: BU-035AX

; CURRENT APPLICATION NUMBER: US/10/133,210

; CURRENT FILING DATE: 2002-04-26

; NUMBER OF SEQ ID NOS: 281

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 18

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-133-210-18

Query Match 100.0%; Score 3; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 54

US-09-863-054-24

; Sequence 24, Application US/09863054
 ; Publication No. US20030021809A1
 ; GENERAL INFORMATION:

; APPLICANT: Chisari, Francis V.

; TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
 ; Lymphocyte Responses to Hepatitis B Virus

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/863,054

; FILING DATE: 21-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/935,898

; FILING DATE: 26-AUG-1992

; APPLICATION NUMBER: US 08/024,120

; FILING DATE: 26-FEB-1993

; APPLICATION NUMBER: US 08/396,283

; FILING DATE: 27-FEB-1995

; APPLICATION NUMBER: US 08/463,486

; FILING DATE: 05-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lockyer, Jean M.

; REGISTRATION NUMBER: 44,879

; REFERENCE/DOCKET NUMBER: 014740-000421US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-863-054-24

Query Match 100.0%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 55

US-03-572-404B-781

; Sequence 781, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 781
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in APOB at 2799-2808 and may interact with Sequ
; OTHER INFORMATION: in this patent.
US-09-572-404B-781

Query Match 100.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 6 LNF 8

RESULT 56
US-09-572-404B-839
; Sequence 839, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 839
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in APOB at 2798-2807 and may interact with Sequ
; OTHER INFORMATION: in this patent.
US-09-572-404B-839

Query Match 100.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 7 LNF 9

RESULT 57
US-10-072-419-1
; Sequence 1, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Hum
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Schistosomera gregaria
US-10-072-419-1

Query Match 100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 58
US-10-072-419-35
; Sequence 35, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Hum
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Schistosomera gregaria
US-10-072-419-35

Query Match 100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 59
US-10-072-419-36
; Sequence 36, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Hum
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Tenthredo arcuata
US-10-072-419-36

Query Match 100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 60
US-10-226-629A-453
; Sequence 453, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection

; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 453
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-453

Query Match 100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 4 LNF 6

RESULT 61

US-10-226-629A-466
; Sequence 466, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 466
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-466

Query Match 100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 5 LNF 7

RESULT 62

US-10-226-629A-479
; Sequence 479, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 479
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-479

Query Match 100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 6 LNF 8

RESULT 63

US-10-226-629A-492
; Sequence 492, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 492
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-492

Query Match 100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 7 LNF 9

RESULT 64

US-10-226-629A-505
; Sequence 505, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 505
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-505

Query Match 100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

```

Db      |||
      8 LNF 10

RESULT 65
US-09-573-822C-16
; Sequence 16, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG241 at 66-75 and may interact with Sequence
; US-09-573-822C-16

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 66
US-09-573-822C-18
; Sequence 18, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG241 at 65-74 and may interact with Sequence
; US-09-573-822C-18

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 67
US-09-573-822C-40
; Sequence 40, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C

Db      |||
      3 LNF 5

RESULT 68
US-09-573-822C-153
; Sequence 153, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 153
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG256 at 202-211 and may interact with Sequence
; US-09-573-822C-153

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      3 LNF 5

RESULT 69
US-10-371-069-343
; Sequence 343, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15

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; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0151)
US-10-371-069-343
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Query Match
Best Local Similarity 100.0%; Score 3; DB 12; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LNF 3
   |||
Db 3 LNF 5
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RESULT 70

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US-10-371-645-343
; Sequence 343, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
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; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0151)
US-10-371-645-343
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Query Match
Best Local Similarity 100.0%; Score 3; DB 12; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LNF 3
   |||
Db 3 LNF 5
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RESULT 71

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US-10-033-662-65
; Sequence 65, Application US/10033662
; Publication No. US20030092197A1
; GENERAL INFORMATION:
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; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Card
; FILE REFERENCE: 9195-081
; CURRENT APPLICATION NUMBER: US/10/033,662
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-662-65
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Query Match
Best Local Similarity 100.0%; Score 3; DB 15; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LNF 3
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Db 6 LNF 8
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RESULT 72

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US-09-974-879-319
; Sequence 319, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2
; CURRENT APPLICATION NUMBER: US/09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,987
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 319
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-319
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Query Match
Best Local Similarity 100.0%; Score 3; DB 11; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LNF 3
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Db 6 LNF 8

RESULT 73
US-09-305-736-319
; Sequence 319, Application US/09305736
; Publication No. US20030088078A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/09/305,736
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: PCT/US98/23435
; EARLIER FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/064,911
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,912
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,983
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,900
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,988
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,987
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,908
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,984
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,985
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/066,094
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,100
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,089
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,095
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,090
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 319
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-305-736-319

Query Match 100.0%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 6 LNF 8

RESULT 74
US-10-226-629A-454
; Sequence 454, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01

; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 454
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-454

Query Match 100.0%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
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Db 4 LNF 6

RESULT 75
US-10-226-629A-467
; Sequence 467, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 467
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-467

Query Match 100.0%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
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Db 5 LNF 7

Search completed: November 25, 2003, 20:37:09
Job time : 5.81395 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 2.42442 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3
Sequence: 1 INF 3

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3	100.0	4	2	US-08-667-001-1	Sequence 1, Appl
3	3	100.0	4	2	US-08-667-001-2	Sequence 2, Appl
4	3	100.0	4	2	US-08-667-001-4	Sequence 4, Appl
5	3	100.0	4	2	US-08-667-001-5	Sequence 5, Appl
6	3	100.0	4	2	US-08-667-001-9	Sequence 9, Appl
7	3	100.0	4	3	US-09-357-952-54	Sequence 54, Appl
8	3	100.0	4	3	US-09-357-952-85	Sequence 85, Appl
9	3	100.0	4	3	US-09-053-941-24	Sequence 24, Appl
10	3	100.0	4	4	US-09-521-650-54	Sequence 54, Appl
11	3	100.0	4	4	US-09-521-650-85	Sequence 85, Appl
12	3	100.0	4	4	US-09-168-888-54	Sequence 54, Appl
13	3	100.0	4	4	US-09-168-888-85	Sequence 85, Appl
14	3	100.0	4	4	US-09-817-413-24	Sequence 24, Appl
15	3	100.0	4	4	US-09-536-785A-39	Sequence 39, Appl
16	3	100.0	5	3	US-08-485-324-24	Sequence 24, Appl
17	3	100.0	5	3	US-08-447-506-24	Sequence 24, Appl
18	3	100.0	5	3	US-08-235-437-24	Sequence 24, Appl
19	3	100.0	5	3	US-08-981-122-17	Sequence 17, Appl
20	3	100.0	5	3	US-08-447-515-24	Sequence 24, Appl
21	3	100.0	5	3	US-09-357-952-82	Sequence 82, Appl
22	3	100.0	5	3	US-09-357-952-84	Sequence 84, Appl
23	3	100.0	5	3	US-09-357-952-132	Sequence 132, Appl
24	3	100.0	5	4	US-09-521-650-82	Sequence 82, Appl
25	3	100.0	5	4	US-09-521-650-84	Sequence 84, Appl
26	3	100.0	5	4	US-09-521-650-132	Sequence 132, Appl
27	3	100.0	5	4	US-09-168-888-82	Sequence 82, Appl

28	3	100.0	5	4	US-09-168-888-84	Sequence 84, Appl
29	3	100.0	5	4	US-09-168-888-132	Sequence 132, Appl
30	3	100.0	6	3	US-09-357-952-81	Sequence 81, Appl
31	3	100.0	6	3	US-09-357-952-83	Sequence 83, Appl
32	3	100.0	6	3	US-09-357-952-123	Sequence 123, Appl
33	3	100.0	6	4	US-09-521-650-81	Sequence 81, Appl
34	3	100.0	6	4	US-09-521-650-83	Sequence 83, Appl
35	3	100.0	6	4	US-09-521-650-123	Sequence 123, Appl
36	3	100.0	6	4	US-09-168-888-81	Sequence 81, Appl
37	3	100.0	6	4	US-09-168-888-83	Sequence 83, Appl
38	3	100.0	6	4	US-09-168-888-123	Sequence 123, Appl
39	3	100.0	6	6	5342922-20	Patent No. 5342922
40	3	100.0	7	1	US-08-401-512-75	Sequence 75, Appl
41	3	100.0	7	1	US-08-401-512-76	Sequence 76, Appl
42	3	100.0	7	2	US-08-598-873-40	Sequence 40, Appl
43	3	100.0	7	3	US-09-226-012-110	Sequence 110, Appl
44	3	100.0	7	3	US-09-226-012-111	Sequence 111, Appl
45	3	100.0	7	3	US-08-605-430-40	Sequence 40, Appl
46	3	100.0	7	3	US-09-357-952-34	Sequence 34, Appl
47	3	100.0	7	3	US-09-357-952-80	Sequence 80, Appl
48	3	100.0	7	3	US-09-082-279B-1065	Sequence 1065, Ap
49	3	100.0	7	4	US-09-521-650-34	Sequence 34, Appl
50	3	100.0	7	4	US-09-521-650-80	Sequence 80, Appl
51	3	100.0	7	4	US-09-168-888-34	Sequence 34, Appl
52	3	100.0	7	4	US-09-168-888-80	Sequence 80, Appl
53	3	100.0	7	4	US-09-315-304B-1065	Sequence 1065, Ap
54	3	100.0	7	4	US-09-834-784-1065	Sequence 1065, Ap
55	3	100.0	7	6	5342922-21	Patent No. 5342922
56	3	100.0	8	1	US-08-030-731A-12	Sequence 12, Appl
57	3	100.0	8	1	US-08-045-264A-20	Sequence 20, Appl
58	3	100.0	8	2	US-08-922-267A-71	Sequence 71, Appl
59	3	100.0	8	2	US-08-599-455B-33	Sequence 33, Appl
60	3	100.0	8	3	US-08-925-002-37	Sequence 37, Appl
61	3	100.0	8	3	US-09-144-759-8	Sequence 8, Appl
62	3	100.0	8	3	US-09-069-781B-33	Sequence 33, Appl
63	3	100.0	8	4	US-09-137-132-33	Sequence 33, Appl
64	3	100.0	8	4	US-08-864-564A-33	Sequence 33, Appl
65	3	100.0	8	4	US-09-084-410-33	Sequence 33, Appl
66	3	100.0	8	4	US-08-708-1230-33	Sequence 33, Appl
67	3	100.0	8	4	US-08-583-153A-33	Sequence 33, Appl
68	3	100.0	8	4	US-09-570-267-8	Sequence 8, Appl
69	3	100.0	8	4	US-08-638-524B-33	Sequence 33, Appl
70	3	100.0	9	1	US-08-435-241A-5	Sequence 5, Appl
71	3	100.0	9	1	US-09-053-941-25	Sequence 25, Appl
72	3	100.0	9	4	US-09-817-413-25	Sequence 25, Appl
73	3	100.0	9	4	US-09-311-784A-220	Sequence 220, Appl
74	3	100.0	9	4	US-09-311-784A-354	Sequence 354, Appl
75	3	100.0	10	1	US-08-185-448-10	Sequence 10, Appl
76	3	100.0	10	1	US-08-122-792-1	Sequence 1, Appl
77	3	100.0	10	1	US-08-464-235-24	Sequence 24, Appl
78	3	100.0	10	3	US-08-800-213A-1	Sequence 1, Appl
79	3	100.0	10	3	US-08-800-213A-3	Sequence 3, Appl
80	3	100.0	10	3	US-08-800-213A-4	Sequence 4, Appl
81	3	100.0	10	3	US-08-800-213A-5	Sequence 5, Appl
82	3	100.0	10	3	US-08-800-213A-7	Sequence 7, Appl
83	3	100.0	10	3	US-08-800-213A-8	Sequence 8, Appl
84	3	100.0	10	3	US-08-800-213A-11	Sequence 11, Appl
85	3	100.0	10	3	US-08-338-056-2	Sequence 2, Appl
86	3	100.0	10	3	US-08-463-486-24	Sequence 24, Appl
87	3	100.0	10	3	US-09-053-941-20	Sequence 20, Appl
88	3	100.0	10	4	US-08-992-877-40	Sequence 40, Appl
89	3	100.0	10	4	US-09-817-413-20	Sequence 20, Appl
90	3	100.0	10	4	US-09-311-784A-343	Sequence 343, Appl
91	3	100.0	10	5	US-09-311-784A-343	Sequence 343, Appl
92	3	100.0	11	1	US-08-355-888A-17	Sequence 17, Appl
93	3	100.0	11	2	US-08-693-697-17	Sequence 17, Appl
94	3	100.0	11	2	US-08-693-697-17	Sequence 17, Appl
95	3	100.0	11	3	US-08-693-697-17	Sequence 17, Appl
96	3	100.0	11	3	US-07-861-458C-106	Sequence 106, Appl
97	3	100.0	11	4	US-09-357-914-17	Sequence 17, Appl
98	3	100.0	12	2	US-08-551-459-1	Sequence 1, Appl
99	3	100.0	12	3	US-09-258-754-93	Sequence 93, Appl
100	3	100.0	12	4	US-09-042-107-93	Sequence 93, Appl
					US-09-430-221-8	Sequence 8, Appl

ALIGNMENTS

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RESULT 1
US-09-641-803-33
; Sequence 33, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-33

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Query Match      100.0%; Score 3; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 LNF 3
Db      1 LNF 3

```

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RESULT 2
US-08-667-001-1
; Sequence 1, Application US/08667001
; Patent No. 5827827
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D.
; APPLICANT: Wirsching, Peter
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,001
; FILING DATE: 20-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,039
; FILING DATE: 16-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lewis, Donald G.
; REGISTRATION NUMBER: 28,636
; REFERENCE/DOCKET NUMBER: TSRI 282.1
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "serine is linked to CH3C(O)
; OTHER INFORMATION: - in formula (V A) or (V B)"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 4
; OTHER INFORMATION: /note= "Pro-Ile-Val-OCH3 is
; OTHER INFORMATION: connected to Phe via Psi[] in formula (V A) or (V
; OTHER INFORMATION: B)"
US-08-667-001-1
Query Match      100.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LNF 3
Db      2 LNF 4

```

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RESULT 3
US-08-667-001-2
; Sequence 2, Application US/08667001
; Patent No. 5827827
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D.
; APPLICANT: Wirsching, Peter
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,001
; FILING DATE: 20-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,039
; FILING DATE: 16-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lewis, Donald G.
; REGISTRATION NUMBER: 28,636
; REFERENCE/DOCKET NUMBER: TSRI 282.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal

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RESULT 6
 US-08-667-001-9
 ; Sequence 9, Application US/08667001
 ; Patent No. 5827827
 ; GENERAL INFORMATION:
 ; APPLICANT: Janda, Kim D.
 ; APPLICANT: Wirsching, Peter
 ; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
 ; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8
 ; CITY: La Jolla
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/667,001
 ; FILING DATE: 20-JUN-1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/335,039
 ; FILING DATE: 16-FEB-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lewis, Donald G.
 ; REGISTRATION NUMBER: 28,636
 ; REFERENCE/DOCKET NUMBER: TSRI 282.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 554-2937
 ; TELEFAX: (619) 554-6312
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: 1
 ; OTHER INFORMATION: /note= "sequence = Y1 in formula
 ; OTHER INFORMATION: (III A) and (III B)"
 US-08-667-001-9

Query Match 100.0%; Score 3; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNF 3
 Db 2 LNF 4
 RESULT 7
 US-09-357-952-54
 ; Sequence 54, Application US/09357952
 ; Patent No. 6248904
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Han-Zhong
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Yang, Wu
 ; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof
 ; FILE REFERENCE: 1735.0030001

; CURRENT APPLICATION NUMBER: US/09/357,952
 ; CURRENT FILING DATE: 1999-07-21
 ; EARLIER APPLICATION NUMBER: US 60/093,642
 ; EARLIER FILING DATE: 21-JUL-1998
 ; NUMBER OF SEQ ID NOS: 139
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 54
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 ; OTHER INFORMATION: Peptide
 US-09-357-952-54

Query Match 100.0%; Score 3; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 Db 2 LNF 4

RESULT 8
 US-09-357-952-85
 ; Sequence 85, Application US/09357952
 ; Patent No. 6248904
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Han-Zhong
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Yang, Wu
 ; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease:
 ; FILE REFERENCE: 1735.0030001
 ; CURRENT APPLICATION NUMBER: US/09/357,952
 ; CURRENT FILING DATE: 1999-07-21
 ; EARLIER APPLICATION NUMBER: US 60/093,642
 ; EARLIER FILING DATE: 21-JUL-1998
 ; NUMBER OF SEQ ID NOS: 139
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 85
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 ; OTHER INFORMATION: Peptide
 US-09-357-952-85

Query Match 100.0%; Score 3; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
 Db 1 LNF 3

RESULT 9
 US-09-053-941-24
 ; Sequence 24, Application US/09053941
 ; Patent No. 6271354
 ; GENERAL INFORMATION:
 ; APPLICANT: SRINIVASAN, ALGARSAMY
 ; APPLICANT: KOPROWSKI, HILARY
 ; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
 ; FILE REFERENCE: Chimeric Viral Proteins
 ; CURRENT APPLICATION NUMBER: US/09/053,941
 ; CURRENT FILING DATE: 1998-04-02
 ; EARLIER APPLICATION NUMBER: 60/043,380

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; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-053-941-24

Query Match          100.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      2 LNF 4

RESULT 10
US-09-521-650-54
; Sequence 54, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-54

Query Match          100.0%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      1 LNF 3

RESULT 12
US-09-168-888-54
; Sequence 54, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-54

Query Match          100.0%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      2 LNF 4

RESULT 13
US-09-168-888-54
; Sequence 85, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
```

US-09-168-888-85
 ; Sequence 85, Application US/09168888
 ; Patent No. 6342611
 ; GENERAL INFORMATION:
 ; APPLICANT: Weber, Eckard
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Keana, John F.W.
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Zhang, Han-Zhong
 ; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
 ; TITLE OF INVENTION: Use Thereof
 ; FILE REFERENCE: 1735-0290002
 ; CURRENT APPLICATION NUMBER: US/09/168,888
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,582
 ; EARLIER FILING DATE: 1997-10-10
 ; EARLIER APPLICATION NUMBER: US 09/033,661
 ; EARLIER FILING DATE: 1998-03-03
 ; NUMBER OF SEQ ID NOS: 142
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 85
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 ; US-09-168-888-85

Query Match 100.0%; Score 3; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 1 LNF 3

RESULT 14
 US-09-817-413-24
 ; Sequence 24, Application US/09817413
 ; Patent No. 6436648
 ; GENERAL INFORMATION:
 ; APPLICANT: SRINIVASAN, ALGARSAMY
 ; APPLICANT: KOPROWSKI, HILARY
 ; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
 ; FILE REFERENCE: Chimeric Viral Proteins
 ; CURRENT APPLICATION NUMBER: US/09/817,413
 ; CURRENT FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/043,380
 ; PRIOR FILING DATE: 1999-04-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 24
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 ; US-09-817-413-24

Query Match 100.0%; Score 3; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 15
 US-09-536-785A-39
 ; Sequence 39, Application US/09536785A

; Patent No. 6541450
 ; GENERAL INFORMATION:
 ; APPLICANT: BARBIER, JEAN-RENE
 ; APPLICANT: MORLEY, PAUL
 ; APPLICANT: NEUGEBAUER, WITOLD
 ; APPLICANT: ROSS, VIRGINIA J.S.
 ; APPLICANT: WHITFIELD, JAMES F.
 ; APPLICANT: WILLICK, GORDON E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
 ; TITLE OF INVENTION: OSTEOPOROSIS
 ; FILE REFERENCE: 1339-9
 ; CURRENT APPLICATION NUMBER: US/09/536,785A
 ; CURRENT FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 08/904,760
 ; PRIOR FILING DATE: 1997-08-01
 ; PRIOR APPLICATION NUMBER: 08/691,647
 ; PRIOR FILING DATE: 1996-08-02
 ; PRIOR APPLICATION NUMBER: 08/262,495
 ; PRIOR FILING DATE: 1994-06-20
 ; PRIOR APPLICATION NUMBER: 60/040,560
 ; PRIOR FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 39
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-536-785A-39

Query Match 100.0%; Score 3; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
 |||
 Db 2 LNF 4

RESULT 16
 US-08-485-324-24
 ; Sequence 24, Application US/08485324
 ; Patent No. 6043093
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlstatder, Jacob
 ; TITLE OF INVENTION: SELECTION METHODS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Curtis, Morris, & Safford
 ; ADDRESSEE: c/o Barry Evans
 ; STREET: 530 Fifth Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,324
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/235,437
 ; FILING DATE: 29-APR-1994
 ; APPLICATION NUMBER: US 07/852,412
 ; FILING DATE: 16-MAR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Evans, Barry
 ; REGISTRATION NUMBER: 22,802
 ; REFERENCE/DOCKET NUMBER: 370132-2000
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-324-24

Query Match 100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3
Db 3 LNF 5

RESULT 17
US-08-447-506-24
Sequence 24, Application US/08447506
Patent No. 6066499
GENERAL INFORMATION:
APPLICANT: Wohlstatder, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESS: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,506
FILING DATE: 23-MAY-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-506-24

Query Match 100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3
Db 3 LNF 5

RESULT 18
US-08-235-437-24
Sequence 24, Application US/08235437
Patent No. 6087177
GENERAL INFORMATION:
APPLICANT: Wohlstatder, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESS: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,437
FILING DATE: 29-APR-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-235-437-24

Query Match 100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3
Db 3 LNF 5

RESULT 19
US-08-981-122-17
Sequence 17, Application US/08981122B
Patent No. 6127339
GENERAL INFORMATION:
APPLICANT: Hatanaka, Yoshihiro
ADDRESS: Arimoto, Masaharu
TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/08/981,122B
CURRENT FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: JP 7-176904
PRIOR FILING DATE: 1995-06-21
PRIOR APPLICATION NUMBER: PCT/JP96/01734
PRIOR FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 5
TYPE: PPT
ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Sequence of a peptide synthesized in Example 2 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetide
; OTHER INFORMATION: synthesizing system (RaMPs)
US-08-981-122-17

Query Match 100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 1 LNF 3

RESULT 20
US-08-447-515-24
; Sequence 24, Application US/08447515
; Patent No. 6162640
; GENERAL INFORMATION:
; APPLICANT: Wohlstaetter, Jacob
; TITLE OF INVENTION: SELECTION METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris, & Safford
; ADDRESSEE: c/o Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,515
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,437
; FILING DATE: 29-APR-1994
; APPLICATION NUMBER: US 07/852,412
; FILING DATE: 16-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370132-2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-447-515-24

Query Match 100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 3 LNF 5

RESULT 21
US-09-357-952-82
; Sequence 82, Application US/09357952

; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease:
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-82

Query Match 100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 22
US-09-357-952-84
; Sequence 84, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease:
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-84

Query Match 100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 1 LNF 3

RESULT 23
US-09-357-952-132

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; Sequence 132, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-132

Query Match 100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred.No.2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
DB 2 LNF 4

RESULT 24
US-09-521-650-82
; Sequence 82, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-82

Query Match 100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred.No.2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
DB 2 LNF 4

RESULT 25
US-09-521-650-84
; Sequence 84, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-84

Query Match 100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No.2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
DB 1 LNF 3

RESULT 26
US-09-521-650-132
; Sequence 132, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-82

Query Match 100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No.2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; SEQ ID NO 132
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-132

Query Match 100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 2 LNF 4

RESULT 27
US-09-168-888-82
; Sequence 82, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168.888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-82

Query Match 100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 2 LNF 4

RESULT 28
US-09-168-888-84
; Sequence 84, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof

; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168.888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-84

Query Match 100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 1 LNF 3

RESULT 29
US-09-168-888-132
; Sequence 132, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168.888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-132

Query Match 100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
|||
Db 2 LNF 4

RESULT 30
US-09-357-952-81
; Sequence 81, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:

```
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-81

Query Match 100.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 2 LNF 4

RESULT 31
US-09-357-952-83
; Sequence 83, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-83

Query Match 100.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 1 LNF 3

RESULT 32
US-09-357-952-123
; Sequence 123, Application US/09357952
; Patent No. 6248904
```

```
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-123

Query Match 100.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 2 LNF 4

RESULT 33
US-09-521-650-81
; Sequence 81, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; EARLIER FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-81

Query Match 100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 1 LNF 3
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```
Db          2 LNF 4

RESULT 34
US-09-521-650-83
; Sequence 83, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-521-650-83

Query Match          100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LNF 3
           |||
Db          1 LNF 3

RESULT 35
US-09-521-650-123
; Sequence 123, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-521-650-123

Query Match          100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LNF 3
           |||
Db          1 LNF 3

RESULT 36
US-09-168-888-81
; Sequence 81, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-168-888-81

Query Match          100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LNF 3
           |||
Db          2 LNF 4

RESULT 37
US-09-168-888-83
; Sequence 83, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
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;/ CURRENT FILING DATE: 1998-10-09
;/ EARLIER APPLICATION NUMBER: US 60/061,582
;/ EARLIER FILING DATE: 1997-10-10
;/ EARLIER APPLICATION NUMBER: US 09/033,661
;/ EARLIER FILING DATE: 1998-03-03
;/ NUMBER OF SEQ ID NOS: 142
;/ SOFTWARE: PatentIn Ver. 2.0
;/ SEQ ID NO 83
;/ LENGTH: 6
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Description of Artificial Sequence:Synthetic
;/ OTHER INFORMATION: Peptide
US-09-168-888-83

Query Match 100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 1 LNF 3

RESULT 38
US-09-168-888-123
;/ Sequence 123, Application US/0916888
;/ Patent No. 6342611
;/ GENERAL INFORMATION:
;/ APPLICANT: Weber, Eckard
;/ APPLICANT: Cai, Sui Xiong
;/ APPLICANT: Keana, John P.W.
;/ APPLICANT: Drewe, John A.
;/ APPLICANT: Zhang, Han-Zhong
;/ TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
;/ TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
;/ TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
;/ TITLE OF INVENTION: Use Thereof
;/ FILE REFERENCE: 1735.0290002
;/ CURRENT APPLICATION NUMBER: US/09/168,888
;/ CURRENT FILING DATE: 1998-10-09
;/ EARLIER APPLICATION NUMBER: US 60/061,582
;/ EARLIER FILING DATE: 1997-10-10
;/ EARLIER APPLICATION NUMBER: US 09/033,661
;/ EARLIER FILING DATE: 1998-03-03
;/ NUMBER OF SEQ ID NOS: 142
;/ SOFTWARE: PatentIn Ver. 2.0
;/ SEQ ID NO 123
;/ LENGTH: 6
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Description of Artificial Sequence:Synthetic
;/ OTHER INFORMATION: Peptide
US-09-168-888-123

Query Match 100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 39
5342922-20
;/ Patent No. 5342922
;/ APPLICANT: MARSHALL, GARLAND R.;TOTH, MIHALY V.
;/ TITLE OF INVENTION: INHIBITORS OF RETROVIRAL PROTEASE
;/ NUMBER OF SEQUENCES: 23
;/ CURRENT APPLICATION DATA:

;/ APPLICATION NUMBER: US/07/320,742
;/ FILING DATE: 08-MAR-1989
;/ SEQ ID NO:20:
;/ LENGTH: 6
5342922-20

Query Match 100.0%; Score 3; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 1 LNF 3

RESULT 40
US-08-401-512-75
;/ Sequence 75, Application US/08401512
;/ Patent No. 5599673
;/ GENERAL INFORMATION:
;/ APPLICANT: Keating, Mark T.
;/ APPLICANT: Curran, Mark E.
;/ APPLICANT: Wang, Qing
;/ TITLE OF INVENTION: Long QT Syndrome Genes
;/ NUMBER OF SEQUENCES: 81
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Venable, Baetjer, Howard & Civiletti,LLP
;/ STREET: 1201 New York Avenue, Suite 1000
;/ CITY: Washington
;/ STATE: DC
;/ COUNTRY: USA
;/ ZIP: 20005-3917
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/401,512
;/ FILING DATE: 09-MAR-1995
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Saxe, Stephen A.
;/ REGISTRATION NUMBER: 38,609
;/ REFERENCE/DOCKET NUMBER: 19780-113879
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-962-4848
;/ TELEFAX: 202-962-8300
;/ INFORMATION FOR SEQ ID NO: 75:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 7 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ HYPOTHETICAL: NO
US-08-401-512-75

Query Match 100.0%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 4 LNF 6

RESULT 41
US-08-401-512-76
;/ Sequence 76, Application US/08401512
;/ Patent No. 5599673
;/ GENERAL INFORMATION:
;/ APPLICANT: Keating, Mark T.
;/ APPLICANT: Curran, Mark E.

; APPLICANT: Wang, Qing
; TITLE OF INVENTION: Long QT Syndrome Genes
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3917
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/401,512
; FILING DATE: 09-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 19780-113879
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-401-512-76

Query Match 100.0%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 42
US-08-598-873-40
; Sequence 40, Application US/08598873
; Patent No. 5928884
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Huebner, Kay
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
; METHODS BASED THEREON
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/598,873
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258

; REFERENCE/DOCKET NUMBER: 8666-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-598-873-40

Query Match 100.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 1 LNF 3

RESULT 43
US-09-226-012-110
; Sequence 110, Application US/09226012
; Patent No. 8207383
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; SYNDROME GENE
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/226,012
; CURRENT FILING DATE: 1999-01-06
; EARLIER APPLICATION NUMBER: 09/122,847
; EARLIER FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 110
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-226-012-110

Query Match 100.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 44
US-09-226-012-111
; Sequence 111, Application US/09226012
; Patent No. 8207383
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; SYNDROME GENE
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/226,012
; CURRENT FILING DATE: 1999-01-06
; EARLIER APPLICATION NUMBER: 09/122,847
; EARLIER FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 111
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown

; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:See Warmke and
; OTHER INFORMATION: Ganetzky, 1994.
US-09-226-012-111

Query Match 100.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 4 LNF 6

RESULT 45
US-08-605-430-40
; Sequence 40, Application US/08605430
; Patent No. 6242212
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Huebner, Kay
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,430
; FILING DATE: 22-FEB-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8666-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-605-430-40

Query Match 100.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 1 LNF 3

RESULT 46
US-09-357-952-34
; Sequence 34, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.

; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-34

Query Match 100.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 47
US-09-357-952-80
; Sequence 80, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-80

Query Match 100.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 48
US-09-082-279B-1065
; Sequence 1065, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly

```

; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1065
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-1065

```

```

Query Match      100.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 LNF 3
      |||
Db      1 LNF 3

```

RESULT 49

```

US-09-521-650-34
; Sequence 34, Application US/09521650
; Patent No. 6335429

```

```

; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong

```

```

; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof

```

```

; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 7

```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-34

```

```

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 LNF 3
      |||
Db      2 LNF 4

```

RESULT 50

```

US-09-521-650-80

```

```

; Sequence 80, Application US/09521650

```

```

; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-80

```

```

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 LNF 3
      |||
Db      2 LNF 4

```

RESULT 51

```

US-09-168-888-34
; Sequence 34, Application US/09168888
; Patent No. 6342611

```

```

; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong

```

```

; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof

```

```

; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 7

```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-34

```

```

Query Match      100.0%; Score 3; DB 4; Length 7;

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```
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1065

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 52
US-09-168-888-80
; Sequence 80, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewna, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-80

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 53
US-09-315-304B-1065
; Sequence 1065, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M. D.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1065
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:

; OTHER INFORMATION: Core polypeptide
US-09-834-784-1065

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      1 LNF 3

RESULT 54
US-09-834-784-1065
; Sequence 1065, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1065
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-1065

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      1 LNF 3

RESULT 55
5342922-21
; Patent No. 5342922
; APPLICANT: MARSHALL, GARLAND R.; TOTH, MIHALY V.
; TITLE OF INVENTION: INHIBITORS OF RETROVIRAL PROTEASE
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/320,742
; FILING DATE: 08-MAR-1989
; SEQ ID NO: 21
; LENGTH: 7
5342922-21

Query Match      100.0%; Score 3; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 56
US-08-030-731A-12
; Sequence 12, Application US/08030731A
```

; Patent No. 5426036
; GENERAL INFORMATION:
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Riess, Guenther Johannes
; APPLICANT: Uhlmann, Eugen
; APPLICANT: Wallmeier, Holger
; TITLE OF INVENTION: Processes for the Preparation of Foreign
; TITLE OF INVENTION: Proteins in Streptomycetes
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,731A
; FILING DATE: 12-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/189,840
; FILING DATE: 03-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/430,622
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/687,610
; FILING DATE: 19-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,757
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 37 14 866.4
; FILING DATE: 05-MAY-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 38 37 273.8
; FILING DATE: 03-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 39 27 449.7
; FILING DATE: 19-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 12 818.0
; FILING DATE: 21-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirschner Michael K.
; REGISTRATION NUMBER: 34,851
; REFERENCE/DOCKET NUMBER: 02481-0593-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-030-731A-12

Query Match 100.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 57
US-08-264A-20
; Sequence 20, Application US/08045264A
; Patent No. 5436131
; GENERAL INFORMATION:
; APPLICANT: CONDR, JON H.
; APPLICANT: GRAHAM, DONALD J.
; APPLICANT: GOTLIB, LEAH
; TITLE OF INVENTION: COLOR SCREENING ASSAY FOR IDENTIFYING
; TITLE OF INVENTION: DRUG-RESISTANT HIV PROTEASE MUTANTS AND INHIBITORS
; TITLE OF INVENTION: THEREOF.
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc. Lincoln Ave.
; STREET: PO Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh IIfx
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/045,264A
; FILING DATE: 02-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEREDITH, ROY, D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18936
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; DESCRIPTION: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal fragment
US-08-045-264A-20

Query Match 100.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 2 LNF 4

RESULT 58
US-08-322-267A-71
; Sequence 71, Application US/08922267A
; Patent No. 5861239
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,267A
FILING DATE: 2-SEP-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/829,553
FILING DATE: 28-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/631,200
FILING DATE: 12-APR-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-922-267A-71

Query Match 100.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 5 LNF 7

RESULT 59
US-08-599-455B-33
Sequence 33, Application US/08599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-599-455B-33

Query Match 100.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

RESULT 60
US-08-925-002-37
Sequence 37, Application US/08925002
Patent No. 6048527
GENERAL INFORMATION:
APPLICANT: Granoff, Dan M.
APPLICANT: Moe, Gregory R.
TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
EPITOPES IN THE PREPARATION OF VACCINE
COMPOSITIONS
FILE REFERENCE: 1238.002
CURRENT APPLICATION NUMBER: US/08/925,002
CURRENT FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 37
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sequence from
a phage display peptide library
US-08-925-002-37

Query Match 100.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 1 LNF 3

RESULT 61
US-09-144-759-8
Sequence 8, Application US/09144759
Patent No. 6117639
GENERAL INFORMATION:
APPLICANT: Hooch, Thomas
APPLICANT: Germann, Ursula

; APPLICANT: Kwong, Ann
; TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS
; FILE REFERENCE: VPI/98-08
; CURRENT APPLICATION NUMBER: US/09/144,759
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-144-759-8

Query Match 100.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 2 LNF 4

RESULT 62
US-09-069-781B-33
; Sequence 33, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,781B
; FILING DATE: 29-APRIL-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: US 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: US 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: US 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: US 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: US 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: US 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: US 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: US 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283

; REFERENCE/DOCKET NUMBER: 07334/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-069-781B-33

Query Match 100.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
|||
Db 4 LNF 6

RESULT 63
US-09-137-132-33
; Sequence 33, Application US/09137132
; Patent No. 6380363
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,132
; FILING DATE: 18-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019004

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-864-564A-33

Query Match 100.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

RESULT 64
US-08-864-564A-33
; Sequence 33, Application US/08864564A
; Patent No. 6395498
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,564A
; FILING DATE: 28-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154

```

; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-094-410-33

Query Match 100.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

RESULT 66
US-08-708-123D-33
; Sequence 33, Application US/08708123D
; Patent No. 6482927
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,123D
FILING DATE: 03-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996

APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown

; MOLECULE TYPE: peptide
US-08-708-123D-33

Query Match 100.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

RESULT 67
US-08-583-153A-33
; Sequence 33, Application US/08583153A
; Patent No. 6506877
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,153A
FILING DATE: 28-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/016001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-583-153A-33

Query Match 100.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

```
RESULT 68
US-09-570-267-8
; Sequence 8, Application US/09570267
; Patent No. 6528276
; GENERAL INFORMATION:
; APPLICANT: Hock, Thomas
; APPLICANT: Hermann, Ursula
; APPLICANT: Kwong, Ann
; TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS
; TITLE OF INVENTION: USEFUL FOR MEASURING PROTEASE ACTIVITY
; FILE REFERENCE: VPI/98-08
; CURRENT APPLICATION NUMBER: US/09/570,267
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 09/144,759
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-570-267-8

Query Match 100.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 2 LNF 4

RESULT 69
US-08-638-524B-33
; Sequence 33, Application US/08638524B
; Patent No. 6548269
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OB
; TITLE OF INVENTION: CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,524B
; FILING DATE: 26-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/593,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/018001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-638-524B-33

Query Match 100.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 70
US-08-435-241A-5
; Sequence 5, Application US/08435241A
; Patent No. 5674833
; GENERAL INFORMATION:
; APPLICANT: Mikkelsen et al.
; TITLE OF INVENTION: Detergent Compositions Containing Protease And
; TITLE OF INVENTION: No. 5674833el Inhibitors For Use Therein
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5674833o No. 5674833disk of No. 5674833th America, Inc.
; STREET: 405 Lexington Ave., Suite 6200
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,241A
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 252
; ATTORNEY/AGENT INFORMATION:
; NAME: Elias J. Lambiris, Esq.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3486.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 867-0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-435-241A-5

Query Match 100.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 6 LNF 8
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RESULT 71
 US-09-053-941-25
 ; Sequence 25, Application US/09053941
 ; Patent No. 6271354
 ; GENERAL INFORMATION:
 ; APPLICANT: SRINIVASAN, ALGARSAMY
 ; APPLICANT: KOPROWSKI, HILARY
 ; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
 ; FILE REFERENCE: Chimeric Viral Proteins
 ; CURRENT APPLICATION NUMBER: US/09/053,941
 ; CURRENT FILING DATE: 1998-04-02
 ; EARLIER APPLICATION NUMBER: 60/043,380
 ; EARLIER FILING DATE: 1999-04-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 25
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Flag
 ; OTHER INFORMATION: protein--HIV-1 protease chimera
 US-09-053-941-25

Query Match 100.0%; Score 3; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 Db 7 LNF 9

RESULT 72
 US-09-817-413-25
 ; Sequence 25, Application US/09817413
 ; Patent No. 6436648
 ; GENERAL INFORMATION:
 ; APPLICANT: SRINIVASAN, ALGARSAMY
 ; APPLICANT: KOPROWSKI, HILARY
 ; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
 ; FILE REFERENCE: Chimeric Viral Proteins
 ; CURRENT APPLICATION NUMBER: US/09/817,413
 ; CURRENT FILING DATE: 2001-03-25
 ; PRIOR APPLICATION NUMBER: 60/043,380
 ; PRIOR FILING DATE: 1999-04-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 25
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Flag
 ; OTHER INFORMATION: protein--HIV-1 protease chimera
 US-09-817-413-25

Query Match 100.0%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 Db 7 LNF 9

RESULT 73
 US-09-311-784A-220
 ; Sequence 220, Application US/09311784A
 ; Patent No. 6534482
 ; GENERAL INFORMATION:
 ; APPLICANT: FIKES, JOHN D.

; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; TITLE OF INVENTION: Immune Response and Methods of Using the Same
 ; FILE REFERENCE: 39963-20022.01
 ; CURRENT APPLICATION NUMBER: US/09/311,784A
 ; CURRENT FILING DATE: 1999-05-13
 ; PRIOR APPLICATION NUMBER: US 60/085,751
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 220
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HBV ENV 197 (peptide 20.0137)
 US-09-311-784A-220

Query Match 100.0%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 Db 6 LNF 8

RESULT 74
 US-09-311-784A-354
 ; Sequence 354, Application US/09311784A
 ; Patent No. 6534482
 ; GENERAL INFORMATION:
 ; APPLICANT: FIKES, JOHN D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; TITLE OF INVENTION: Immune Response and Methods of Using the Same
 ; FILE REFERENCE: 39963-20022.01
 ; CURRENT APPLICATION NUMBER: US/09/311,784A
 ; CURRENT FILING DATE: 1999-05-13
 ; PRIOR APPLICATION NUMBER: US 60/085,751
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 354
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0041)
 US-09-311-784A-354

Query Match 100.0%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LNF 3
 Db 2 LNF 4

RESULT 75
 US-08-185-448-10
 ; Sequence 10, Application US/08185448

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; Patent No. 5580747
; GENERAL INFORMATION:
; APPLICANT: SHULTZ, JOHN W.
; APPLICANT: WHITE, DOUGLAS H.
; TITLE OF INVENTION: NON-RADIOACTIVE KINASE,
; TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDRUS, SCARLES, STARKE & SAWALL
; STREET: 100 E. WISCONSIN AVENUE, SUITE 1100
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,448
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,928
; FILING DATE: 12-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SARA, CHARLES S
; REGISTRATION NUMBER: 30492
; REFERENCE/DOCKET NUMBER: F.3347-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 255-2022
; TELEFAX: (608) 255-2182
; TELEX: 26832 ANDSTARK
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1
; OTHER INFORMATION: /label= LABEL
; OTHER INFORMATION: /note= "LOCATION OF LISSAMINE RHODAMINE
; OTHER INFORMATION: DETECTION TAG"
; US-08-185-448-10
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Query Match 100.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 3 LNF 5
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Search completed: November 25, 2003, 20:30:09
Job time : 3.42442 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 10.2907 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-34

Perfect score: 15

Sequence: 1 MHQPPQLPPTWFP 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4	26.7	8	SI0783	enamelin f - bovin
2	4	26.7	12	PN0863	dystrophin-associ
3	4	26.7	13	I84603	deoxynucleotidyltr
4	4	26.7	19	PH1352	Ig heavy chain DJ
5	4	26.7	20	PC2030	tumor-derived adhe
6	3	20.0	7	S71299	ICL2 protein - Par
7	3	20.0	7	PT0283	Ig heavy chain CRD
8	3	20.0	8	SI6324	hypothetical prote
9	3	20.0	9	B38740	Ig kappa chain C r
10	3	20.0	10	PC2171	triacylglycerol li
11	3	20.0	10	SI8396	probable glucose-6
12	3	20.0	10	C39745	sphingomyelinase -
13	3	20.0	11	XASNBA	bradykinin-potent
14	3	20.0	11	YHRT	morphogenetic neur
15	3	20.0	11	YHUU	morphogenetic neur
16	3	20.0	11	YHBO	morphogenetic neur
17	3	20.0	11	YHXAE	morphogenetic neur
18	3	20.0	11	YHJFY	seed protein ws-18
19	3	20.0	11	C61497	173K exoantigen -
20	3	20.0	11	I33098	hypothetical 1.2K
21	3	20.0	12	C39109	ATP synthase D cha
22	3	20.0	12	PN0046	inhibin alpha chai
23	3	20.0	13	A60856	actin 7 - soybean
24	3	20.0	13	SI5755	neural cell adhesi
25	3	20.0	13	D39690	cell surface glyco
26	3	20.0	13	A40207	Ig lambda chain V-
27	3	20.0	13	G61458	18K iron-sulfur pr
28	3	20.0	14	PQ0152	223K exoantigen -
29	3	20.0	14	C33098	

30	3	20.0	14	2	PH1566	cerebrin 30 - huma
31	3	20.0	14	2	PH1348	Ig heavy chain DJ
32	3	20.0	14	2	H83778	hypothetical prote
33	3	20.0	15	2	PQ0545	capsid protein VPI
34	3	20.0	15	2	B39109	hypothetical 1.5K
35	3	20.0	15	2	S29386	nigerythrin - Desu
36	3	20.0	15	2	PA0014	seed storage prote
37	3	20.0	15	2	PN0173	seed storage prote
38	3	20.0	15	2	PA0060	protein QF200037 -
39	3	20.0	15	2	B61457	alpha-glucosidase
40	3	20.0	15	2	A60221	apolipoprotein A-I
41	3	20.0	16	2	F44908	chitinase (EC 3.2.
42	3	20.0	16	2	A54877	alpha-conotoxin Pn
43	3	20.0	16	2	B54877	alpha-conotoxin Pn
44	3	20.0	16	2	E58503	superoxide dismuta
45	3	20.0	16	2	S01104	hypothetical prote
46	3	20.0	16	2	PH0763	T-cell receptor be
47	3	20.0	16	2	PH0759	T-cell receptor be
48	3	20.0	17	2	SI5754	actin 6 - soybean
49	3	20.0	17	2	S32587	L-ascorbate peroxi
50	3	20.0	17	2	S59481	hydroxyproline-ric
51	3	20.0	17	2	I55612	thyroid hormone re
52	3	20.0	17	2	SI0786	enamelin, 26K - bo
53	3	20.0	18	2	S04229	N4-(beta-N-acetylgl
54	3	20.0	18	2	PC2280	prolylendopeptidas
55	3	20.0	18	2	S39845	2-aminobenzoate-Co
56	3	20.0	18	2	B45138	arsenite oxidase I
57	3	20.0	18	2	SI0452	hypothetical prote
58	3	20.0	18	2	A54195	Na+/K+-exchanging
59	3	20.0	19	2	PC1323	endopeptidase Clp
60	3	20.0	19	2	S60633	H+-transporting tw
61	3	20.0	19	2	C32735	thyroglobulin - pi
62	3	20.0	19	2	B32735	thyroglobulin - Sh
63	3	20.0	19	2	B61409	genome polyprotein
64	3	20.0	19	2	S39486	cell wall protein,
65	3	20.0	19	2	A37968	neural surface pro
66	3	20.0	19	2	A34467	36K microfibril-as
67	3	20.0	20	2	S21737	coumarin 7-monooxy
68	3	20.0	20	2	S29817	cytochrome P450 2C
69	3	20.0	20	2	A33878	notechis II-5b non
70	3	20.0	20	2	A39328	ribulose-bisphosph
71	3	20.0	20	2	A37111	tubulin alpha chai
72	3	20.0	20	2	A54519	apolipoprotein A-I
73	3	20.0	20	2	A05313	acetyl-CoA synthet
74	3	20.0	20	2	T44453	alpha-amylase (EC
75	3	20.0	20	2	PH1380	dimeric protein (B
76	3	20.0	20	2	S65605	glue protein - Cal
77	3	20.0	20	2	A61093	octopamine recepto
78	3	20.0	20	2	S28779	interphotoreceptor
79	3	20.0	20	2	F24417	acidic fibroblast
80	3	20.0	20	2	S03954	somatotropin - syn
81	3	20.0	20	2	I53672	tyrosine protein k
82	3	20.0	20	2	I78890	tyrosine-melanocyt
83	2	13.3	4	2	A32039	starvation-induced
84	2	13.3	4	2	S53508	proctolin - Americ
85	2	13.3	5	1	H0R0HA	peptidyl-dipeptida
86	2	13.3	5	2	JN0860	flagellar protein
87	2	13.3	5	2	E42364	ribulose-bisphosph
88	2	13.3	5	2	PS0324	acid proteinase li
89	2	13.3	5	2	B37988	proctolin - Atlant
90	2	13.3	5	2	A60411	27.5 kDa structura
91	2	13.3	5	2	I44817	27.5K structural p
92	2	13.3	5	2	I44817	27.5K structural p
93	2	13.3	5	2	E44817	28.5K structural p
94	2	13.3	5	2	C44817	28K structural pro
95	2	13.3	5	2	A44817	halo-toxin - Pseud
96	2	13.3	5	2	A61049	hypothetical prote
97	2	13.3	6	2	A37765	contraction-inhibi
98	2	13.3	6	2	B27696	contraction-inhibi
99	2	13.3	6	2	B27696	transferrin - bovi
100	2	13.3	6	2	A19780	

ALIGNMENTS

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RESULT 1
S10783
enamelin f - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10783
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10783
A:Molecule type: protein
A:Residues: 1-8 <STR>
C:Keywords: enamel; phosphoprotein

Query Match      26.7%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
      |||||
Db      2 PLPP 5

RESULT 2
PN0663
dystrophin-associated glycoprotein A3a-II - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C:Accession: PN0663
R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in the plasma membrane of skeletal muscle
A:Reference number: PN0662; MUID:94156881; PMID:8113213
A:Accession: PN0663
A:Molecule type: protein
A:Residues: 1-12 <YCS>
C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C:Keywords: glycoprotein; skeletal muscle

Query Match      26.7%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
      |||||
Db      3 PLPP 6

RESULT 3
I84603
deoxynucleotidyltransferase - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C:Accession: I84603
R:Koizumi, O.; Kaneda, T.; Morishita, R.
Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A:Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man
A:Reference number: I45884; MUID:87213162; PMID:3579900
A:Accession: I84603
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-13 <RES>
A:Cross-references: GB:M26144; NID:g951194; PIDN:AAA74588.1; PID:g951195
C:Genetics:
A:Gene: GDB:DNTT
A:Cross-references: GDB:l19100; OMIM:187410
A:Map position: 10q23-10q24

Query Match      26.7%; Score 4; DB 2; Length 13;

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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QPLP 9
      |||||
Db      8 QPLP 11

RESULT 4
PH1352
Ig heavy chain DJ region (clone C100-115) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1352
R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1352
A:Molecule type: DNA
A:Residues: 1-19 <WAS>
A:Note: the authors translated the stop codon for residue 2 as X
C:Keywords: heterotetramer; immunoglobulin

Query Match      26.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPTV 12
      |||||
Db      8 PPTV 11

RESULT 5
PC2030
tumor-derived adhesion factor - human (fragment)
N:Alternate names: 30K protein
C:Species: Homo sapiens (man)
C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jan-2000
C:Accession: PC2030
R:Akaogi, K.; Okabe, Y.; Funahashi, K.; Yoshitake, Y.; Nishikawa, K.; Yasumitsu, H.; Umehara, K.
Biochem. Biophys. Res. Commun. 198, 1046-1053, 1994
A:Title: Cell adhesion activity of a 30-kDa major secreted protein from human bladder cancer cells
A:Reference number: PC2030; MUID:94161713; PMID:8117260
A:Accession: PC2030
A:Molecule type: protein
A:Residues: 1-20 <AKA>
A:Experimental source: cell line EJ-1
C:Comment: This protein relates with the aberrant cell adhesion of cancer cells.

Query Match      26.7%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
      |||||
Db      16 PLPP 19

RESULT 6
S71299
ICL2 protein - Paramesium tetraurelia (fragment)
C:Species: Paramesium tetraurelia
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
C:Accession: S71299
R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beissson, J.
Eur. J. Biochem. 238, 121-128, 1996
A:Title: Characterization of centrin genes in Paramesium.
A:Reference number: S71298; MUID:96248429; PMID:8665928
A:Accession: S71299
A:Molecule type: protein
A:Residues: 1-7 <MAD>
A:Experimental source: strain d4-2

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C;Genetics:
A;Genetic code: SGC5

Query Match 20.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
|||
Db 2 QPP 4

RESULT 7

PT0283
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0283
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0283
A;Molecule type: DNA
A;Residues: 1-7 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
|||
Db 5 QPP 7

RESULT 8

S16324
hypothetical protein 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C;Accession: S16324
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A;Title: A novel class of plant proteins containing a homeodomain with a closely linked
A;Reference number: S16323; MUID:91266907; PMID:1675603
A;Accession: S16324
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <RUB>
A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 20.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
|||
Db 6 LPP 8

RESULT 9

B38740
Ig kappa chain C region (PY20) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: B38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: B38740

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-9 <RUF>

Query Match 20.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PTV 12
|||
Db 5 PTV 7

RESULT 10

PC2171
triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fra
C;Species: Rhizopus niveus
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: PC2171
R;Kobno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.
Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994
A;Title: Purification, characterization, and crystallization of two types of lipase fr
A;Reference number: PC2171; MUID:94319059; PMID:7765029
A;Accession: PC2171
A;Molecule type: protein
A;Residues: 1-10 <KOH>
A;Comment: This enzyme catalyzes the hydrolysis of the ester bonds.
C;Keywords: carboxylic ester hydrolase

Query Match 20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
|||
Db 5 LPP 7

RESULT 11

S18396
probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Acetobacter hansenii (fra
C;Species: Acetobacter hansenii
C;Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999
C;Accession: S18396
R;Levy, H.R.; Cook, C.
Arch. Biochem. Biophys. 291, 161-167, 1991
A;Title: Purification and properties of NADP-linked glucose-6-phosphate dehydrogenase
A;Reference number: S18396; MUID:92027789; PMID:1929428
A;Accession: S18396
A;Molecule type: protein
A;Residues: 1-10 <LEV>
A;Experimental source: ATCC 23769
C;Function:
A;Description: catalyzes reduction of glucose-6-phosphate to gluconolactone 6-phosphat
A;Pathway: pentose phosphate pathway
C;Keywords: oxidoreductase; homotetramer; NADP; pentose phosphate pathway

Query Match 20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
|||
Db 3 LPP 5

RESULT 12

C39745
spingomyelinase - Rhodococcus sp. (fragment)
C;Species: Rhodococcus sp.
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C;Accession: C39745
R;Ito, M.; Ikegami, Y.; Yamagata, T.

J. Biol. Chem. 266, 7919-7926, 1991
A:Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosceramidases. E1
ble using these activator proteins.
A:Reference number: A39745; MUID:91210321; PMID:1850427
A:Accession: C39745
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <ITO>

Query Match 20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPP 9
|||
Db 3 LPP 5

RESULT 13
XASNEA
bradykinin-potentiating peptide B - mamushi
C:Species: Agkistrodon blomhoffi (mamushi)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
C:Accession: A01254
R:Kato, H.; Suzuki, T.
Proc. Jpn. Acad. 46, 176-181, 1970
A:Reference number: A01254
A:Accession: A01254
A:Molecule type: protein
A:Residues: 1-11 <KAT>
A:Note: the sequence of the natural peptide was confirmed by the synthesis and analysis
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; vena
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
|||
Db 3 LPP 5

RESULT 14
YHBT
morphogenetic neuropeptide - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: A01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical structu
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head
C:Superfamily: unassigned animal peptides
C:Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
|||
Db 1 QPP 3

RESULT 15

YHHU

morphogenetic neuropeptide - human

C:Species: Homo sapiens (man)

C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C:Accession: B01427; A01427

R:Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele

A:Reference number: A93266; MUID:82035850; PMID:7290191

A:Accession: B01427

A:Molecule type: protein

A:Residues: 1-11 <BOD>

R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.

A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis

A:Note: the synthetic peptide was identical with the natural peptide in chemical struct

C:Comment: this peptide was first isolated from nerve cells of hydra and was called head

C:Superfamily: unassigned animal peptides

C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neurope

F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #stat

Query Match 20.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
|||
Db 1 QPP 3

RESULT 16

YHBO

morphogenetic neuropeptide - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C:Accession: C01427; A01427

R:Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele

A:Reference number: A93266; MUID:82035850; PMID:7290191

A:Accession: C01427

A:Molecule type: protein

A:Residues: 1-11 <BOD>

R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.

A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis

A:Note: the synthetic peptide was identical with the natural peptide in chemical struct

C:Comment: This peptide was first isolated from nerve cells of hydra and was called head

C:Superfamily: unassigned animal peptides

C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neurope

F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #stat

Query Match 20.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
|||
Db 1 QPP 3

RESULT 17

YHXA
morphogenetic neuroepitide - sea anemone (Anthopleura elegantissima)
N/Alternate names: head activator
C/Species: Anthopleura elegantissima
C/Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C/Accession: A93900; A01427
R/Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
A/Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A/Reference number: A93900
A/Accession: A93900
A/Molecule type: protein
A/Residues: 1-11 <SCH>
R/Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A/Title: Synthesis of a new neuroepitide, the head activator from hydra.
A/Reference number: A91296; PMID:82050803; PMID:7297679
A/Contents: annotation; synthesis
A/Note: The synthetic peptide was identical with the natural peptide in chemical structure
C/Comment: This peptide was first isolated from nerve cells of hydra and was called head activator.
n mammalian intestine and hypothalamus.
C/Superfamily: unassigned animal peptides
C/Keywords: growth factor; hormone; neuroepitide; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
|||
Db 1 QPP 3

RESULT 18

YHJFY
morphogenetic neuroepitide - Hydra attenuata
N/Alternate names: head activator
C/Species: Hydra attenuata
C/Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C/Accession: B93900; A01427
R/Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
A/Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A/Reference number: A93900
A/Accession: B93900
A/Molecule type: protein
A/Residues: 1-11 <SCH>
R/Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A/Title: Synthesis of a new neuroepitide, the head activator from hydra.
A/Reference number: A91296; PMID:82050803; PMID:7297679
A/Contents: annotation; synthesis
A/Note: The synthetic peptide was identical with the natural peptide in chemical structure
C/Comment: This peptide was first isolated from nerve cells of hydra and was called head activator.
n mammalian intestine and hypothalamus.
C/Superfamily: unassigned animal peptides
C/Keywords: growth factor; hormone; neuroepitide; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
|||
Db 1 QPP 3

RESULT 19

C61497
seed protein ws-18 - winged bean (fragment)

C/Species: Psophocarpus tetragonolobus (winged bean)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C/Accession: C61497
R/Hirano, H.

J. Protein Chem. 8, 115-130, 1989
A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis
A/Reference number: A61491; PMID:89351606; PMID:2765119
C/Accession: C61497

A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-11 <HIR>
C/Keywords: glycoprotein; seed

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12
|||
Db 3 PTV 5

RESULT 20

I33098
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C/Species: Plasmodium falciparum
C/Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C/Accession: I33098
R/Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990
A/Reference number: A33098
A/Accession: I33098
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-11 <NIC>

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
|||
Db 2 LPP 4

RESULT 21

C39109
hypothetical 1.2K protein - hepatitis C virus
N/Alternate names: hypothetical protein 3
C/Species: hepatitis C virus
C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C/Accession: C39109; JQ1586
R/Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A/Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A/Reference number: A39109; PMID:91156678; PMID:1705704
A/Accession: C39109
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-12 <HAN>
R/Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992

A/Title: Cloning and sequencing of the structural region and expression of putative coat protein gene of hepatitis C virus
A/Reference number: JQ1584; PMID:92300349; PMID:1318944
A/Accession: JQ1586
A/Molecule type: genomic RNA
A/Residues: 1-12 <KUM>
A/Experimental source: strain U.K.

Query Match 20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
|||
Db 1 QPP 3

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Qy      4 PPQ 6
      |||
Db      8 PPQ 10

RESULT 22
PN0046
A:Title: ATP synthase D chain, mitochondrial - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C:Accession: PN0046
R:Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro
A:Reference number: PN0041
A:Accession: PN0046
A:Molecule type: protein
A:Residues: 1-12 <KAT>
A:Experimental source: neuroblastoma cell
C:Comment: The molecular mass is 24,400 and the pI is 5.37. The amino-terminus is blocked
C:Keywords: brain; mitochondrion

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 HQP 4
      |||
Db      6 HQP 8

RESULT 23
A60856
inhibin alpha chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60856
R:Levensha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenthal
J. Endocrinol. 113, 213-221, 1997
A:Title: Isolation of inhibin from ovine follicular fluid.
A:Reference number: A60856; MUID:87224684; PMID:3585232
A:Accession: A60856
A:Molecule type: protein
A:Residues: 1-13 <LEV>
C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C:Superfamily: inhibin
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 HQP 4
      |||
Db      6 HQP 8

RESULT 24
S15755
actin 7 - soybean (fragment)
C:Species: Glycine max (soybean)
C:Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C:Accession: S15755
R:Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A:Reference number: S15754; MUID:91346640; PMID:2102831
A:Accession: S15755
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <PEA>
A:Cross-references: EMBL:X17120; NID:g18527; PIDN:CAA34980.1; PID:g18528

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C:Superfamily: actin
C:Keywords: cytoskeleton; structural protein

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 QPL 8
      |||
Db      8 QPL 10

RESULT 25
D39690
neural cell adhesion molecule, cardiac splice form +, -, + - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: D39690
R:Reyes, A.A.; Small, S.J.; Akeson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule m
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: D39690
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A:Molecule type: mRNA
A:Residues: 1-13 <REV>
A:Cross-references: GB:M63970
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PPQ 6
      |||
Db      7 PPQ 9

RESULT 26
A40207
cell surface glycoprotein gp150 - slime mold (Dictyostelium discoideum) (fragment)
C:Species: Dictyostelium discoideum
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 31-Dec-1993
C:Accession: A40207
R:Gao, E.N.; Shier, P.; Siu, C.H.
J. Biol. Chem. 267, 9409-9415, 1992
A:Title: Purification and partial characterization of a cell adhesion molecule (gp150)
A:Reference number: A40207; MUID:92250549; PMID:1577768
A:Accession: A40207
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <GAO>
C:Keywords: glycoprotein

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PPT 11
      |||
Db      3 PPT 5

RESULT 27
G61458
Ig lambda chain V-II region (AZI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: G61458; PI0159
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-ass

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A;Reference number: A61458; MUID:90039128; PMID:2478651
A;Accession: G61458
A;Molecule type: protein
A;Residues: 1-13 <BRO>
C;Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycoprotein
C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
|||
Db 6 QPP 8

RESULT 28

PQ0152
18K iron-sulfur protein - Chlamydomonas reinhardtii chloroplast (fragment)
C;Alternate names: frxB homolog
C;Species: Chlamydomonas reinhardtii

C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-Sep-1993
C;Accession: PQ0152
R;Wu, M.; Nie, Z.Q.; Yang, J.

Plant Cell 1, 551-557, 1989

A;Title: The 18-KD protein that binds to the chloroplast DNA replicative origin is an iron-sulfur protein

A;Reference number: PQ0152; MUID:92404720; PMID:2562513

A;Accession: PQ0152

A;Molecule type: protein

A;Residues: 1-14 <WUM>

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 MFP 15
|||
Db 1 MFP 3

RESULT 29

C33098
223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C;Accession: C33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: C33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <NIC>

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
|||
Db 2 LPP 4

RESULT 30

PH1566

cerebrin 30 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C;Accession: PH1566

R;Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.

J. Neurochem. 61, 533-540, 1993

A;Title: Micropurification of two human cerebrospinal fluid proteins by high performance liquid chromatography

A;Reference number: PH1566; MUID:93329419; PMID:8336140

A;Accession: PH1566

A;Molecule type: protein

A;Residues: 1-14 <LEO>

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8
|||
Db 9 QPL 11

RESULT 31

PH1348

IG heavy chain DJ region (clone C100-106) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1348

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1348

A;Molecule type: DNA

A;Residues: 1-14 <WAS>

C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPT 11
|||
Db 4 PPT 6

RESULT 32

H83778

hypothetical protein BH1032 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C;Accession: H83778

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai, T.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and its relationship to other Bacillus species

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: H83778

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-14 <STO>

A;Cross-references: GB:AP001510; GB:BA000004; NID:G10173440; PIDN:BAB04751.1; GSPDB:GNO

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH1032

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TVM 13
|||
Db 8 TVM 10

RESULT 33

PQ0545

capsid protein VP19C - human herpesvirus 1 (fragment)

C;Species: human herpesvirus 1

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

```

C;Accession: PQ0545
R;Davison, M.D.; Rixon, F.J.; Davison, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A;Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes
A;Reference number: PQ0544; MUID:93019027; PMID:1328483
A;Accession: PQ0545
A;Molecule type: protein
A;Residues: 1-15 <DAV>
A;Experimental source: strain 17
C;Genetics:
A;Gene: UL38
C;Keywords: capsid protein

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 P L P 9
Db      5 P L P 7

RESULT 34
B39109
hypothetical 1.5K protein - hepatitis C virus
N;Alternate names: hypothetical protein 2
C;Species: hepatitis C virus
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C;Accession: B39109; JQ1585
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A;Reference number: A39109; MUID:91156678; PMID:1705704
A;Accession: B39109
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-15 <HAN>
A;Cross-references: GB:M58406
R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A;Title: Cloning and sequencing of the structural region and expression of putative core
A;Reference number: JQ1584; MUID:92300349; PMID:1318944
A;Accession: JQ1585
A;Molecule type: genomic RNA
A;Residues: 1-15 <KOM>
A;Experimental source: strain U.K.

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 Q P P 5
Db      5 Q P P 7

RESULT 35
S29386
nigerythrins - Desulfovibrio vulgaris
C;Species: Desulfovibrio vulgaris
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C;Accession: S29386
R;Pierik, A.J.; Wolbert, R.B.G.; Portier, G.L.; Verhagen, M.F.J.M.; Hagen, W.R.
Eur. J. Biochem. 212, 237-245, 1993
A;Title: Nigerythrins and rubrythrins from Desulfovibrio vulgaris each contain two mononit
A;Reference number: S29385; MUID:93185629; PMID:8383040
A;Accession: S29386
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <PIE>

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C;Accession: PQ0545
R;Davison, M.D.; Rixon, F.J.; Davison, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A;Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes
A;Reference number: PQ0544; MUID:93019027; PMID:1328483
A;Accession: PQ0545
A;Molecule type: protein
A;Residues: 1-15 <DAV>
A;Experimental source: strain 17
C;Genetics:
A;Gene: UL38
C;Keywords: capsid protein

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 P T V 12
Db      8 P T V 10

RESULT 36
PA0014
seed storage protein 12S 3 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C;Accession: PA0014
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimension
A;Reference number: PA0001
A;Accession: PA0014
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: seed
C;Keywords: seed; storage protein

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 P Q Q 6
Db      7 P Q Q 9

RESULT 37
PN0173
seed storage protein 12S4 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 23-Mar-2001
C;Accession: PN0173
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A;Description: Two dimensional electrophoresis of plant proteins and standardization of
A;Reference number: PN0173
A;Accession: PN0173
A;Molecule type: protein
A;Residues: 1-15 <TSU>
A;Experimental source: seeds

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 P Q Q 6
Db      7 P Q Q 9

RESULT 38
PA0060
protein QF200037 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0060
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A;Reference number: PA0051
A;Accession: PA0060
A;Molecule type: protein
A;Residues: 1-15 <CHO>

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY .7 PLP 9
 Db 4 PLP 6
 RESULT 39
 B61457
 alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
 C/Species: Tetrahymena pyriformis
 C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
 C/Accession: B61457
 R/Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
 J. Protozool. 36, 562-567, 1989
 A/Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification
 A/Reference number: A61457; PMID:90095988; PMID:2689637
 A/Accession: B61457
 A/Molecule type: protein
 A/Residues: 1-15 <BAN>
 C/Genetics:
 A/Genetic code: SGC5
 C/Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monomeric
 Query Match 20.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 LPP 10
 Db 2 LPP 4
 RESULT 40
 A60221
 apolipoprotein A-I - common carp (fragment)
 C/Species: Cyprinus carpio (common carp)
 C/Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-1993
 C/Accession: A60221
 R/Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.
 J. Neurochem. 55, 1237-1243, 1990
 A/Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve regeneration
 A/Reference number: A60221; PMID:90376100; PMID:2118944
 A/Accession: A60221
 A/Molecule type: protein
 A/Residues: 1-15 <HAR>
 A/Note: protein from plasma and from optic nerve yielded the same sequence
 C/Keywords: lipid binding; lipoprotein
 Query Match 20.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QPP 5
 Db 2 QPP 4
 RESULT 41
 F44908
 chitinase (EC 3.2.1.14), 23.4K - Streptomyces olivaceoviridis (fragment)
 C/Species: Streptomyces olivaceoviridis
 C/Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000
 C/Accession: F44908
 R/Romaguera, A.; Menge, U.; Breves, R.; Diekmann, H.
 J. Bacteriol. 174, 3450-3454, 1992
 A/Title: Chitinases of Streptomyces olivaceoviridis and significance of processing for morphogenesis
 A/Reference number: A44908; PMID:92276319; PMID:1592803
 A/Accession: F44908
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-16 <ROM>
 A/Experimental source: ATCC 11238
 A/Note: sequence extracted from NCBI backbone (NCBIP:104594)
 C/Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation
 Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 MFP 15
 Db 6 MFP 8
 RESULT 42
 A54877
 alpha-conotoxin PnIA [validated] - cone shell (Conus pennaceus)
 N/Alternate names: alpha-Crx-PnIA
 C/Species: Conus pennaceus
 C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
 C/Accession: A54877
 R/Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlot
 Biochemistry 33, 9523-9529, 1994
 A/Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine release
 A/Reference number: A54877; PMID:94347719; PMID:8068627
 A/Accession: A54877
 A/Molecule type: protein
 A/Residues: 1-16 <FAI>
 R/Hu, S.H.; Gehrman, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.
 submitted to the Brookhaven Protein Data Bank, January 1996
 A/Reference number: A66355; PDB:1PEN
 A/Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16
 C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic
 C/Superfamily: alpha-conotoxin
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 F/2-8,3-16/Disulfide bonds: #status experimental
 F/16/Modified site: amidated carboxyl end (Cys) #status experimental
 Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 LPP 10
 Db 5 LPP 7
 RESULT 43
 B54877
 alpha-conotoxin PnIB - cone shell (Conus pennaceus)
 C/Species: Conus pennaceus
 C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
 C/Accession: B54877
 R/Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlot
 Biochemistry 33, 9523-9529, 1994
 A/Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine release
 A/Reference number: A54877; PMID:94347719; PMID:8068627
 A/Accession: B54877
 A/Molecule type: protein
 A/Residues: 1-16 <FAI>
 C/Comment: This alpha-conotoxin
 C/Superfamily: alpha-conotoxin
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 F/2-8,3-16/Disulfide bonds: #status experimental
 F/16/Modified site: amidated carboxyl end (Cys) #status experimental
 Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 LPP 10
 Db 5 LPP 7

RESULT 44

E58503
 superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)
 N;Alternate names: 21.3K bladder and kidney stone protein
 C;Species: unidentified bacterium
 C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 05-Mar-1999
 C;Accession: E58503
 R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996
 A;Description: The proteins of kidney and gallbladder stones.
 A;Reference number: A58501

A;Accession: E58503

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <BIN>

A;Experimental source: human bladder and kidney stones

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C;Keywords: metalloprotein; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10

Db |||

5 LPP 7

RESULT 45

S01104
 hypothetical protein 3 - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jul-2000

C;Accession: S01104

R;Eveloth, D.D.; Marsh, J.L.

Mol. Gen. Genet. 209, 290-298, 1987

A;Title: Overlapping transcription units in *Drosophila*: sequence and structure of the C5
 A;Reference number: S01102; MUID:88038375; PMID:3478553

A;Accession: S01104

A;Molecule type: DNA

A;Residues: 1-16 <EVE>

A;Cross-references: EMBL:X05991; NID:g7759; PIDN:CAA29407.1; PID:g7762

C;Genetics:

A;Cross-references: FlyBase:FBgn0002036

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12

Db |||

13 PTV 15

RESULT 46

PH0763
 T-cell receptor beta chain (F15) - mouse (fragment)

C;Species: *Mus musculus* (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C;Accession: PH0763

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-x
 allelic exclusion and antigen-specific repertoire

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0763

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>

A;Cross-references: EMBL:X60857; NID:g50933; PIDN:CAA43247.1; PID:g50934

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6

Db |||

5 PPQ 7

RESULT 47

PH0759

T-cell receptor beta chain (QB7.3.2) - mouse (fragment)

C;Species: *Mus musculus* (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C;Accession: PH0759

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0759

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>

A;Cross-references: EMBL:X60854; NID:g53878; PIDN:CAA43244.1; PID:g53879

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6

Db |||

5 PPQ 7

RESULT 48

S15754

actin 6 - soybean (fragment)

C;Species: Glycine max (soybean)

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999

C;Accession: S15754; S08049

R;Pearson, L.; Meagher, R.B.

Plant Mol. Biol. 14, 513-526, 1990

A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
 A;Reference number: S15754; MUID:91346640; PMID:2102831

A;Accession: S15754

A;Molecule type: DNA

A;Residues: 1-17 <PEA>

A;Cross-references: EMBL:X17119; NID:g18525; PIDN:CAA34979.1; PID:g18526

C;Superfamily: actin

C;Keywords: cytoskeleton

Query Match 20.0%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPL 8

Db |||

8 QPL 10

RESULT 49

S32587

L-ascorbate peroxidase (EC 1.11.1.11) isozyme II - spinach (fragment)

C;Species: *Spinacia oleracea* (spinach)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993

C;Accession: S32587; S15878

R;Kubo, A.; Saji, H.; Tanaka, K.; Tanaka, K.; Kondo, N.

Plant Mol. Biol. 18, 691-701, 1992

A;Title: Cloning and sequencing of a cDNA encoding ascorbate peroxidase from *Arabidopsis*;
 A;Reference number: S20866; MUID:92216045; PMID:1558944

A;Accession: S32587
 A;Molecule type: protein
 A;Residues: 1-17 <KUB>
 A;Note: this is a revision to the sequence from reference S15878
 R;Tanaka, K.; Takeuchi, E.; Kubo, A.; Sakaki, T.; Haraguchi, K.; Kawamura, Y.
 Arch. Biochem. Biophys. 286, 371-375, 1991
 A;Title: Two immunologically different isozymes of ascorbate peroxidase from spinach leaves
 A;Reference number: S15878; MUID:91378325; PMID:1897962
 A;Accession: S15878
 A;Molecule type: protein
 A;Residues: 1,3-17 <TAN>
 A;Note: this sequence has been revised in reference S20866
 C;Keywords: chloroplast; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PTV 12
 ||||
 Db 5 PTV 7

RESULT 50

S59481
 hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
 C;Species: Phaseolus vulgaris (kidney bean)
 C;Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
 A;Accession: S59481
 R;Wojtaszek, P.; Iretowan, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A;Title: Specificity in the immobilisation of cell wall proteins in response to different
 A;Reference number: S59481; MUID:96011753; PMID:7548825
 A;Accession: S59481
 A;Molecule type: protein
 A;Residues: 1-17 <WQ>
 C;Keywords: Glycoprotein; hydroxyproline
 F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
 ||||
 Db 4 LPP 6

RESULT 51

I55612
 thyroid hormone receptor beta - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C;Accession: I55612
 R;Adams, M.; Matthews, C.; Collingwood, T.N.; Tone, Y.; Beck-Peccoz, P.; Chatterjee, K.K.
 J. Clin. Invest. 94, 506-515, 1994
 A;Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to th
 A;Reference number: I55612; MUID:94314950; PMID:8040303
 A;Accession: I55612
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-17 <RES>
 A;Cross-references: GB:S72623; NID:G633779; PIDN:AA831420.1; PID:G633780
 C;Genetics:
 A;Gene: TRbeta

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
 ||||
 Db 5 LPP 7

RESULT 52

S10786
 enamel, 26K - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
 C;Accession: S10786
 R;Strawich, E.; Glimcher, M.J.
 Eur. J. Biochem. 191, 47-56, 1990
 A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelins' is alt
 A;Reference number: S10780; MUID:90336641; PMID:2379503
 A;Accession: S10786
 A;Molecule type: protein
 A;Residues: 1-17 <STR>
 C;Keywords: enamel; phosphoprotein

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
 ||||
 Db 3 QPP 5

RESULT 53

S04229
 N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)
 N;Alternate names: Glycosylasparaginase
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
 C;Accession: S04229
 R;Tollersrud, O.K.; Aronson Jr., N.N.
 Biochem. J. 260, 101-108, 1989
 A;Title: Purification and characterization of rat liver glycosylasparaginase.
 A;Reference number: S04228; MUID:89374025; PMID:2775174
 A;Accession: S04229
 A;Molecule type: protein
 A;Residues: 1-18 <TOL>
 C;Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase
 C;Keywords: hydrolase

Query Match 20.0%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9
 ||||
 Db 3 PLP 5

RESULT 54

PC2280
 prolylendopeptidase-inhibiting peptide - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 28-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-May-1997
 C;Accession: PC2280
 R;Omori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.
 Biochem. Biophys. Res. Commun. 202, 809-815, 1994
 A;Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.
 A;Reference number: PC2280; MUID:94324971; PMID:8048952
 A;Accession: PC2280
 A;Molecule type: protein
 A;Residues: 1-18 <OHM>
 A;Experimental source: brain
 C;Superfamily: cytoskeletal keratin

Query Match 20.0%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9

```
Db          |||
            4 PLP 6

RESULT 55
S39845
2-aminobenzoate-CoA ligase, anaerobic - Pseudomonas sp. (strain KB740) (fragment)
C:Species: Pseudomonas sp.
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S39845
R:Altenschmidt, U.; Fuchs, G.
Eur. J. Biochem. 205, 721-727, 1992
A:Title: Novel aerobic 2-aminobenzoate metabolism. Purification and characterization of
from a denitrifying Pseudomonas sp.
A:Reference number: S22402; MUID:92241310; PMID:1315272
A:Accession: S39845
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10, 'X', 12-14, 'X', 16-18 <ALT>

Query Match      20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 LPP 10
        |||
Db      12 LPP 14

RESULT 56
B45138
arsenite oxidase I - Alcaligenes faecalis (fragment)
C:Species: Alcaligenes faecalis
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 04-Dec-1994
C:Accession: B45138
R:Anderson, G.L.; Williams, J.; Hille, R.
J. Biol. Chem. 267, 23674-23682, 1992
A:Title: The purification and characterization of arsenite oxidase from Alcaligenes faecalis
A:Reference number: A45138; MUID:93054722; PMID:1331097
A:Accession: B45138
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <AND>
A>Note: sequence extracted from NCBI backbone (NCBIP:118543)

Query Match      20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 LPP 10
        |||
Db      9 LPP 11

RESULT 57
S10452
hypothetical protein (bpha 5' region) - Aspergillus niger
C:Species: Aspergillus niger
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
C:Accession: S10452
R:van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken
submitted to the EMBL Data Library, March 1990
A:Reference number: S10452
A:Accession: S10452
A:Molecule type: DNA
A:Residues: 1-18 <VAN>
A:Cross-references: EMBL:X52521; NID:g23336; PID:g2337

Query Match      20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 QPL 8

Db          |||
            4 PLP 6

RESULT 58
A54195
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)
C:Species: Squalus acanthias (spiny dogfish)
C>Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Apr-2002
C:Accession: A54195
R:Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.
Biochemistry 33, 8044-8050, 1994
A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase
A:Reference number: A54195; MUID:94297020; PMID:8025109
A:Accession: A54195
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <ESM>
A:Experimental source: rectal gland
A>Note: sequence extracted from NCBI backbone (NCBIP:149363)
C:Keywords: hydrolase

Query Match      20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PPT 11
        |||
Db      9 PPT 11

RESULT 59
PC1323
endopeptidase Clp (EC 3.4.21.92) chain P [similarity] - curled-leaved tobacco chloroplast
C:Species: chloroplast Nicotiana glauca (curled-leaved tobacco)
C>Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 08-Dec-2000
C:Accession: PC1323
R:Rejes, E.; Engler, D.; Maliga, P.
Theor. Appl. Genet. 79, 28-32, 1990
A:Title: Extensive homologous chloroplast DNA recombination in the pt14 Nicotiana glauca
A:Reference number: PC1323
A:Accession: PC1323
A:Molecule type: DNA
A:Residues: 1-19 <FEJ>
C:Genetics: chloroplast
A:Genome: chloroplast
C:Function:
A>Description: ATP-driven cleavage of proteins to small peptides
A>Note: magnesium required
C:Superfamily: endopeptidase Clp chain P
C:Keywords: ATP; chloroplast; hydrolase; serine proteinase
F/3/Active site: His #status predicted

Query Match      20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 HQP 4
        |||
Db      3 HQP 5

RESULT 60
S60633
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion
C:Species: mitochondrion Artemia sp. (brine shrimp)
A:Variety: strain La Mata
C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002
C:Accession: S60633
R:Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.
J. Mol. Evol. 38, 156-168, 1994
A:Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and par
```

A;Accession: S60633
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-19 <PER>
A;Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211
A;Experimental source: strain La Mata
A;Note: the source is designated as Artemia parthenogenetica
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Genetics:
A;Gene: ATP8
A;Genome: mitochondrion
A;Genetic code: SGC4
C;Superfamily: H⁺-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9
|||
Db 6 PLP 8
|||

RESULT 61
C32735
thyroglobulin - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Apr-1997
C;Accession: C32735
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
Biochem. Biophys. Res. Commun. 118, 423-429, 1984
A;Title: The isolation of identical thyroxine containing amino acid sequences from bovine thyroglobulin
A;Reference number: A32735; MUID:84153804; PMID:6704086
A;Accession: C32735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <RAW>
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homology
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8
|||
Db 10 QPL 12
|||

RESULT 62
B32735
thyroglobulin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Apr-1997
C;Accession: B32735
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
Biochem. Biophys. Res. Commun. 118, 423-429, 1984
A;Title: The isolation of identical thyroxine containing amino acid sequences from bovine thyroglobulin
A;Reference number: A32735; MUID:84153804; PMID:6704086
A;Accession: B32735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <RAW>
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homology
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8
|||
Db 10 QPL 12
|||

RESULT 63
B61409
genome polyprotein (clone L3/S2) - Skalica virus (fragment)
C;Species: Skalica virus
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Nov-2000
C;Accession: B61409
R;Guirakhoo, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Gresikova, M.
J. Gen. Virol. 72, 333-338, 1991
A;Title: The relationship between the flaviviruses Skalica and Langat as revealed by molecular biology
A;Reference number: A61409; MUID:91132129; PMID:1847173
A;Accession: B61409
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: genomic RNA
A;Residues: 1-19 <GUI>
C;Superfamily: yellow fever virus genome polyprotein

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
|||
Db 1 LPP 3
|||

RESULT 64
S59486
cell wall protein, 22K - kidney bean (fragment)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S59486
R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A;Title: Specificity in the immobilisation of cell wall proteins in response to different lectins
A;Reference number: S59481; MUID:96011753; PMID:7548825
A;Accession: S59486
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <WOJ>

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
|||
Db 3 QPP 5
|||

RESULT 65
A37968
neural surface protein Bravo - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 15-Aug-1997
C;Accession: A37968; A36345
R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, L.
J. Cell Biol. 112, 1049, 1991
A;Reference number: A37968; MUID:91154309; PMID:1999455
A;Contents: erratum
A;Accession: A37968
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19
R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, L.
J. Cell Biol. 111, 3087-3096, 1990
A;Title: Topologically restricted appearance in the developing chick retinotectal system
A;Reference number: A36345; MUID:91100421; PMID:2269667
A;Accession: A36345

A:Molecule type: protein
A:Residues: 1-7,9-19 <DE2>

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
Db 15 QPP 17

RESULT 66

A34467
36K microfibril-associated protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 18-Jun-1993
C:Accession: A34467
R:Kobayashi, R.; Tashima, Y.; Masuda, H.; Shozawa, T.; Numata, Y.; Miyauchi, K.; Hayakawa, J. Biol. Chem. 264, 17437-17444, 1989
A:Title: Isolation and characterization of a new 36-kDa microfibril-associated glycoprotein
A:Reference number: A34467; MUID:90008913; PMID:2793866
A:Accession: A34467
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <KOB>

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8
Db 16 QPL 18

RESULT 67

S21737
coulmarin 7-monoxygenase (EC 1.14.14.-) cytochrome P450 2A7 - western baboon (fragment)
N:Alternate names: coumarin 7-hydroxylase
C:Species: Papio papio (western baboon)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Mar-1999
C:Accession: S21737
R:Dalet-Beluche, I.; Boulenc, X.; Fabre, G.; Maurel, P.; Bonfils, C.
Eur. J. Biochem. 204, 641-648, 1992
A:Title: Purification of two cytochrome P450 isozymes related to CYP2A and CYP3A gene families
A:Reference number: S21176; MUID:92174920; PMID:1541278
A:Accession: S21737
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <DAL>
C:Genetics:
A:Gene: CYP2A7
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TVM 13
Db 16 TVM 18

RESULT 68

S29817
cytochrome P450 2C23 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Mar-1999
C:Accession: S29817
R:Marie, S.; Roussel, F.; Cresteil, T.
Biochim. Biophys. Acta 1172, 124-130, 1993

A:Title: Age- and tissue-dependent expression of CYP2C23 in the rat.
A:Reference number: S29817; MUID:93176794; PMID:7679925

A:Accession: S29817
A:Molecule type: mRNA
A:Residues: 1-20 <MAR>
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; transmembrane protein

Query Match 20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9
Db 4 PLP 6

RESULT 69

A33878
myosin light chain kinase, smooth muscle - turkey (fragment)
C:Species: Meleagris gallopavo (common turkey)
C>Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 07-Nov-1997
C:Accession: A33878
R:Ikebe, M.; Maruta, S.; Reardon, S.
J. Biol. Chem. 264, 6967-6971, 1989
A:Title: Location of the inhibitory region of smooth muscle myosin light chain kinase.
A:Reference number: A33878; MUID:89214114; PMID:2708351
A:Accession: A33878
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <IKE>
C:Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat homology
C:Keywords: smooth muscle

Query Match 20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPO 6
Db 14 PPO 16

RESULT 70

A39328
notechis II-Sb nontoxic venom protein - common tiger snake (fragment)
C:Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 30-Sep-1993
C:Accession: A39328
R:Yang, C.C.; Chang, L.S.; Wu, F.S.
Toxicol. 29, 1337-1344, 1991
A:Title: Venom constituents of Notechis scutatus scutatus (Australian tiger snake) from
A:Reference number: A39328; MUID:92263371; PMID:1814009
A:Accession: A39328
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <YAN>
C:Superfamily: phospholipase A2

Query Match 20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8
Db 17 QPL 19

RESULT 71

A37111
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C>Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 12-Apr-1995

```
C;Accession: A37111
R;Sato, M.H.; Hisabori, T.; Yoshida, M.
J. Biol. Chem. 265, 13419-13422, 1990
A;Title: The 55-kDa polypeptide released from spinach thylakoid membranes with 1 M LiCl
A;Reference number: A37111; MUID:90337936; PMID:2143183
A;Accession: A37111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <SAT>
A;Superfamily: ribulose-bisphosphate carboxylase small chain
C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match      20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 LPP 10
        |||
Db      18 LPP 20

RESULT 72
A54519
tubulin alpha chain - Leishmania enriettii (fragment)
C;Species: Leishmania enriettii
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 13-Aug-1999
C;Accession: A54519
R;Wirth, D.F.; Slater, C.
Mol. Biochem. Parasitol. 9, 83-92, 1983
A;Title: Isolation and characterization of an alpha-tubulin gene from Leishmania enriettii
A;Reference number: A54519; MUID:84142075; PMID:6321982
A;Accession: A54519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-20 <WIR>
A;Cross-references: GE:M28001; NID:g159409; PIDN:AAA29273.1; PID:g159410
C;Superfamily: tubulin

Query Match      20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 PTV 12
        |||
Db      2 PTV 4

RESULT 73
A05313
apolipoprotein A-I - red guenon (fragment)
N;Alternate names: apo-A-I
C;Species: Erythrocebus patas (red guenon, hussar)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 11-May-2000
C;Accession: A05313
R;Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
Biochemistry 15, 1928-1933, 1976
A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus
A;Reference number: A90395; MUID:76184721; PMID:178359
A;Accession: A05313
A;Molecule type: protein
A;Residues: 1-20 <MAH>
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipoprotein

Query Match      20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PPQ 6
        |||
Db      3 PPQ 5

RESULT 74
T44453
acetyl-CoA synthetase [imported] - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44453
R;Nishijyo, T.; Park, S.M.; Lu, C.D.; Itoh, Y.; Abdelal, A.T.
J. Bacteriol. 180, 5559-5566, 1998
A;Title: Molecular characterization and regulation of an operon encoding a system for
A;Reference number: Z22777; MUID:9908987; PMID:9791103
A;Accession: T44453
A;Status: preliminary; translated from GE/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-20 <NTS>
A;Cross-references: EMBL:AF012537; NID:g2668593; PIDN:AAC71069.1; PID:g2668594
A;Experimental source: strain PA01

Query Match      20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PLP 9
        |||
Db      11 PLP 13

RESULT 75
PH1380
alpha-amylase (EC 3.2.1.1) (Haim sensitive) - Bacillus sp. (fragment)
C;Species: Bacillus sp.
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 07-May-1999
C;Accession: PH1380
R;Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.
Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992
A;Title: Purification and some properties of a Haim-sensitive alpha-amylase from newly
A;Reference number: PH1380; MUID:93113087; PMID:11369074
A;Accession: PH1380
A;Molecule type: protein
A;Residues: 1-20 <KAW>
A;Experimental source: strain N0.195
C;Comment: This enzyme has an optimum pH of 7.0.
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match      20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 VMP 14
        |||
Db      11 VMP 13

Search completed: November 25, 2003, 19:36:14
Job time : 10.2907 secs
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 5.31977 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-34

Perfect score: 15

Sequence: 1 MHQPPQLPPTVMFP 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	26.7	12	1 FIF1_SARBU	P83349 sarcophaga
2	3	20.0	8	1 CPD1_ENTFA	P13269 enterococcu
3	3	20.0	9	1 AL10_CARMA	P81813 carcinus ma
4	3	20.0	9	1 RT33_BOVIN	P82926 bos taurus
5	3	20.0	10	1 PAR6_PANAE	P82660 panagrellus
6	3	20.0	11	1 BFPB_AGRFA	P01021 agkistrodon
7	3	20.0	11	1 MORN_HUMAN	P01163 homo sapien
8	3	20.0	11	1 TIN4_HOPTI	P82654 hoplobatr
9	3	20.0	12	1 TIN2_HOPTI	P82652 hoplobatr
10	3	20.0	12	1 TIN3_HOPTI	P82653 hoplobatr
11	3	20.0	13	1 ACT7_SOYEN	P15987 glycine max
12	3	20.0	14	1 EDCD_LYMDI	P80940 lymantria d
13	3	20.0	15	1 PRP_MYCBO	P80149 mycobacteri
14	3	20.0	16	1 AF2S_MALPA	P83142 malva parvi
15	3	20.0	16	1 CXAA_CONPE	P50984 conus penna
16	3	20.0	16	1 CXAB_CONPE	P50985 conus penna
17	3	20.0	17	1 ACT6_SOYEN	P15986 glycine max
18	3	20.0	18	1 UC21_MAIZE	P80627 zea mays (m
19	3	20.0	20	1 AIBG_EYUAS	P33090 equus asinu
20	3	20.0	20	1 APAL_ERYPA	P18647 erythrocebu
21	3	20.0	20	1 BULB_NARPS	P80554 narcissus p
22	3	20.0	20	1 CPA7_PAPSP	P80055 papio sp. (
23	3	20.0	20	1 OAR_PHOXY	P14803 photinus py
24	2	13.3	5	1 E104_LITRU	P82100 litoria rub
25	2	13.3	5	1 PAP2_PARMA	P81864 pardachirus
26	2	13.3	5	1 PRCT_PERAM	P01373 periplaneta
27	2	13.3	6	1 CIP1_MYTED	P13736 mytilus edu
28	2	13.3	6	1 CIP2_MYTED	P13737 mytilus edu
29	2	13.3	6	1 TMOF_SARBU	P41495 sarcophaga
30	2	13.3	6	1 TRPI_PSEPU	P36414 pseudomonas
31	2	13.3	6	1 VP19_HSVIK	P23210 herpes simp
32	2	13.3	7	1 LANC_CARUI	P36960 carnobacter
33	2	13.3	7	1 MNP1_LEPDE	P42984 leptinotars

34	2	13.3	7	1 TPFY_PACDA	P83455 pachymedusa
35	2	13.3	7	1 UP04_MOUSE	P38642 mus musculu
36	2	13.3	7	1 UN06_PINPS	P81675 pinus pinas
37	2	13.3	8	1 ACI_THUAL	P18691 thunnus alb
38	2	13.3	8	1 ALL5_CALVO	P41841 calliphora
39	2	13.3	8	1 ALL6_CYDPO	P82157 cydia pomon
40	2	13.3	8	1 COW2_CONPU	P58785 conus purpu
41	2	13.3	8	1 NP8_BOVIN	P15507 bos taurus
42	2	13.3	8	1 PPK2_PERAM	P82692 periplaneta
43	2	13.3	9	1 COXE_THUOB	P80975 thunnus obe
44	2	13.3	9	1 FAR1_CALVO	P41856 calliphora
45	2	13.3	9	1 FAR3_PENMO	P83318 penaeus mon
46	2	13.3	9	1 FAR4_PENMO	P83319 penaeus mon
47	2	13.3	9	1 FAR5_ASCSU	P43170 ascaris suu
48	2	13.3	9	1 FAR9_ASCSU	P43172 ascaris suu
49	2	13.3	9	1 FLA2_TREHY	P80159 treponema h
50	2	13.3	9	1 FRF1_SARBU	P83350 sarcophaga
51	2	13.3	9	1 KNL3_BOMVA	P83058 bombina var
52	2	13.3	9	1 LMT3_LOCMI	P41489 locusta mig
53	2	13.3	9	1 OXYA_SOUAC	P42999 squalus aca
54	2	13.3	9	1 OXYT_EISFO	P42998 eisenia foe
55	2	13.3	9	1 OXYT_RABIT	P32878 oryctolagus
56	2	13.3	9	1 OXYT_RAJCL	P42994 raja clavav
57	2	13.3	9	1 SAMP_MUSCA	P19095 mustelus ca
58	2	13.3	9	1 TKC1_CALVO	P41517 calliphora
59	2	13.3	9	1 UP33_HUMAN	P30089 homo sapien
60	2	13.3	9	1 YBFR_AZQVI	P25825 azotobacter
61	2	13.3	10	1 AH3_FRUSE	P29261 prunus sero
62	2	13.3	10	1 AL19_CARMA	P81822 carcinus ma
63	2	13.3	10	1 BPP2_BOTIN	P30422 bothrops in
64	2	13.3	10	1 BPP2_BOTJA	P01022 bothrops ja
65	2	13.3	10	1 BPP8_BOTIN	P30426 bothrops in
66	2	13.3	10	1 BPP_VIPAS	P31351 viperia aspi
67	2	13.3	10	1 BRK_ONCMY	Q9prz1 oncorhynch
68	2	13.3	10	1 CATB_SHEEP	P83205 ovis aries
69	2	13.3	10	1 COXM_RAT	P80431 rattus norv
70	2	13.3	10	1 COXQ_RABIT	P80336 oryctolagus
71	2	13.3	10	1 COXQ_SHEEP	P80337 ovis aries
72	2	13.3	10	1 GONI_ALLEMI	P37041 alligator m
73	2	13.3	10	1 GON3_ONCKE	P20367 oncorhynch
74	2	13.3	10	1 GONL_SQUAC	P27429 squalus aca
75	2	13.3	10	1 LABA_JATMU	P13270 jatrophia mu
76	2	13.3	10	1 LPK2_LOCMI	P41488 locusta mig
77	2	13.3	10	1 NS1_MYCTU	P81135 mycobacteri
78	2	13.3	10	1 ODP2_BOVIN	P11180 bos taurus
79	2	13.3	10	1 PVK_LOCMI	P83382 locusta mig
80	2	13.3	10	1 Q2OB_COMTE	P80465 comamonas t
81	2	13.3	10	1 SIAP_BACTG	P49325 bacillus th
82	2	13.3	10	1 TEMK_RANTE	P56923 rana tempor
83	2	13.3	10	1 TKL2_LOCMI	P16224 locusta mig
84	2	13.3	10	1 TKL3_LOCMI	P30249 locusta mig
85	2	13.3	10	1 TNK1_PIG	P01292 sus scrofa
86	2	13.3	10	1 TNOF_AEDAE	P19425 aedes aegyp
87	2	13.3	10	1 UHA3_HUMAN	P40930 homo sapien
88	2	13.3	10	1 UPA2_HUMAN	P30088 homo sapien
89	2	13.3	10	1 UPA5_HUMAN	P30091 homo sapien
90	2	13.3	10	1 UPA9_HUMAN	P30095 homo sapien
91	2	13.3	10	1 URE3_MORMO	P17339 morganella
92	2	13.3	11	1 ASL1_BACSE	P83146 bacteroides
93	2	13.3	11	1 BPP3_BOTIN	P30423 bothrops in
94	2	13.3	11	1 BPP4_BOTIN	P30424 bothrops in
95	2	13.3	11	1 BPP_AGKHP	P04562 agkistrodon
96	2	13.3	11	1 BRK_MEGFL	P12797 megascollia
97	2	13.3	11	1 CEPI_ACHFU	P22790 achatina fu
98	2	13.3	11	1 EFG_CLOPA	P81350 clostridium
99	2	13.3	11	1 LADD_ONCMY	P81018 oncorhynch
100	2	13.3	11	1 LPW_THETH	P05624 thermus the

ALIGNMENTS

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FIF1_SARBU
ID_FIF1_SARBU STANDARD; PRT; 12 AA.
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FIRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 26.7%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQP 7
DB 2 PPQP 5

RESULT 2
CPDI_ENTFA
ID_CPDI_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPD1.";
RL Science 226:849-850(1984).
CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOGIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 VMF 14
DB 3 VMF 5

RESULT 3
AL10_CARMA

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ID_AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 963 MW; 372D79CDB4776C7 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQP 7
DB 2 PQP 4

RESULT 4
RT33_BOVIN
ID_RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRP33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPL 8
DB 5 QPL 7

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RESULT 5
FAR6_PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FWRamide-like neuropeptide FF6 (NGAPQFVR-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRamide-related
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus."
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -1- FUNCTION: MYOACTIVE.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POP 7
DB |||
4 POP 6

RESULT 6
BPPE_ACKHA
ID BPPE_ACKHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii."
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181 (1970).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
DB |||
3 LPP 5

RESULT 7
MORN_HUMAN
ID MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RC MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
RT from coelenterates to humans."
RL Nature 293:579-580 (1981).
RN [2]
SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004 (1981).
RN [3]
SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuropeptide, the head activator from hydra."
RL FEBS Lett. 131:317-321 (1981).
RN [4]
FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition."
RL EMBO J. 8:3311-3318 (1989).
CC -1- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
CC IN THE G2/MITOSIS TRANSITION.
CC -1- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHXAE.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHUPHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
DB |||
1 QPP 3

RESULT 8
TIN4_HOPTI

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ID TIN4 HOPTI STANDARD; PRT; 11 AA.
 AC P82654;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tigerin-4.
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
 RT tigerina.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
 CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
 KW Amphibian defense peptide; Antibiotic.
 FT DISULFID 3 11
 FT SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 20.0%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9
 DB 7 PLP 9

RESULT 9
 TIN2 HOPTI STANDARD; PRT; 12 AA.
 AC P82652;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tigerin-2.
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
 RT tigerina.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
 CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT DISULFID 3 11
 FT MOD RES 12 12
 FT SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9
 DB 7 PLP 9

RESULT 10
 TIN3 HOPTI STANDARD; PRT; 12 AA.
 AC P82653;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tigerin-3.
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
 RT tigerina.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
 CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT DISULFID 3 11
 FT MOD RES 12 12
 FT SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9
 DB 7 PLP 9

RESULT 11
 ACT7 SOYBN STANDARD; PRT; 13 AA.
 AC P15987;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Actin 7 (Fragment).
 GN SACT.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Wayne;
 RX MEDLINE=91346640; PubMed=2102831;
 RA Pearson L., Meagher R.B.;
 RT "Diverse soybean actin transcripts contain a large intron in the 5',
 RT untranslated leader: structural similarity to vertebrate muscle actin
 RT genes.";
 RL Plant Mol. Biol. 14:513-526(1990).
 CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
 CC IN ALL EUKARYOTIC CELLS.

CC -|- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
 CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
 CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -|- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
 CC -|- SIMILARITY: Belongs to the actin family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X17120; CAA34980.1; -;
 CC PIR; S15755; S15755.
 CC InterPro; IPR004001; Actin.
 CC InterPro; IPR004000; Actin like.
 CC PROSITE; PS00406; ACTINS_1; PARTIAL.
 CC PROSITE; PS00432; ACTINS_2; PARTIAL.
 CC PROSITE; PS01132; ACTINS_ACT-LIKE; PARTIAL.
 CC Structural protein; Multigene family.
 FT NON TER 13
 FT 13
 SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred.No.1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 QPL 8
 Db |||
 8 QPL 10

RESULT 12
 ECDC LYMDI STANDARD; PRT; 14 AA.
 AC P80940;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE Testis ecdysiotropin peptide C (TE).
 DE Lymantria dispar (Gypsy moth).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Lymantriidae; Lymantria.
 OX NCBI_TaxID=13123;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=97387807; PubMed=9243792;
 RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
 RA Bell R.A.;
 RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
 RT gonadotropin isolated from brains of Lymantria dispar pupae."
 RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
 CC -|- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
 CC OF LARVAE AND PUPAE.
 CC SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred.No.1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PLP 9
 Db |||
 9 PLP 11
 RESULT 13
 PRP_MYCBO STANDARD; PRT; 15 AA.
 ID PRP_MYCBO

AC P80149;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Proline-rich protein (Fragment).
 OS Mycobacterium bovis.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=BCG / Paris 1173 P2;
 RX MEDLINE=93281750; PubMed=8506381;
 RA Romain F., Augier J., Pescher P., Marchal G.A.;
 RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-
 RT type hypersensitivity reactions only in guinea pigs immunized with
 RT living mycobacteria."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- DISEASE: IMMUNODOMINANT FOR DELAYED-TYPE HYPERSENSITIVITY
 CC REACTIONS IN GUINEA PIGS.
 FT NON TER 15
 FT 15
 SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred.No.1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PPQ 6
 Db |||
 9 PPQ 11
 RESULT 14
 AF2S MALPA STANDARD; PRT; 16 AA.
 AC P83142;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antifungal protein 2 small subunit (CW-2) (Fragment).
 OS Malva parviflora (Little mallow) (Cheeseweed).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosidis II; Malvales; Malvaceae; Malvoideae; Malva.
 OX NCBI_TaxID=145753;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Seed;
 RX MEDLINE=20568734; PubMed=11118343;
 RA Wang X., Bunkers G.J.;
 RT "Potent heterologous antifungal proteins from cheeseweed (Malva
 RT parviflora).";
 RL Biochem. Biophys. Res. Commun. 279:669-673(2000).
 CC -|- FUNCTION: Possesses antifungal activity against P.infestans but
 CC not F.graminearum.
 CC -|- SUBUNIT: Heterodimer of a large and a small subunit.
 CC -|- MISCELLANEOUS: Antimicrobial activity is not affected by salt
 CC concentration.
 CC GO; GO:0003799; F:antifungal peptide activity; IDA.
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.
 KW Fungicide; Antibiotic.
 FT NON TER 16
 FT 16
 SQ SEQUENCE 16 AA; 2027 MW; 9998D9EB8FB7BE65 CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred.No.1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PPQ 6
 Db |||
 9 PPQ 11

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RESULT 15
CXAB_CONPE
ID _CXAA_CONPE STANDARD; PRT; 16 AA.
AC P50984;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Pn1A.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hesson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=96311277; PubMed=8740364;
RA Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
RA Martin J.L.;
RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
RT antagonist, alpha-conotoxin Pn1A from Conus pennaceus.";
RL Structure 4:417-423(1996).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; A54877; A54877.
DR PDB; 1PEN; 21-APR-97.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15 SULFATION.
FT MOD_RES 16 16 AMIDATION.
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
SQ SEQUENCE 16 AA; 1628 MW; 05310FF5EC99005 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY , 8 LPP 10
Db |||
5 LPP 7

RESULT 16
ACT6_SOYBN
ID _ACT6_SOYBN STANDARD; PRT; 17 AA.
CXAB_CONPE
ID _CXAA_CONPE STANDARD; PRT; 16 AA.
AC P50985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Pn1B.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hesson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=97444322; PubMed=9298951;
RA Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
RT "Crystal structure at 1.1-A resolution of alpha-conotoxin Pn1B:
RT comparison with alpha-conotoxins Pn1A and GI.";
RL Biochemistry 36:11323-11330(1997).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; B54877; B54877.
DR PDB; 1AKG; 20-MAY-98.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15 SULFATION.
FT MOD_RES 16 16 AMIDATION.
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
SQ SEQUENCE 16 AA; 1643 MW; 05310FF5ED86AF5 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY , 8 LPP 10
Db |||
5 LPP 7

RESULT 17
ACT6_SOYBN
ID _ACT6_SOYBN STANDARD; PRT; 17 AA.

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AC P15986;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 6 (Fragment).
GN SAC6.

OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Wayne;
RC MEDLINE=91346640; PubMed=2102831;
RX Pearson L., Meagher R.B.;
RA "Diverse soybean actin transcripts contain a large intron in the 5',
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
CC -----
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CC -----
DR EMBL; X17119; CRA34979.1; -.
DR PIR; S15754; S15754.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; actin; 1.
DR PROSITE; PS00406; ACTINS 1; PARTIAL.
DR PROSITE; PS00432; ACTINS 2; PARTIAL.
DR PROSITE; PS01132; ACTINS ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 17
FT SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPL 8
DB 8 QPL 10

RESULT 18
UC21_MAIZE
ID UC21_MAIZE STANDARD; PRT; 18 AA.
AC P80627;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;

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RN SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.
CC -!- SIMILARITY: TO L-ASCORBATE PEROXIDASES.
CC Maize-2DPAGE; P80627; COLEOPTILE.
DR MaizeDB; 123953; -.
DR NON_TER 1
FT NON_TER 18
FT SEQUENCE 18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12
DB 5 PTV 7

RESULT 19
A1BG_EQUAS
ID A1BG_EQUAS STANDARD; PRT; 20 AA.
AC P39090;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-1B-glycoprotein (Alpha-1-B glycoprotein) (Postalbumin)
DE (Fragment).
GN A1BG.
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;
[1]
RN SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=9130579; PubMed=1868686;
RA Patterson S.D., Bell K., Shaw D.C.;
RT "Donkey and horse alpha 1 B-glycoprotein: partial characterization
RT and new alleles.";
RL Comp. Biochem. Physiol. 98B:523-528(1991).
CC -!- FUNCTION: Unknown.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
KW Immunoglobulin domain; Glycoprotein; Plasma.
FT NON_TER 20
FT SEQUENCE 20 AA; 2197 MW; 65857DFDA68EBD9F CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POP 7
DB 6 POP 8

RESULT 20
APAL_ERYPA
ID APAL_ERYPA STANDARD; PRT; 20 AA.
AC P18647;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein A-I (Apo-AI) (Fragment).
GN APOA1.

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OS Erythrocebus patas (Red guenon) (Ruszar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=76184721; PubMed=178359;
RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
RT "Characterization of the plasma lipoproteins and apoproteins of the
RL Erythrocebus patas monkey."
CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
DR PIR; A05313; A05313
KW Plasma; Lipid transport; HDL; Cholesterol metabolism.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQ 6
Db 3 PPQ 5

RESULT 21
BULB NARPS
ID BULB NARPS STANDARD; PRT; 20 AA.
AC P80554;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Bulb protein (Fragment).
OS Narcissus pseudonarcissus (Daffodil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Narcissus.
OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Golden Harvest; TISSUE=Bulb;
RA Partis M.D., Barker P., Thomas B.;
RL Submitted (FEB-1996) to the SWISS-PROT data bank.
FT UNSURE 2 2 OR N.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2077 MW; 76212FF3A468AD38 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
Db 13 LPP 15

RESULT 22
CPA7 PAPSP
ID CPA7 PAPSP STANDARD; PRT; 20 AA.
AC P80055;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome P450 2A7 (EC 1.14.14.1) (CYPIA7) (P450 FT) (Coumarin 7-
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DE hydroxylase) (Fragment).
GN CYP2A7.
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=61183;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=92174920; PubMed=1541278;
RA Dalet-Beluche I., Boulenc X., Fabre G., Maurel P., Bonfils C.;
RT "Purification of two cytochrome P450 isozymes related to CYP2A and
RT CYP3A gene families from monkey (baboon, Papio papio) liver
RT microsomes. Cross reactivity with human forms."
RL Bur. J. Biochem. 204:641-648(1992).
CC -!- FUNCTION: EXHIBITS A HIGH COUMARIN 7-HYDROXYLASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- INDUCTION: By phenobarbital.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR InterPro; IPR001128; CYTOCHROME_P450.
DR PROSITE; PS00086; CYTOCHROME_P450; PARTIAL.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT UNSURE 14 14
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2045 MW; 693102A1F0B50C96 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TVM 13
Db 16 TVM 18

RESULT 23
OAR PHOPY
ID OAR PHOPY STANDARD; PRT; 20 AA.
AC P14803;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Octopamine receptor (Octopamine binding protein) (Fragment).
DE Photinus pyralis (North American firefly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia;
OC Cantharoides; Lampyridae; Photinus.
OX NCBI_TaxID=7054;
RN [1]
RP SEQUENCE.
RC TISSUE=Light organ;
RX MEDLINE=90092510; PubMed=2513233;
RA Nathanson J.A., Kantham L., Hunnicutt E.J.;
RT "Isolation and N-terminal amino acid sequence of an octopamine ligand
RT binding protein."
RL FEBS Lett. 259:117-120(1989).
CC -!- FUNCTION: PUTATIVE RECEPTOR FOR OCTOPAMINE. OCTOPAMINE (OA) IS A
CC NEUROTRANSMITTER. NEUROHORMONE, AND NEUROMODULATOR IN
CC INVERTEBRATES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR PIR; S28779; S28779.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PARTIAL.
KW G-protein coupled receptor.
FT UNSURE 2 2
FT UNSURE 9 9
FT UNSURE 19 19
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FT NON TER      20      20
SQ SEQUENCE 20 AA; 2500 MW; ACBC81A11B8D4AB CRC64;

Query Match      20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MHQ 3
      |||
Db      18 MHQ 20

RESULT 24
EI04_LITRU
ID _EI04_LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 4.
OS Litorea rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella";
RL Aust. J. Chem. 52:639-645 (1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A0S9A00000 CRC64;

Query Match      13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TV 12
      |||
Db      3 TV 4

RESULT 25
PAP2_PAPMA
ID _PAP2_PAPMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moles sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleoidei; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moles sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713 (1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
      properties. Forms voltage-dependent, ion-permeable channels

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CC      in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARDAXIN FAMILY.
KW Toxin.
FT NON TER      5      5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match      13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 FP 15
      |||
Db      4 FP 5

RESULT 26
PRCT_PERAM
ID _PRCT_PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256 (1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569 (1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211 (1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas; PubMed=2872661;
RX MEDLINE=96232789; PubMed=2872661;
RA Stangler J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72 (1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
CC -!- MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
      THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

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Query Match 13.3%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
 ||
 Db 3 LP 4

RESULT 27
 CIP1 MYTED STANDARD; PRT; 6 AA.
 ID CIP1 MYTED
 AC P13736;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Contraction-inhibiting peptide I (MIP I).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides.";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -I- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN MUSCLES.
 CC -I- SIMILARITY: TO MIP II.
 CC DR PIR; A27696; A27696.
 KW Hormone; Amidation.
 FT MOD RES 6
 SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;
 Amidation.

Query Match 13.3%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MF 14
 ||
 Db 4 MF 5

RESULT 28
 CIP2 MYTED STANDARD; PRT; 6 AA.
 ID CIP2 MYTED
 AC P13737;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Contraction-inhibiting peptide II (MIP II).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides.";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -I- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN MUSCLES.
 CC -I- SIMILARITY: TO MIP I.
 CC DR PIR; B27696; B27696.
 KW Hormone; Amidation.
 FT MOD RES 6
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;
 Amidation.

Query Match 13.3%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MF 14
 ||
 Db 4 MF 5

RESULT 29
 TMOF SARB STANDARD; PRT; 6 AA.
 ID TMOF SARB
 AC P41435;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Trypsin-modulating oostatic factor (TMOF).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Ovary;
 RX MEDLINE=94211930; PubMed=8159807;
 RA Eylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
 RA de Loof A.;
 RT "Sequencing and characterization of trypsin modulating oostatic factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria (Sarcophaga) bullata.";
 RL Regul. Pept. 50:61-72(1994).
 CC -I- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN OF OOCYTE CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE DEVELOPMENT.
 CC -I- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR EPITHELIUM AFTER A BLOOD MEAL.
 KW Hormone.
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PT 11
 ||
 Db 2 PT 3

RESULT 30
 TRPI_PSEPU STANDARD; PRT; 6 AA.
 ID TRPI_PSEPU
 AC P36414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE trpBA operon transcriptional activator (fragment).
 GN TRPI.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PPG1 C1S;
 RX MEDLINE=89335826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas putida.";
 RL Biochimie 71:521-531(1989).
 CC -I- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE

CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.

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DR EMBL; X13299; CAA31660.1; -;
DR InterPro: IPR000847; HTH_LysR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.
KW Tryptophan biosynthesis; Transcription regulation; Activator;
KW DNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
||
Db 5 LP 6

RESULT 31
ID VP19 HSV1K STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Capsid assembly and DNA maturation protein (Varion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
EN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.

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DR EMBL; M57646; AAA45830.1; -;
KW Capsid assembly; Coat protein; DNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PL 8
||
Db 5 PL 6

RESULT 32
LANC CARUI STANDARD; PRT; 7 AA.
ID _LANC_CARUI
AC P36960; 1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin UI49 (Fragment).
OS Carnobacterium sp. (strain UI49).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
CC -!- ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON TER 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
||
Db 5 QP 6

RESULT 33
MNPI LEPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myotropic neuropeptide 1 (led-MNP-I).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head.
RX MEDLINE=95380343; PubMed=7651886;
RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata.";
RL Peptides 16:365-374(1995).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PL 8
 ||
 Db 5 PL 6

RESULT 34
 ID_TPFY_PACDA STANDARD; PRT; 7 AA.
 AC P83455;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tryptophyllin-1 (Pdt-1).
 OS Pachymedusa dactinolor (Giant Mexican leaf frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Phyllomedusinae; Pachymedusa.
 OX NCBI_TaxID=75988;
 RN [1]
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF PRO-7.
 RC TISSUE=Skin secretion;
 RA Chen T.B., Orr D.F., Shaw C.;
 RT "Pachymedusa dactinolor tryptophyllin-1 (Pdt-1): structural characterization, pharmacological activity and cloning of precursor cDNA."
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.
 CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular smooth muscle.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0045986; P:negative regulation of smooth muscle contractility; NAS.
 KW Amphibian defense peptide; Amidation; Hydroxylation.
 FT MOD_RES 3 3 HYDROXYLATION.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
 ||
 Db 2 PP 3

RESULT 35
 ID_UF04_MOUSE STANDARD; PRT; 7 AA.
 AC P38642;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins using preparative two-dimensional gel electrophoresis."
 RL Electrophoresis 15:735-745(1994).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
 ||
 Db 3 PP 4

RESULT 36
 ID_UN06_PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Plomneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomieu C.;
 RT "Separation and characterization of needle and xylem maritime pine proteins."
 RL Electrophoresis 20:1098-1108(1999).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
 ||
 Db 5 LP 6

RESULT 37
 ID_ACI_THUAL STANDARD; PRT; 8 AA.
 AC P18691;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Angiotensin-converting enzyme inhibitor.
 OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8236;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Muscle;
 RX MEDLINE=88326322; PubMed=3415688;
 RA Kohana Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
 RT "Isolation of angiotensin-converting enzyme inhibitor from tuna muscle."
 RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
 DR PIR: A31570; A31570.
 SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PT 11
Db 1 PT 2

RESULT 38

ALL5 CALVO
ID -ALL5_CALVO STANDARD; PRT; 8 AA.

AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.

RA MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.

RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; E47393; E47393
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD RES 3 3 HYDROXYLATION (20%).
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
Db 2 PP 3

RESULT 39

ALL6 CYDPO
ID -ALL6_CYDPO STANDARD; PRT; 8 AA.

AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydia pomonella (Coddling moth).
OS Cydia pomonella (Coddling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.

RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
Db 1 LP 2

RESULT 40

CONW2 CONPU
ID -CONW2_CONPU STANDARD; PRT; 8 AA.

AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-F.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=9338839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
Db 5 LP 6

RESULT 41

NPB BOVIN
ID -NPB_BOVIN STANDARD; PRT; 8 AA.

AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

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[1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 4 QP 5

RESULT 42
FPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPR-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;

[1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tissue-specific distribution of FXPRlamides in the nervous system of
RL the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY)
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=WALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 43

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COXE_THUOB STANDARD; PRT; 9 AA.
ID COXE_THUOB
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 3 QP 4

RESULT 44
FARL_CALVO STANDARD; PRT; 9 AA.
ID FARL_CALVO
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.

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DR PIR; A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQ 6
DB 2 PQ 3

RESULT 45
FAR3_PENMO
ID FAR3_PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP3 (AQPSMLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petson A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1105 MW; CDD107340685A776 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 2 QP 3

RESULT 46
FAR4_PENMO
ID FAR4_PENMO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP4 (SQPSMLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petson A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk

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of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 2 QP 3

RESULT 47
FAR5_ASCSU
ID FAR5_ASCSU STANDARD; PRT; 9 AA.
AC P43170;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF5.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
Ascaris suum."
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1052 MW; 340B0059D1B76338 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PT 11
DB 4 PT 5

RESULT 48
FAR9_ASCSU
ID FAR9_ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
Ascaris suum."
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

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CC CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1012 MW; 524F0737741176877 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PL 8
DB 6 PL 7

RESULT 49
FLA2 TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (Fragment).
GN FLA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RC STRAIN=C5;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,
RA van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are
RT composed of two sheath proteins and three core proteins.";
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -!- SUBUNIT: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
CC -!- FUNCTION: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
CC SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE
CC THAT CONTAINS THREE PROTEINS FLA1 (37 kDa), FLA2 (34 kDa) AND
CC FLA3 (32 kDa).
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagella; Periplasmic.
FT UNSURE 2
FT UNSURE 8
FT NON TER 9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C58B4772D1 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TV 12
DB 2 TV 3

RESULT 50
PRF1 SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FWRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;

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RX MEDLINE=22342733; PubMed=12438695;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 51
KNL3 BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McLean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RT Submitted (JUL-2001) to the swiss-prot data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 52
LMT3 LOCM1 STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.

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OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db |||
3 QP 4

RESULT 53
OXYA SQUAC
ID -OXYA SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Asparagocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PL 8
Db |||
7 PL 8

RESULT 54
OXYT_EISFO
ID -OXYT_EISFO STANDARD; PRT; 9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE.
RC TISSUE=Putrinary;
RX MEDLINE=94121660; PubMed=8292046;
RA Umi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC NEPHRIDIAL FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; PC2021; PC2021.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
KW PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PT 11
Db |||
7 PT 8

RESULT 55
OXYT_RABIT
ID -OXYT_RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit).
OS Hippopotamus amphibius (Hippopotamus),
OS Balanoptera physalus (Finback whale) (Common rorqual),
OS Tachylophus aculeatus aculeatus (Australian echidna), and
OS Hydrolagus colliiei (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophysial hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;

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RA Ferguson D.R., Pickering B.T.;
 RT "Arginine and lysine vasopressins in the hippopotamus
 RL neurohypophysis.";
 RL Gen. Comp. Endocrinol. 13:425-429 (1969).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=B.physalus;
 RA Acher R., Chauvet J., Chauvet M.-T.;
 RT "Isolation of finback whale oxytocin and vasopressin.";
 RL Nature 201:191-192 (1964).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=A. aculeatus;
 RX MEDLINE=7323515; PubMed=4515919;
 RA Acher R., Chauvet J., Chauvet M.-T.;
 RT "Neurohypophyseal hormones and evolution of tetrapods.";
 RL Nature New Biol. 244:124-126 (1973).
 RN [5]
 RP SEQUENCE.
 RC SPECIES=H.colliel;
 RX MEDLINE=7008110; PubMed=5366118;
 RA Pickering B.T., Heller H.;
 RT "Oxytocin as a neurohypophyseal hormone in the holoccephalian
 RL elasmobranch fish, *Hydrolagus collei*.";
 RL J. Endocrinol. 45:597-606 (1969).
 CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
 CC UTERUS AND OF THE MAMMARY GLAND.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; A91466; A91466.
 DR PIR; A92774; A92774.
 DR PIR; A93147; A93147.
 DR PIR; A93408; A93408.
 DR PIR; B90667; B90667.
 DR PDB; 1XY1; 15-OCT-90.
 DR PDB; 1XY2; 15-OCT-90.
 DR InterPro; IPR000981; Neurhyp horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Hypothalamus; Amidation; 3D-structure.
 FT DISULFID 1 6
 MOD RES 9 9
 SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;
 Qy Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 7 PL 8
 7 PL 8
 RESULT 56
 OXYT_RAJCL
 ID OXYT_RAJCL STANDARD; PRT; 9 AA.
 AC P42994;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Glumitocin.
 OS Raja clavata (Thornback ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalia; Hyposqualea; Pristioralea; Batoidae;
 OC Rajiformes; Rajidae; Raja.
 OX NCBI_TaxID=7781;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=66123415; PubMed=5880565;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Phylogeny of neurohypophyseal peptides: isolation of a new hormone,
 RL glumitocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,
 the ray (*Raja clavata*).";
 RL Biochim. Biophys. Acta 107:393-396 (1965).

CC -!- FUNCTION: ANTIDIURETIC HORMONE.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro; IPR000981; Neurhyp_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 MOD RES 9 9
 SEQUENCE 9 AA; 984 MW; 17E9C76EB45B04B CRC64;
 Qy Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 5 PQ 6
 7 PQ 8
 RESULT 57
 SAMP_MUSCA
 ID SAMP_MUSCA STANDARD; PRT; 9 AA.
 AC P19095;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum amyloid P-component (SAP) (Fragment).
 OS *Mustelus canis* (Smooth dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
 OC *Mustelus*.
 OX NCBI_TaxID=7812;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83160932; PubMed=6403520;
 RA Robey F.A., Tanaka T., Liu T.-Y.;
 RT "Isolation and characterization of two major serum proteins from the
 RT dogfish, *Mustelus canis*, C-reactive protein and amyloid P
 RT component.";
 RL J. Biol. Chem. 258:3889-3894 (1983).
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 DR PIR; B20569; B20569.
 DR InterPro; IPR001759; Pentaxin.
 DR PROSITE; PS00289; PENTAXIN; PARTIAL.
 KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
 FT DOMAIN 1 >9
 NON_TER 9
 SEQUENCE 9 AA; 965 MW; D05B5735B386769 CRC64;
 Qy Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 14 FP 15
 2 FP 3
 RESULT 58
 TKC1_CALVO
 ID TKC1_CALVO STANDARD; PRT; 9 AA.
 AC P41517;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin I.
 OS *Calliphora vomitoria* (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: MYOACTIVE PEPTIDE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PT 11
DB 2 PT 3

RESULT 59
ID UP33 HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Pasquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6. ITS MW IS: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PL 8
DB 2 PL 3

RESULT 60
ID YBFR AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).

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OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; M83692; AAA22122.1; -
DR PIR; B41983; B41983.
KW Hypothetical protein.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

RESULT 61
ID AH3 PRUSE STANDARD; PRT; 10 AA.
AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC Glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

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Db          3 PP 4
RESULT 62
AL19 CARMA
ID AL19_CARMA STANDARD; PRT; 10 AA.
AC P81822;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 19.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 10 10
FT SEQUENCE 10 AA; 1101 MW; 96687CD5A8569AB1 CRC64;
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PT 11
DB 2 PT 3

RESULT 63
BPP2_BOTIN
ID BPP2_BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; B37196; B37196.
FT MOD RES 1 1
FT SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 9 PP 10

RESULT 64
BPP2_BOTJA
ID BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
DE inhibitor V-6-II).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of the
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01255; XAVI6B.
FT MOD RES 1 1
FT SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 9 PP 10

RESULT 65
BPP8_BOTIN
ID BPP8_BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; B37196; B37196.
FT MOD RES 1 1
FT SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 9 PP 10

```

CC It acts as an indirect hypotensive agent.
 DR PIR; M37196; M37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1173 MW; 2F835545761F6D8 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
 Db 9 PP 10

RESULT 66
 BPP VIPAS STANDARD; PRT; 10 AA.
 AC P31351;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).
 OS Vipera aspis (Aspic viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 OX NCBI_TaxID=8706;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Venom;
 RC MEDLINE=90382616; PubMed=2169439;
 RA Komori Y., Sugihara H.;
 RT enzyme from the venom of Vipera aspis aspis.";
 RL Int. J. Biochem. 22:767-771(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A60377; XASNPC.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327696773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
 Db 9 PP 10

RESULT 67
 BRK ONCMY STANDARD; PRT; 10 AA.
 AC Q9PZL1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lysyl-bradykinin-like.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94039817; PubMed=8224232;
 RA Conlon J.M., Olson K.R.;
 RT "Purification of a vasoactive peptide related to lysyl-bradykinin from

RT trout plasma.";
 RL FEBS Lett. 334:75-78(1993).
 CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
 DR PIR; S39030; S39030.
 KW Bradykinin; Vasodilator.
 SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
 Db 3 PP 4

RESULT 68
 CAIB SHEEP STANDARD; PRT; 10 AA.
 ID AC P83205;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
 GN CTSB.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=23394055; PubMed=12506352;
 RA El Amiri B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z., Mboko H.B., Beckers J.-F.M.P.;
 RT "Isolation and partial characterization of three pregnancy-associated glycoproteins from the ewe placenta.";
 RL Mol. Reprod. Dev. 64:199-206(2003).
 CC -!- FUNCTION: Thiol protease which is believed to participate in intracellular degradation and turnover of proteins. Has also been implicated in tumor invasion and metastasis.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in small molecule substrates (thus differing from cathepsin L). In addition to being an endopeptidase, shows peptidyl-dipeptidase activity, liberating C-terminal dipeptides.
 CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked by a disulfide bond (By similarity).
 CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 DR InterPro; IPR000169; Shprot.acsite.
 DR PROSITE; PS00640; THIOI_PROTEASE_ASN; PARTIAL.
 DR PROSITE; PS00139; THIOI_PROTEASE_CYS; PARTIAL.
 DR PROSITE; PS00639; THIOI_PROTEASE_HIS; PARTIAL.
 KW Hydrolase; Thiol protease; Lysosome.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
 Db 1 LP 2

RESULT 69

COXM RAT
ID COXM RAT STANDARD; PRT; 10 AA.
AC P80431;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
DE (Fragment).
GN COX7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform."
RL Eur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC PIR; S65387; S65387.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HQ 3
Db 2 HQ 3

RESULT 70
COXM RABIT
ID COXM RABIT STANDARD; PRT; 10 AA.
AC P80336;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
GN COX8H.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RA Freund R., Kadenbach B.;
RX Submitted (MAR-1994) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HQ 3
Db 2 HQ 3

RESULT 71
COXQ SHEEP
ID COXQ SHEEP STANDARD; PRT; 10 AA.
AC P80337;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RA Freund R., Kadenbach B.;
RX Submitted (MAR-1994) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PT 11
Db 9 PT 10

RESULT 72
CONI ALLMI
ID CONI ALLMI STANDARD; PRT; 10 AA.
AC P37041; P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)
DE (Luliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A60066; RUAQ1.
DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QP 4
 DB 8 QP 9

RESULT 73
 GON3 ONCKE STANDARD; PRT; 10 AA.
 AC P20367; P81751;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberein III (Gonadotropin-releasing hormone III) (GNRH-III) (LH-RH III) (Luliberin III).
 GN GNRH3.
 OS Oncorhynchus keta (Chum salmon), and Clupea pallasii (Pacific herring).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8018, 30724;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=O.keta;
 RX MEDLINE=83195140; PubMed=6341999;
 RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
 RT "Characterization of a teleost gonadotropin-releasing hormone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
 RN [2]
 RP SEQUENCE, AND FUNCTION.
 RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
 RX MEDLINE=20114351; PubMed=10650929;
 RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
 RA Chang J.P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure and function of three gonadotropin-releasing hormones, including a novel form, from an ancient teleost, herring.";
 RL Endocrinology 141:505-512(2000).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC PIR: A21114; A21114.
 DR InterPro; IPR002012; GNRH.
 DR Pfam; PF00446; GNRH; 1.
 DR PROSITE; PS00473; GNRH; 1.
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LP 9
 DB 8 LP 9

RESULT 74
 GONL_SQUAC STANDARD; PRT; 10 AA.
 AC P27429;

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QP 4
 DB 8 QP 9

RESULT 75
 LABA JATMU STANDARD; PRT; 10 AA.
 AC P13270;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Labaditin.
 OS Jatropha multifida (Physic nut).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Jatropha.
 OX NCBI_TaxID=3996;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Latex;
 RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
 RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha multifida L. (Euphorbiaceae). Isolation and sequence determination by means of two-dimensional NMR.";
 RL FEBS Lett. 256:91-96(1989).
 CC -!- FUNCTION: LABADITIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY SEEMS TO BE BASED ON AN INTERACTION WITH C1.
 CC -!- PTM: This is a cyclic peptide.
 CC -!- DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR TREATMENT OF INFECTED WOUNDS, SKINS INFECTIONS AND SCABIES.
 SQ SEQUENCE 10 AA; 1089 MW; D98AAB6362D1B362 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 TV 12

Db ||
 5 TV 6

Search completed: November 25, 2003, 19:28:28
Job time : 5.3912 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 28.1686 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-34

Perfect score: 15

Sequence: 1 MHQPPQPLPPTVMFP 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	26.7	9	10	P82429
2	4	26.7	12	2	Q8KZ86
3	4	26.7	12	4	Q9BZ49
4	4	26.7	13	2	Q9L8K1
5	4	26.7	13	4	Q14182
6	4	26.7	15	10	Q9S8N8
7	4	26.7	15	10	Q40562
8	4	26.7	15	10	Q40563
9	4	26.7	16	13	Q9PRU6
10	4	26.7	17	13	Q9PRU7
11	4	26.7	18	12	Q84129
12	4	26.7	19	2	Q9RBV1
13	4	26.7	20	2	Q46499
14	4	26.7	20	4	Q9UCAB
15	4	26.7	20	10	Q9S8A8
16	4	26.7	20	13	Q9PRN3

17	3	20.0	9	2	P83157	P83157 anabaena sp
18	3	20.0	9	4	Q9UCS8	Q9UCS8 homo sapien
19	3	20.0	9	5	Q9TWV0	Q9TWV0 anthopleura
20	3	20.0	9	10	Q9S8J8	Q9S8J8 oryza sativ
21	3	20.0	9	16	Q935G1	Q935G1 salmonella
22	3	20.0	10	2	Q9R5T2	Q9R5T2 acetobacter
23	3	20.0	10	4	Q14096	Q14096 homo sapien
24	3	20.0	10	11	Q9QVF7	Q9QVF7 rattus sp.
25	3	20.0	10	11	Q8VHM9	Q8VHM9 mus musculus
26	3	20.0	10	12	Q8JV78	Q8JV78 polyomaviru
27	3	20.0	10	13	Q90ZV8	Q90ZV8 psittacus e
28	3	20.0	11	2	Q47569	Q47569 escherichia
29	3	20.0	11	4	Q60761	Q60761 homo sapien
30	3	20.0	11	4	Q9UCR1	Q9UCR1 homo sapien
31	3	20.0	11	6	Q9GL48	Q9GL48 sus scrofa
32	3	20.0	11	10	Q9S8Z9	Q9S8Z9 psophocarpu
33	3	20.0	11	13	Q8UUP1	Q8UUP1 xenopus lae
34	3	20.0	12	4	Q9P116	Q9P116 homo sapien
35	3	20.0	12	4	Q9NTQ2	Q9NTQ2 homo sapien
36	3	20.0	12	6	Q9TRU1	Q9TRU1 bos taurus
37	3	20.0	12	10	P82329	P82329 pisum sativ
38	3	20.0	13	4	Q9UEE2	Q9UEE2 homo sapien
39	3	20.0	13	4	Q14890	Q14890 homo sapien
40	3	20.0	13	4	Q9UNV6	Q9UNV6 homo sapien
41	3	20.0	13	6	Q9TRW6	Q9TRW6 bos taurus
42	3	20.0	13	10	Q42373	Q42373 solanum tub
43	3	20.0	13	11	Q88176	Q88176 mus musculus
44	3	20.0	13	12	Q67604	Q67604 squash leaf
45	3	20.0	14	8	Q9T2K7	Q9T2K7 chlamydomon
46	3	20.0	14	10	P82326	P82326 pisum sativ
47	3	20.0	14	11	Q70599	Q70599 rattus norv
48	3	20.0	14	16	Q9K326	Q9K326 bacillus ha
49	3	20.0	15	2	Q9R5D5	Q9R5D5 chromatium
50	3	20.0	15	6	Q9TR62	Q9TR62 oryctolagus
51	3	20.0	15	11	Q9QV25	Q9QV25 rattus sp.
52	3	20.0	15	12	Q69353	Q69353 herpes simp
53	3	20.0	16	2	Q9R5K7	Q9R5K7 streptomyce
54	3	20.0	16	4	Q9NNZ2	Q9NNZ2 homo sapien
55	3	20.0	16	4	Q9UCH1	Q9UCH1 homo sapien
56	3	20.0	16	5	Q18378	Q18378 drosophila
57	3	20.0	16	6	Q9TRR1	Q9TRR1 oryctolagus
58	3	20.0	16	8	P92732	P92732 fejevarya
59	3	20.0	16	11	Q9JHB6	Q9JHB6 mus musculus
60	3	20.0	17	2	Q8VMB2	Q8VMB2 pseudomonas
61	3	20.0	17	2	P97135	P97135 mycobacteri
62	3	20.0	17	3	Q06800	Q06800 saccharomyc
63	3	20.0	17	4	Q15276	Q15276 homo sapien
64	3	20.0	17	4	Q96P96	Q96P96 homo sapien
65	3	20.0	17	4	Q14001	Q14001 homo sapien
66	3	20.0	17	6	Q9TRU8	Q9TRU8 bos taurus
67	3	20.0	17	10	P83061	P83061 spinacia ol
68	3	20.0	17	12	Q8B4C4	Q8B4C4 hepatitis b
69	3	20.0	18	2	Q9RSU2	Q9RSU2 pseudomonas
70	3	20.0	18	2	Q9R5F9	Q9R5F9 alcaligenes
71	3	20.0	18	2	Q9R4V9	Q9R4V9 campylobact
72	3	20.0	18	2	Q9EYW5	Q9EYW5 erwinia ste
73	3	20.0	18	2	Q9R4C6	Q9R4C6 agrobacteri
74	3	20.0	18	4	Q9UCG7	Q9UCG7 homo sapien
75	3	20.0	18	4	Q96F98	Q96F98 homo sapien
76	3	20.0	18	4	Q16244	Q16244 homo sapien
77	3	20.0	18	4	Q9UCT9	Q9UCT9 homo sapien
78	3	20.0	18	4	Q8NFB4	Q8NFB4 homo sapien
79	3	20.0	18	10	Q9S915	Q9S915 triticum tu
80	3	20.0	18	11	Q9JIE9	Q9JIE9 mus musculus
81	3	20.0	19	2	Q9K4X0	Q9K4X0 planktothri
82	3	20.0	19	4	Q9UC80	Q9UC80 homo sapien
83	3	20.0	19	4	Q9UCFL2	Q9UCFL2 homo sapien
84	3	20.0	19	4	Q9UCNK6	Q9UCNK6 homo sapien
85	3	20.0	19	8	Q31687	Q31687 artemia par
86	3	20.0	19	8	Q9GI97	Q9GI97 sargassum p
87	3	20.0	19	10	Q9S8F5	Q9S8F5 beta vulgar
88	3	20.0	19	12	Q69099	Q69099 herpes simp
89	3	20.0	19	13	Q9PRT0	Q9PRT0 gallus gall

90 Q9prn4 petromyzon
 91 Q90f8 human immun
 92 Q905e8 human immun
 93 Q905k8 human immun
 94 Q90rg5 human immun
 95 Q9r4m9 pseudomonas
 96 Q93ill1 vibrio harv
 97 Q53370 escherichia
 98 Q50180 pseudomonas
 99 Q9r5e8 bacillus sp
 100 Q96t45 homo sapien

ALIGNMENTS

RESULT 1
 P82429 PRELIMINARY; PRT; 9 AA.
 ID P82429
 AC P82429
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DE 44 kDa cell wall protein (fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Siabes A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture."
 RL Planta 0:0-0(2000).
 CC -I- SUBCELLULAR LOCATION: CELL WALL.
 CC -I- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON TER
 SQ SEQUENCE 9 AA; 986 MW; C22CCAADC6C77776 CRC64;

Query Match 26.7%; Score 4; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPO 6
 DB 2 QPPO 5

RESULT 2
 Q8KZ86 PRELIMINARY; PRT; 12 AA.
 ID Q8KZ86
 AC Q8KZ86
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Class I integron DNA integrase (fragment).
 GN INT11.
 OS Acinetobacter baumannii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=204A;
 RA Dolzani L., Gombac F., Legatolla C., Riccio M.L., Rossolini G.M.,
 RA Tonin E., Monti-Bragadin C.;
 RT "Carriage of class I and II integrons in Italian clinical isolates of
 RT Acinetobacter baumannii."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ313334; CAC85941.1; -
 FT NON TER
 SQ SEQUENCE 12 AA; 1296 MW; 90426B8F5E376DC1 CRC64;
 Query Match 26.7%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
 DB 7 PLPP 10

RESULT 3
 Q9BZ49 PRELIMINARY; PRT; 12 AA.
 ID Q9BZ49
 AC Q9BZ49
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE Glycophorin C (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,
 RA Zimmerman P.A.;
 RT "The association of the glycoprotein C exon 3 deletion with
 RT ovalocytosis and malaria susceptibility in the Wosera, Papua New
 RT Guinea".
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF342984; AAK01459.1; -
 FT NON TER
 FT NON TER
 SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

Query Match 26.7%; Score 4; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
 DB 7 PLPP 10

RESULT 4
 Q9L8K1 PRELIMINARY; PRT; 13 AA.
 ID Q9L8K1
 AC Q9L8K1
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Vans (Fragment).
 GN VANSB.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BM4281.
 RX MEDLINE=20307504; PubMed=10846225;
 RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundsfjord A.;
 RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin
 RT resistant enterococci and characterization of two novel insertion
 RT sequences."
 RL Microbiology 146:1469-1479(2000).
 DR EMBL: AF201896; AAF73374.1; -
 FT NON TER
 SQ SEQUENCE 13 AA; 1502 MW; 8D0E282189F9672A CRC64;

Query Match 26.7%; Score 4; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPT 11
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|
|
Db 7 LPPT 10

RESULT 5

ID Q14182 PRELIMINARY; PRT; 13 AA.
AC Q14182;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Deoxynucleotidyltransferase (Fragment).
GN DNTT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87213162; PubMed=3579900;
RA Koitai O., Kaneda T., Morishita R.;
RT "Analysis of human terminal deoxynucleotidyl transferase cDNA
RT expressible in mammalian cells."
RL Biochem. Biophys. Res. Commun. 144:185-190 (1987).
DR EMBL; M26144; AAA74588.1; -.
KW Transferase.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match 26.7%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLP 9
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Db 8 QPLP 11

RESULT 6

ID Q9S8N8 PRELIMINARY; PRT; 15 AA.
AC Q9S8N8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein E-22 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RX MEDLINE=941170739; PubMed=8125056;
RA Flengrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional
RT electrophoresis."
RL Electrophoresis 14:1060-1066 (1993).
SQ SEQUENCE 15 AA; 1752 MW; C7D69337B908B9E CRC64;

Query Match 26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQ 6
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|
|
Db 4 QPPQ 7

RESULT 7

ID Q40562 PRELIMINARY; PRT; 15 AA.
AC Q40562;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Small ras-related protein (Fragment).
GN RAN-A2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SR1;
RA MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein."
RL Plant J. 6:555-565 (1994).
DR EMBL; L16786; AAA73564.1; -.
KW GTP-binding.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1707 MW; 8A889F924EA30CAF CRC64;

Query Match 26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLP 9
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Db 3 QPLP 6

RESULT 8

ID Q40563 PRELIMINARY; PRT; 15 AA.
AC Q40563;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Small ras-related protein (Fragment).
GN RAN-B2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SR1;
RA MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein."
RL Plant J. 6:555-565 (1994).
DR EMBL; L16788; AAA73565.1; -.
KW GTP-binding.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1604 MW; 9A57F48F1FFFFFAF CRC64;

Query Match 26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLP 9
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Db 4 QPLP 7

RESULT 9
Q9PRU6 PRELIMINARY; PRT; 16 AA.
AC Q9PRU6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-Crk in VIVO (Fragment).
DE (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=95105151; PubMed=7806494;
RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J., Yazaki Y., Hirai H.;
RT "Characterization, partial purification, and peptide sequencing of p130, the main phosphoprotein associated with v-Crk oncoprotein.";
RL J. Biol. Chem. 269:32740-32746(1994).
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1480 MW; CAB880A931F8873F CRC64;

Query Match 26.7%; Score 4; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQP 7
Db 13 PPQP 16

RESULT 10
Q9PRU7 PRELIMINARY; PRT; 17 AA.
AC Q9PRU7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-Crk in VIVO (Fragment).
DE (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=95105151; PubMed=7806494;
RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J., Yazaki Y., Hirai H.;
RT "Characterization, partial purification, and peptide sequencing of p130, the main phosphoprotein associated with v-Crk oncoprotein.";
RL J. Biol. Chem. 269:32740-32746(1994).
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1608 MW; 52EAB880A931F887 CRC64;

Query Match 26.7%; Score 4; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQP 7
Db 13 PPQP 16

RESULT 11
Q84129

ID Q84129 PRELIMINARY; PRT; 18 AA.
AC Q84129
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg 8), COOH terminus of NS1 (Fragment).
DE 8).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses.
OC NCBI_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural proteins of influenza A virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL: K00959; AAA43541.1; -;
DR InterPro: IPR000256; Flu_NS1.
DR Pfam: PF00600; Flu_NS1; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FEBEF CRC64;

Query Match 26.7%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 12 PLPP 15

RESULT 12
Q9REB1 PRELIMINARY; PRT; 19 AA.
AC Q9REB1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Integrase (Fragment).
OS Pseudomonas sp. R9.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
OC NCBI_TaxID=1011164;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=R9; TRANSPOS=Trn1404;
RX MEDLINE=20011227; PubMed=10543801;
RA Schnabel E.L., Jones A.L.;
RT "Distribution of tetracycline resistance genes and transposons among phyloplane bacteria in Michigan apple orchards.";
RL Appl. Environ. Microbiol. 65:4898-4907(1999).
DR EMBL: AF157798; AAD47998.1; -;
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2065 MW; 19EF26DDCA6290F0 CRC64;

Query Match 26.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 7 PLPP 10

RESULT 13
Q46499 PRELIMINARY; PRT; 20 AA.
AC Q46499
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)

```
DE Periplasmic (Fragment).
OS Desulfovibrio desulfuricans.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=876;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M6;
RA Lim S.K., Lee S.J., Kim B.H.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U49192; AAA91808.1; -.
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 1996 MW; E93207D26C22999B CRC64;

  Query Match      26.7%; Score 4; DB 2; Length 20;
  Best Local Similarity 100.0%; Pred. No. 8e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQLP 8
Db 10 PQLP 13

RESULT 14
Q9UCA8 PRELIMINARY; PRT; 20 AA.
ID Q9UCA8
AC Q9UCA8
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Tumor-derived adhesion factor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94161713; PubMed=8117260;
RA Akagiri K., Okabe Y., Funahashi K., Yoshitake Y., Nishikawa K.,
RA Yasumitsu H., Umeda M., Miyazaki K.;
RT "Cell adhesion activity of a 30-kDa major secreted protein from human
RT bladder carcinoma cells.";
RL Biochem. Biophys. Res. Commun. 198;1046-1053(1994).
SQ SEQUENCE 20 AA; 1979 MW; EF6F9DC6DCA0A8E8D CRC64;

  Query Match      26.7%; Score 4; DB 4; Length 20;
  Best Local Similarity 100.0%; Pred. No. 8e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 16 PLPP 19

RESULT 15
Q9S8A8 PRELIMINARY; PRT; 20 AA.
ID Q9S8A8
AC Q9S8A8
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Gamma-35 SECALIN isoform P9-12 (COELIAC immunoreactive protein)
DE (Fragment).
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE.
RX MEDLINE=96283789; PubMed=8679669;
RA Rocher A., Calero M., Soriano F., Mendez E.;

  Query Match      26.7%; Score 4; DB 10; Length 20;
  Best Local Similarity 100.0%; Pred. No. 8e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLP 9
Db 16 QPLP 19

RESULT 16
Q9PRN3 PRELIMINARY; PRT; 20 AA.
ID Q9PRN3
AC Q9PRN3
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Melanotropin MSH-B.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=96122167; PubMed=8537171;
RA Takahashi A., Anemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RA Kawauchi H.;
RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands.";
RL Int. J. Pept. Protein Res. 46;197-204(1995).
SQ SEQUENCE 20 AA; 2403 MW; AC4DAD67CC69AB0D CRC64;

  Query Match      26.7%; Score 4; DB 13; Length 20;
  Best Local Similarity 100.0%; Pred. No. 8e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLP 9
Db 17 QPLP 20

RESULT 17
P83157 PRELIMINARY; PRT; 9 AA.
ID P83157
AC P83157
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=23412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR PROSITE; PS00088; SOD MN; PARTIAL.
DR Oxidoreductase; Iron; Metal-binding.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;
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Db          ||||
           5 QPP 7

RESULT 22
Q9R5T2      PRELIMINARY;      PRT;      10 AA.
AC Q9R5T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
OS Acetobacter hansenii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=436;
RN [1]_TaxID=436;
RP SEQUENCE.
RX MEDLINE=92027789; PubMed=1929428;
RA Levy H.R., Cook C.;
RT "Purification and properties of NADP-linked glucose-6-phosphate
RT dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
RL Arch. Biochem. Biophys. 291:161-167(1991).
FT NON_TER 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D77767 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
Db |||
   3 LPP 5

RESULT 23
Q14096      PRELIMINARY;      PRT;      10 AA.
AC Q14096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYP2B6 gene cryptic exon 3A of cytochrome P450IIB6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174922; PubMed=2308828;
RA Miles J.S., McLaren A.W., Gonzalez F.J., Wolf C.R.;
RT "Alternative splicing in the human cytochrome P450IIB6 gene: use of a
RT cryptic exon within intron 3 and splice acceptor site within exon 4.";
RL Nucleic Acids Res. 18:189-189(1990).
DR EMBL; X16864; CAA34754.1;
SQ SEQUENCE 10 AA; 885 MW; 4181BD9D87DC77767 CRC64;

Query Match      20.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
Db |||
   3 LPP 5

RESULT 24
Q9QVF7      PRELIMINARY;      PRT;      10 AA.
AC Q9QVF7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta 2-glycoprotein I, beta 2-GPI (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]_TaxID=10118;
RP SEQUENCE.
RX MEDLINE=92135065; PubMed=1777418;
RA Matsuura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
RA Yasuda T., Koike T.;
RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
RT cDNA cloning and inter-species differences of beta 2-GPI in
RT alternation of anticardiolipin binding.";
RL Int. Immunol. 3:1217-1221(1991).
FT NON_TER 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1100 MW; 94E681B767376EA1 CRC64;

Query Match      20.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPP 9
Db |||
   5 LPP 7

RESULT 25
Q8VHM9      PRELIMINARY;      PRT;      10 AA.
AC Q8VHM9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interferon receptor 2a' (Fragment).
GN IFNAR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The genomic structure and expression patterns of the gene encoding
RT the second chain of the murine interleukin 10 receptor, IL-10R2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The organization, transcriptional regulation and chromosomal
RT localization of the locus encoding the gene for the murine type I
RT interferon receptor, Ifnar2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440786; AAL40944.1;
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1139 MW; 322A36A72449C737 CRC64;

Query Match      20.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
Db |||
   1 LPP 3

RESULT 26
Q8JUV78     PRELIMINARY;      PRT;      10 AA.
ID Q8JUV78

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AC Q8JV78;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OC NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USAL;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
  Girones R.;
RT "Potential transmission of human polyomaviruses through the
  gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303946; AAM97796.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1183 MW; 4CD6A96731A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
DB 7 LPP 9

RESULT 27
Q90ZV8 PRELIMINARY; PRT; 10 AA.
ID Q90ZV8
AC Q90ZV8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adenylate kinase (Fragment).
OS Psittacus erithacus (grey parrot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Psittaciformes; Psittacidae; Psittacus.
OC NCBI_TaxID=57247;
RN [1]
RP SEQUENCE FROM N.A.
RA Shapero L.H., Dumbacher J.P.;
RT "Adenylate kinase intron 5: a new nuclear locus for avian
  systematics.";
RL Auk 118:248-255(2001).
DR EMBL; AF307895; AAK43534.1; -.
FT NON TER 1 1
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1099 MW; 22847A272731B777 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPT 11
DB 3 PPT 5

RESULT 28
Q47569 PRELIMINARY; PRT; 11 AA.
ID Q47569
AC Q47569;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE Hypothetical 1.3 kDa protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

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OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K-12;
RX MEDLINE=94162733; PubMed=7764507;
RA Yamada M., Yanai S., Talkuder A.;
RT "Analysis of products of the Escherichia coli genomic genes and
  regulation of their expressions; an applicable procedure for genomic
  analysis of other microorganisms.";
RL Biosci. Biotechnol. Biochem. 58:117-120(1994).
DR EMBL; D21156; BAA04692.1; -.
KW Hypothetical protein.
FT NON TER 11
SQ SEQUENCE 11 AA; 1322 MW; C0B8E40E37672732 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQ 3
DB 1 MHQ 3

RESULT 29
O60761 PRELIMINARY; PRT; 11 AA.
ID O60761
AC O60761;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NPT-1 protease (Fragment).
GN NPT-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98207718; PubMed=9545579;
RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,
  Tatsumi S., Morita K., Takeda E.;
RT "Characterization of the 5' flanking region of the human NPT-1
  Na+/phosphate cotransporter gene.";
RL Biochim. Biophys. Acta 1396:267-272(1998).
DR EMBL; D83236; BAA25645.1; -.
FT NON TER 11
FT NON TER 11
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 20.0%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
DB 7 LPP 9

RESULT 30
Q9UCR1 PRELIMINARY; PRT; 11 AA.
ID Q9UCR1
AC Q9UCR1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1171 MW; 273615AA0437737 CRC64;

Query Match
Best Local Similarity 20.0%; Score 3; DB 4; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPL 8
Db 3 QPL 5

RESULT 31
Q9GL48
ID Q9GL48 PRELIMINARY; PRT; 11 AA.
AC Q9GL48;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE G protein-coupled receptor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagasaka T., Boulday G., Coupel S., Coulon F., Tesson L.,
RA Heslan J.-M., Souillou J.-P., Chazreau B.;
RT "Alternative double screening for differentially expressed genes by
RT modified RNA differential display and semi-quantitative Reverse
RT Northern blot.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF319662; AAG33870.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1298 MW; 822261F10861BB41 CRC64;

Query Match
Best Local Similarity 20.0%; Score 3; DB 6; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPT 11
Db 2 PPT 4

RESULT 32
Q9S8Z9
ID Q9S8Z9 PRELIMINARY; PRT; 11 AA.
AC Q9S8Z9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE W1 peptide (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eursoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytochemistry 31:731-735(1992).
FT NON_TER 1

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FT NON_TER 11
SQ SEQUENCE 11 AA; 1120 MW; 8391BABC77772D1 CRC64;

Query Match
Best Local Similarity 20.0%; Score 3; DB 10; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12
Db 3 PTV 5

RESULT 33
Q8UUP1
ID Q8UUP1 PRELIMINARY; PRT; 11 AA.
AC Q8UUP1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Beta-TrCP protein (Fragment).
GN BETA-TRCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Carnevali F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus
RT laevis.";
RL Thesis (2001), Department of Genetica e Biologia Molecolare,
RL University of Rome La Sapienza, Rome, Italy.
DR EMBL; AJ428930; CAD21927.1; -.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match
Best Local Similarity 20.0%; Score 3; DB 13; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
Db 9 QPP 11

RESULT 34
Q9P116
ID Q9P116 PRELIMINARY; PRT; 12 AA.
AC Q9P116;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Apolipoprotein E receptor 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Korschneck I., Gharehbaghi-Schnell E., Lang I., Binder R.B.;
RT "Expression of Apolipoprotein E Receptor 2 in atherosclerosis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF129170; AAF66440.1; -.
KW Lipoprotein; Receptor.
FT NON_TER 1
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1467 MW; 4E8935410404877 CRC64;

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Query Match 20.0%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPT 11
 ||||
 Db 1 PPT 3

RESULT 35

Q9NTQ2 Q9NTQ2 PRELIMINARY; PRT; 12 AA.
 AC Q9NTQ2;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE D40219.1 (Mu opiate receptor (MOR1)) (Fragment).
 GN D40219.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Phillimore B.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL132774; CAB76846.1; -.
 KW Receptor.
 FT NON TER 1 1
 SQ SEQUENCE 12 AA; 1296 MW; 58479422BDABIDB CRC64;

Query Match 20.0%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9
 ||||
 Db 10 PLP 12

RESULT 36

Q9TRU1 Q9TRU1 PRELIMINARY; PRT; 12 AA.
 AC Q9TRU1;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE 43 kDa CYANOGEN bromide fragment PEAK 7 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=92132498; PubMed=1734497;
 RA Vaiboy O.P., Sletten K., Husby G., Nordstoga K.;
 RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
 of bovine kidney.";
 RL Scand. J. Immunol. 35:63-69(1992).
 FT NON TER 1 1
 SQ SEQUENCE 12 AA; 1257 MW; 0D5C94FDE9B76AA4 CRC64;

Query Match 20.0%; Score 3; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY * 10 PTV 12
 ||||
 Db 7 PTV 9

RESULT 37

P82329 P82329 PRELIMINARY; PRT; 12 AA.
 AC P82329;
 DT 01-JUN-2000 (Tremblrel. 14, Created)
 DT 01-JUN-2000 (Tremblrel. 14, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE Unknown protein from 2D-page of thylakoid lumen (SPOT111) (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OC NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
 RX MEDLINE=20181728; PubMed=10715320;
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
 RA Adamska I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 targeting analysis of luminal and peripheral thylakoid proteins.";
 RL Plant Cell 12:319-341(2000)
 CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
 CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.5, ITS MW IS: 24.1 KDA.
 KW Chloroplast; Thylakoid membrane.
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1244 MW; CBE0AD74B3D5B862 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
 ||||
 Db 9 LPP 11

RESULT 38

Q9UEE2 Q9UEE2 PRELIMINARY; PRT; 13 AA.
 AC Q9UEE2;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE ERGB transcription factor (Fragment).
 GN FL11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;
 RT "Molecular analysis on the breakpoint region of a t(11;22)
 translocation in Ewing's sarcoma.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB012625; BAA32806.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 13 AA; 1541 MW; 2C677798CB566AB7 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POP 7
 ||||
 Db 4 POP 6

RESULT 39

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Q14890
ID Q14890 PRELIMINARY; PRT; 13 AA.
AC Q14890;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mucin (Fragment).
GN MUC5AC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=tracheobronchial mucosa;
RA Guyonnet-Duperat V., Audie J., Debailleul V., Laine A., Buisine M.,
RA Zouitina-Gallegue S., Pigny P., Degand P., Aubert J., Porchet N.;
RT "Characterization of the human mucin gene MUC5AC: a consensus
RT cysteine-rich domain for l1p15 mucin genes.";
RL Biochem. J. 0:0-0(1994).
DR EMBL; Z34280; CAA84034.1; -.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1580 MW; 535DF5A5183B7767 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
DB 6 LPP 8

RESULT 40
Q9UNV6 PRELIMINARY; PRT; 13 AA.
AC Q9UNV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Inosine monophosphatase 2 (Fragment).
GN INPA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97463449; PubMed=9322233;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Detera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=20284187;
RA Yoshikawa T., Padigar M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Detera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF085628; AAD22141.1; -.
DR EMBL; AF085627; AAD22141.1; JOINED.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1491 MW; E8154075786DD401 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 10 PTV 12
DB 9 PTV 11

RESULT 41
Q9TRW6 PRELIMINARY; PRT; 13 AA.
ID Q9TRW6;
AC Q9TRW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 25 kDa protein P25, peptide P3 (Fragment).
OS Bos taurus (Sovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA Shiratsuchi A., Uchida T., Imahori K.;
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
RL FEBS Lett. 289:37-43(1991).
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1375 MW; 2C2822494805D1B7 CRC64;

Query Match 20.0%; Score 3; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12
DB 6 PTV 8

RESULT 42
Q42373 PRELIMINARY; PRT; 13 AA.
ID Q42373;
AC Q42373;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Patatin class I (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=88226014; PubMed=3371664;
RA Mignery G.A., Pikaard C.S., Park W.D.;
RT "Molecular characterization of the patatin multigene family of
RT potato.";
RL Gene 62:27-44(1988).
DR EMBL; M18882; AAA33830.1; -.
DR EMBL; M18881; AAA33829.1; -.
FT NON TER 13
FT NON TER 13
SQ SEQUENCE 13 AA; 1456 MW; 916595F37A6E29D5 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TVM 13
DB 11 TVM 13

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RESULT 43
O88176 ID O88176 PRELIMINARY; PRT; 13 AA.
AC O88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-c; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9882442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RL of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncaml.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9
Db 3 PLP 5

RESULT 44
O67604 ID O67604 PRELIMINARY; PRT; 13 AA.
AC O67604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Movement protein (Fragment).
GN BCI.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Los Mochis 1;
RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;
RT "Diversity among geminiviruses associated with vegetables from Valle
RT del Fuerte, Sinaloa, Mexico.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; L27273; AAA47820.1; -.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1376 MW; D471DE4D634E76C2 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
Db 7 QPP 9

RESULT 45
O9T2K7 ID O9T2K7 PRELIMINARY; PRT; 14 AA.
AC O9T2K7;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 18-kDa chloroplast DNA-binding iron-sulfur protein (Fragment).
OS Chlamydomonas reinhardtii.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE.
RC MEDLINE=92404720; PubMed=2562513;
RA Wu M., Nie Z.Q., Yang J.;
RT "The 18-kD protein that binds to the chloroplast DNA replicative
RT origin is an iron-sulfur protein related to a subunit of NADH
RT dehydrogenase.";
RL Plant Cell 1:551-557(1989).
SQ SEQUENCE 14 AA; 1698 MW; 7799E02B12C200CB CRC64;

Query Match 20.0%; Score 3; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 MFP 15
Db 1 MFP 3

RESULT 46
P82326 ID P82326 PRELIMINARY; PRT; 14 AA.
AC P82326;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 18.3 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514B1B237 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
Db 5 LPP 7

RESULT 47
O70599 ID O70599 PRELIMINARY; PRT; 14 AA.
AC O70599;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thymidine kinase (EC 2.7.1.21) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Sauer M.;
RL Thesis (1999), University of Vienna, Inst. of Molecular Biology.
DR EMBL; AF006455; CAA07030.1; -.
KW Kinase; Transferase.
FT NON TER 14
SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E8B7 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12
DB 7 PTV 9

RESULT 48
Q9KE26 PRELIMINARY; PRT; 14 AA.
AC Q9KE26;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BH1032.
GN BH1032.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331 (2000).
DR EMBL; AF001510; BAB04751.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 14 AA; 1697 MW; A9A302145A7AE8A6 CRC64;

Query Match 20.0%; Score 3; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TVM 13
DB 8 TVM 10

RESULT 49
Q9R5D5 PRELIMINARY; PRT; 15 AA.
AC Q9R5D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE POLY (3-HYDROXYBUTYRIC acid) granule-associated 40 kDa protein
DE (Fragment).
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Chromatiaceae; Allochromatium.
OX NCBI_TaxID=1049;

[1]
RN RP SEQUENCE.
RX MEDLINE=93146381; PubMed=1490603;
RA Liebergesell M., Schmidt B., Steinbuechel A.;
RT "Isolation and identification of granule-associated proteins relevant
RT for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum
RT D.";
RL FEMS Microbiol. Lett. 78:227-232 (1992).
SQ SEQUENCE 15 AA; 1834 MW; 215B7FCFCF65BB8E CRC64;

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MFP 15
DB 1 MFP 3

RESULT 50
Q9TR62 PRELIMINARY; PRT; 15 AA.
AC Q9TR62;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Apolipoprotein A-IV (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=95329112; PubMed=7605356;
RA Mezdoor H., Yamamura T., Nomura S., Yamamoto A.;
RT "Genetic but not diet-induced hypercholesterolemia causes low
RT apolipoprotein A-IV level in rabbit sera.";
RL Atherosclerosis 113:171-178 (1995).
SQ SEQUENCE 15 AA; 1761 MW; DE115BB7351F0ABC CRC64;

Query Match 20.0%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TVM 13
DB 9 TVM 11

RESULT 51
Q9QV25 PRELIMINARY; PRT; 15 AA.
AC Q9QV25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Sigma receptor cyclophilin-like component (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=94322640; PubMed=8046989;
RA Schuster D.I., Ehrlich G.K., Murphy R.B.;
RT "Purification and partial amino acid sequence of a 28 kDa cyclophilin-
RT like component of the rat liver sigma receptor.";
RL Life Sci. 55:151-151 (1994).
SQ SEQUENCE 15 AA; 1622 MW; 95E384B4EC8D14D4 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      10 PTV 12
Db      3 PTV 5

RESULT 52
Q69353
ID      Q69353      PRELIMINARY;      PRT;      15 AA.
AC      Q69353;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      HSV-2 (333) N terminus of 17.8 kda protein gene (0.642 mu)
DE      (Fragment).
OS      Herpes simplex virus (type 2).
OS      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC      Alphaherpesvirinae; Simplexvirus.
OX      NCBI_TaxID=10310;
RN      [1]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=85033906; PubMed=6092683;
RA      Draper K.G., Frink R.J., Devi G.B., Swain M., Galloway D.,
RA      Wagner E.K.;
RT      "Herpes simplex virus types 1 and 2 homology in the region between
RT      0.58 and 0.68 map units.";
RL      J. Virol. 52:615-623(1984).
DR      EMBL; K03360; AAA45840.1; -.
FT      NON_TER      15
SQ      SEQUENCE      15 AA; 1603 MW; 20B04D60BA4507FE CRC64;

Query Match      20.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      6 QPL 8
Db      11 QPL 13

RESULT 53
Q9R5K7
ID      Q9R5K7      PRELIMINARY;      PRT;      16 AA.
AC      Q9R5K7;
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      23.4-kda chitinase (Fragment).
OS      Streptomyces olivaceoviridis (Streptomyces corchorusii).
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomycineae; Streptomycetaceae; Streptomyces.
OX      NCBI_TaxID=1921;
RN      [1]
RN      SEQUENCE.
RX      MEDLINE=92276319; PubMed=1592803;
RA      Romaguera A., Menge U., Breves R., Diekmann H.;
RA      "Chitinases of Streptomyces olivaceoviridis and significance of
RT      processing for multiplicity.";
RL      J. Bacteriol. 174:3450-3454(1992).
FT      NON_TER      1
FT      NON_TER      16
SQ      SEQUENCE      16 AA; 2014 MW; 0F732A24DC14CE01 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      13 MFP 15
Db      6 MFP 8

RESULT 54
Q9NNZ2
ID      Q9NNZ2      PRELIMINARY;      PRT;      16 AA.
AC      Q9NNZ2;
DT      01-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT      01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE      Integrin alpha-2 subunit (Fragment).
GN      ITGA2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=98421383; PubMed=9746778;
RA      Kritzik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,
RA      Kunicki T.J.;
RT      "Nucleotide polymorphisms in the alpha2 gene define multiple alleles
RT      that are associated with differences in platelet alpha2 beta1
RT      density.";
RL      Blood 92:2382-2388(1998).
DR      EMBL; AF062039; AAF77577.1; -.
FT      NON_TER      16
SQ      SEQUENCE      16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;

Query Match      20.0%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      7 PLP 9
Db      10 PLP 12

RESULT 55
Q9UCH1
ID      Q9UCH1      PRELIMINARY;      PRT;      16 AA.
AC      Q9UCH1;
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE      LIPOAMIDASE (EC 3.1.1.13) (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RN      SEQUENCE.
RX      MEDLINE=93228634; PubMed=8471055;
RA      Hui D.Y., Hayakawa K., Oizumi J.;
RT      "Lipoamidase activity in normal and mutagenized pancreatic cholesterol
RT      esterase (bile salt-stimulated lipase).";
RL      Biochem. J. 291:65-69(1993).
SQ      SEQUENCE      16 AA; 1844 MW; 147321FA60374B3C CRC64;

Query Match      20.0%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      5 POP 7
Db      6 POP 8

RESULT 56
O18378
ID      O18378      PRELIMINARY;      PRT;      16 AA.
AC      O18378;
DT      01-JAN-1998 (TREMBlrel. 05, Created)
DT      01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      Hypothetical 1.5 kda protein in ANON-37CS 5'REGION (ORF3).
GN      ANON-37CC.

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OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88038375; PubMed=3478553;
 RA Eveleth D.D., Marsh J.L.;
 RT "Overlapping transcription units in Drosophila: sequence and structure
 of the Cs gene.";
 RL Mol. Gen. Genet. 209:290-298(1987).
 DR EMBL; X05991; CAA29407.1; -;
 DR FlyBase; FBgn0026744; anon-37Cc.
 KW Hypothetical protein.
 SQ SEQUENCE 16 AA; 1543 MW; F5F881ED5A799277 CRC64;
 Query Match 20.0%; Score 3; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 PTV 12
 Db 13 PTV 15
 RESULT 57
 Q9TRR1 PRELIMINARY; PRT; 16 AA.
 ID Q9TRR1
 AC Q9TRR1
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Fibronectin 47 kDa fragment (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92283375; PubMed=1597256;
 RA Lesot H., Fausser J.L., Akiyama S.K., Staub A., Black D., Kubler M.D.,
 RA Ruch J.V.;
 RT "The carboxy-terminal extension of the collagen binding domain of
 fibronectin mediates interaction with a 165 kDa membrane protein
 involved in odontoblast differentiation.";
 RL Differentiation 49:109-118(1992).
 FT NON_TER 1
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1764 MW; B196CAAC53F5739 CRC64;
 Query Match 20.0%; Score 3; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 POP 7
 Db 2 POP 4
 RESULT 58
 P92732 PRELIMINARY; PRT; 16 AA.
 ID P92732
 AC P92732
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NADH dehydrogenase subunit II (Fragment).
 GN ND2.
 OS Fejervarya limnocharis (Boie's wart frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;

OC Fejervarya.
 OX NCBI_TaxID=110108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153826; PubMed=9000757;
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-strand replication in
 rearrangement of the vertebrate mitochondrial genome.";
 RL Mol. Biol. Evol. 14:91-104(1997).
 DR EMBL; U71324; AAB48287.1; -;
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 16 AA; 1860 MW; DD1C1017F8B19DEE CRC64;
 Query Match 20.0%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 MFP 15
 Db 5 MFP 7
 RESULT 59
 Q9JHB6 PRELIMINARY; PRT; 16 AA.
 ID Q9JHB6
 AC Q9JHB6
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Meprin 1 beta (Fragment).
 GN MEPIB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96147211; PubMed=8567689;
 RA Dietrich J.M., Jiang W., Bond J.S.;
 RT "A novel meprin beta mRNA in mouse embryonal and human colon
 carcinoma cells.";
 RL J. Biol. Chem. 271:2271-2278(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jiang W., Kumar J.M., Bond J.S.;
 RT "Structure of the mouse metalloprotease meprin beta gene (Mep1b):
 alternative splicing in cancer cells.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF160982; AAF80401.1; -;
 DR MGD; MGI:96964; Mep1b.
 FT NON_TER 16
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1979 MW; EB9785A3F6189622 CRC64;
 Query Match 20.0%; Score 3; DB 11; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HOP 4
 Db 5 HOP 7
 RESULT 60
 Q8VME2 PRELIMINARY; PRT; 17 AA.
 ID Q8VME2
 AC Q8VME2
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE PARC protein (Fragment).
 GN PARC.
 OS Pseudomonas putida.

SQ SEQUENCE 17 AA; 1948 MW; AB699819BD70BCEF CRC64;

Query Match 20.0%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9
DB 14 PLP 16

RESULT 65

Q14001 ID Q14001 PRELIMINARY; PRT; 17 AA.
AC Q14001; 17 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclic nucleotide phosphodiesterase (Fragment).
GN CGIPDE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=8921398;
RX MEDLINE=9709687; PubMed=8921398;
RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;
RT "Molecular cloning and chromosomal assignment of the human homologue
of the rat cAMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved
in fat metabolism located at 11p15.1";
RL Genomics 37:211-218(1996).
DR EMBL; X95522; CAA64776.1; .
FT NON_TER 17
SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
DB 15 QPP 17

RESULT 66

Q9TRU8 ID Q9TRU8 PRELIMINARY; PRT; 17 AA.
AC Q9TRU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Leukemia inhibitory factor, LIF=INHIBITOR of aortic endothelial cell
growth (Fragment).
DE growth (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92115728; PubMed=1370585;
RA Ferrara N., Winer J., Hensel W.J.;
RT "Pituitary follicular cells secrete an inhibitor of aortic endothelial
cell growth: identification as leukemia inhibitory factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:698-702(1992).
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 20.0%; Score 3; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9
DB 2 PLP 4

RESULT 67
P83061 ID P83061 PRELIMINARY; PRT; 17 AA.
AC P83061;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans
isomerase) (PPIase) (EC 5.2.1.8) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RA Schubert M., Peterson U., Funk C., Haas B., Schroeder W.P.,
RL Kieselbach T.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR InterPro; IPR001179; FKBP_PPIase.
KW Isomerase; Rotamase; Chloroplast.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1771 MW; E2013F998EFBF908 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
DB 3 LPP 5

RESULT 68

Q8B4C4 ID Q8B4C4 PRELIMINARY; PRT; 17 AA.
AC Q8B4C4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Precore.
OS Hepatitis B virus.
OC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Vaishali C., Acharya S.K., Panda S.K.;
RT "Cryptic Hepatitis B virus infection: analysis of the complete genomic
sequence of HBV from nine patients with seronegative viral
hepatitis".
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY161158; AAO12630.1; .
SQ SEQUENCE 17 AA; 1908 MW; 0B63A9BF82802588 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12
DB 15 PTV 17

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RESULT 69
Q9R5U2      PRELIMINARY;      PRT;      18 AA.
ID Q9R5U2;
AC Q9R5U2;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE 2-amino-benzoate-CoA ligase-B3 (fragment).
OS Pseudomonas.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae.
OX NCBI_TaxID=286;
RN [1]
RP SEQUENCE.
RX MEDLINE=91358327; PubMed=1885526;
RA Altenschnidt U., Oswald B., Fuchs G.;
RT "Purification and characterization of benzoate-coenzyme A ligase and
RT 2-aminobenzoate-coenzyme A ligases from a denitrifying Pseudomonas
RT sp.";
RL J. Bacteriol. 173:5494-5501 (1991).
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2061 MW; C43F8799692771EF CRC64;

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
Db 12 LPP 14

RESULT 70
Q9R5F9      PRELIMINARY;      PRT;      18 AA.
ID Q9R5F9;
AC Q9R5F9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Arsenite oxidase, AOI (fragment).
OS Alcaligenes faecalis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=511;
RN [1]
RP SEQUENCE.
RX MEDLINE=93054722; PubMed=1331097;
RA Anderson G.L., Williams J., Hille R.;
RT "The purification and characterization of arsenite oxidase from
RT Alcaligenes faecalis, a molybdenum-containing hydroxylase.";
RL J. Biol. Chem. 267:23674-23682 (1992).
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1938 MW; 4EDDC418B71A4574 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
Db 9 LPP 11

RESULT 71
Q9R4V9      PRELIMINARY;      PRT;      18 AA.
ID Q9R4V9;
AC Q9R4V9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)

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DE 10 kDa heat shock- and alkaline pH-induced protein (fragment).
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE.
RX MEDLINE=95012609; PubMed=7927682;
RA Wu Y.L., Lee L.H., Rollins D.M., Ching W.M.;
RT "Heat shock- and alkaline pH-induced proteins of Campylobacter jejuni:
RT characterization and immunological properties.";
RL Infect. Immun. 62:4256-4260 (1994).
SQ SEQUENCE 18 AA; 2056 MW; 9E4FED7BB4DA76C4 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8
Db 4 QPL 6

RESULT 72
Q9EYW5      PRELIMINARY;      PRT;      18 AA.
ID Q9EYW5;
AC Q9EYW5;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE RepB.
GN REPB.
OS Erwinia stewartii.
OG Plasmid pSW800.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pantoea.
OX NCBI_TaxID=66271;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu C.-Y., Liu S.-T.;
RT "Erwinia stewartii plasmid pSW800 basic replicon, repA and repB
RT genes.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF310258; AAG47776.1; -.
KW Plasmid.
SQ SEQUENCE 18 AA; 1952 MW; C8FD2873F9CAC66C CRC64;

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8
Db 6 QPL 8

RESULT 73
Q9R4C6      PRELIMINARY;      PRT;      18 AA.
ID Q9R4C6;
AC Q9R4C6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Protocatechuate 3,4-dioxygenase type I alpha subunit (EC 1.13.11.3)
DE (fragment).
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE.
RX MEDLINE=96337865; PubMed=8772173;
RA Hammer A., Stolz A., Knackmuss H.;

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RT "Purification and characterization of a novel type of protocatechuate
RT 3,4-dioxygenase with the ability to oxidize 4-sulfocatechol.",
RL Arch. Microbiol. 166:92-100(1996).
SQ SEQUENCE 18 AA; 2152 MW; BFC56CA8D4376D84 CRC64;
Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 QPL 8
Db 2 QPL 4
RESULT 74
Q9UCG7 PRELIMINARY; PRT; 18 AA.
AC Q9UCG7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Urinary gonadotrophin peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=93229246; PubMed=8471426;
RX Kardana A., Bagshaw K.D., Coles B., Read D., Taylor M.;
RA "Characterisation of UGP and its relationship with beta-core
RT fragment.";
RL Br. J. Cancer 67:686-692(1993).
DR HSP; P10153; IHI2.
SQ SEQUENCE 18 AA; 2214 MW; BB0A2F0B8E933109 CRC64;
Query Match 20.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PPQ 6
Db 2 PPQ 4
RESULT 75
Q96F98 PRELIMINARY; PRT; 18 AA.
AC Q96F98;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011455; AAH11455.1; --
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 18 AA; 2114 MW; 3A6C3E2BF620B9CD CRC64;
Query Match 20.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PPT 11
Db 11

Db 9 PPT 11
Search completed: November 25, 2003, 19:34:16
Job time : 28.1686 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 38.2849 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-34
Perfect score: 15
Sequence: 1 MHQPPPLPTVWFP 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	22	Colostrin deriv
2	15	100.0	15	22	Colostrin peptid
3	15	100.0	15	22	Colostrin consti
4	15	100.0	15	22	Ewe colostrin pe
5	15	100.0	15	22	Colostrin consti
6	15	100.0	15	23	Colostrin consti
7	15	100.0	15	23	Colostrin consti
8	10	66.7	10	22	Neural cell regula
9	10	66.7	10	22	Colostrin deriv

10	10	66.7	10	22	Colostrin peptid
11	10	66.7	10	23	Colostrin consti
12	10	66.7	10	23	Colostrin consti
13	10	66.7	10	23	Neural cell regula
14	9	60.0	11	22	Colostrin peptid
15	9	60.0	12	22	Modified colostrin
16	6	40.0	11	22	Ewe colostrin pe
17	6	40.0	11	23	Human colostrin pe
18	6	40.0	11	23	Human novel secret
19	6	40.0	15	18	Peptide resembling
20	6	40.0	15	23	Human K-ras 10.67
21	6	40.0	16	18	Grb2 N-terminal SH
22	5	33.3	7	20	Mammalian ion chan
23	5	33.3	7	21	SH3 antagonist pep
24	5	33.3	7	22	Colostrin deriv
25	5	33.3	7	22	Colostrin peptid
26	5	33.3	7	22	Colostrin peptid
27	5	33.3	7	23	Ewe colostrin pe
28	5	33.3	7	23	Colostrin consti
29	5	33.3	7	23	Colostrin consti
30	5	33.3	7	23	Neural cell regula
31	5	33.3	7	23	Src homology3 (SH3
32	5	33.3	8	22	Human protein frag
33	5	33.3	8	22	Human protein frag
34	5	33.3	9	22	Clone 1 scFv CDR L
35	5	33.3	9	24	Human cancer-relat
36	5	33.3	9	24	Human cancer-relat
37	5	33.3	10	24	Human cancer-relat
38	5	33.3	10	24	Human cancer-relat
39	5	33.3	12	22	Human protein frag
40	5	33.3	13	16	PI3K protein tyros
41	5	33.3	13	17	Src SH3 domain-bin
42	5	33.3	13	21	Human secreted pro
43	5	33.3	13	23	Escherichia coli 3
44	5	33.3	13	24	Human TPO peptide
45	5	33.3	13	24	Human TPO peptide
46	5	33.3	13	24	Human TPO peptide
47	5	33.3	13	24	Human TPO peptide
48	5	33.3	14	20	Amino acid sequenc
49	5	33.3	14	22	Human protein frag
50	5	33.3	14	22	Bacille Calmette-G
51	5	33.3	14	22	BCG T-cell epitope
52	5	33.3	15	18	Peptide resembling
53	5	33.3	15	18	Peptide resembling
54	5	33.3	15	18	Peptide resembling
55	5	33.3	15	18	Peptide resembling
56	5	33.3	15	22	Growth hormone fam
57	5	33.3	15	24	Human cancer-relat
58	5	33.3	15	24	Human cancer-relat
59	5	33.3	15	24	Human cancer-relat
60	5	33.3	15	24	Human cancer-relat
61	5	33.3	15	24	Human cancer-relat
62	5	33.3	15	24	Human cancer-relat
63	5	33.3	15	24	Human cancer-relat
64	5	33.3	15	24	Human cancer-relat
65	5	33.3	16	18	Yes SH3 domain bin
66	5	33.3	16	18	Src SH3 domain bin
67	5	33.3	16	18	Src SH3 domain bin
68	5	33.3	16	24	G protein-coupled
69	5	33.3	17	21	Human liver peptid
70	5	33.3	18	22	Peptide #9220 enco
71	5	33.3	18	22	Human brain expres
72	5	33.3	18	22	Human bone marrow
73	5	33.3	18	22	Peptide #9548 enco
74	5	33.3	18	22	Human gene 10 enco
75	5	33.3	19	20	Ubiquitin fusion p
76	5	33.3	19	20	Ubiquitin fusion p
77	5	33.3	19	20	MT peptide. Unide
78	5	33.3	19	22	Src SH3 domain-bin
79	5	33.3	20	17	T-cell epitope use
80	5	33.3	20	17	T-cell stimulatory
81	5	33.3	20	18	Heatshock protein
82	5	33.3	20	18	

83 5 33.3 20 19 AAW60693 Mycobacteria heat
 84 5 33.3 20 23 ABB79926 Mycobacterium heat
 85 4 26.7 4 16 AAR80055 Peptidase substrat
 86 4 26.7 5 21 AAY45075 Rat amelogenin N-t
 87 4 26.7 6 13 AAR28486 Casoxin D-like vas
 88 4 26.7 6 16 AAR83532 Zif268 zinc finger
 89 4 26.7 6 19 AAW31463 Transcriptional ac
 90 4 26.7 6 19 AAW31465 Transcriptional ac
 91 4 26.7 6 20 AAW84430 HIV-1 nucleic acid
 92 4 26.7 7 10 AAP90659 New antihypertensi
 93 4 26.7 7 15 AAR60997 Fragment of the 3B
 94 4 26.7 7 16 AAR73883 Rubella virus glyc
 95 4 26.7 7 17 AAW11128 SRC SH3 domain-bin
 96 4 26.7 7 17 AAW17010 SRC SH3 domain-bin
 97 4 26.7 7 17 AAW07013 Synthetic peptide
 98 4 26.7 7 18 AAW25486 SH3 domain binding
 99 4 26.7 7 18 AAW10774 Ferritin motif #17
 100 4 26.7 7 19 AAW79781 Proline-rich pepti

ALIGNMENTS

RESULT 1
 AAB72279
 ID AAB72279 standard; peptide; 15 AA.

XX AAB72279;

XX 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 34.

XX Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokines production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPPQPLPPTVMFP 15

DB 1 MHQPPQPLPPTVMFP 15

RESULT 2

AAB72531
 ID AAB72531 standard; Peptide; 15 AA.

XX AAB72531;

XX 09-MAY-2001 (first entry)

XX Colostrinin peptide #32.

XX Dermatological; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22665.

XX 17-AUG-1999; 99US-0149310.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -

XX Claim 6; Page 26; 48pp; English.

XX The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPPQPLPPTVMFP 15

DB 1 MHQPPQPLPPTVMFP 15

RESULT 3

AAB72563
 ID AAB72563 standard; Peptide; 15 AA.

XX AAB72563;

XX 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #32.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX Unidentified.
 XX OS
 XX WO200112651-A2.
 XX 22-FEB-2001.
 XX 17-AUG-2000; 2000WO-US22774.
 XX PF
 XX 17-AUG-1999; 99US-0149633.
 XX PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX PA
 XX Boldogh I;
 XX PI
 XX WPI; 2001-226545/23.
 XX DR
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX
 XX Claim 6; Page 22; 35pp; English.
 XX PS
 XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 XX
 XX Sequence 15 AA;
 SQ

Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHQPPQPLPPTVMFP 15
 |||||
 Db 1 MHQPPQPLPPTVMFP 15
 |||||

RESULT 4
 AAB59334
 ID AAB59334 standard; Peptide; 15 AA.
 XX AC AAB59334;
 XX XX
 DT 21-MAR-2001 (first entry)
 XX DE Ewe colostrinin peptide fragment C-9.
 XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX OS Ovis sp.
 XX XX
 XX WO200075173-A2.
 XX PN
 XX 14-DEC-2000.
 XX PD
 XX 02-JUN-2000; 2000WO-GB02128.
 XX PF
 XX 02-JUN-1999; 99GB-0012852.
 XX PR
 XX (REGE-) REGEN THERAPEUTICS PLC.
 XX PA
 XX Georgiades JA;
 XX PI
 XX WPI; 2001-071058/08.
 XX DR
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 XX PS Claim 7; Page 27; 63pp; English.
 XX CC
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 XX Sequence 15 AA;
 SQ

Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHQPPQPLPPTVMFP 15
 |||||
 Db 1 MHQPPQPLPPTVMFP 15
 |||||

RESULT 5
 AAE20261
 ID AAE20261 standard; peptide; 15 AA.
 XX AC AAE20261;
 XX XX
 DT 18-JUN-2002 (first entry)
 XX DE Colostrinin constituent peptide #32.
 XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnary.
 XX OS Unidentified.
 XX XX
 XX Key Location/Qualifiers
 FT Modified-site 15 /note= "Optionally C-terminal amide"
 XX FT
 XX WO200213850-A1.
 XX PN
 XX 21-FEB-2002.
 XX PD
 XX 17-AUG-2000; 2000WO-US22776.
 XX PF
 XX 17-AUG-2000; 2000WO-US22776.
 XX PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX PA
 XX Stanton GU, Hughes TK, Boldogh I;
 XX PI
 XX WPI; 2002-269151/31.
 XX DR
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 XX Claim 6; Page 26; 51pp; English.
 XX PS
 XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX Sequence 15 AA;
 Query Match 100.0%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQPPQPLPPTVMFP 15
 |||||
 Db 1 MHQPPQPLPPTVMFP 15

RESULT 6
 AAM51066
 ID AAM51066 standard; Peptide; 15 AA.

XX AAM51066;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide (casein amino acids 159-173).

XX Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 15 /note= "optional C-terminal amidation"

XX WO200213849-A1.

PD 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GU, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 159-173. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

XX Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQPPQPLPPTVMFP 15
 |||||
 Db 1 MHQPPQPLPPTVMFP 15

RESULT 7

AAO14610

ID AAO14610 standard; peptide; 15 AA.

XX AAO14610;

DT 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 32.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX Unidentified.

XX OS

XX Key Location/Qualifiers

FT Modified-site 15 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 22; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPPQPLPPTVMFP 15
DB 1 MHQPPQPLPPTVMFP 15

RESULT 8

AAB72270
ID AAB72270 standard; peptide; 10 AA.

XX
AC AAB72270;

XX
DT 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 25.

XX Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX
PD 22-FEB-2001.

XX
PF 17-AUG-2000; 2000WO-US22818.

XX
PR 17-AUG-1999; 99US-0149311.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -

PS Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX Sequence 10 AA;

Query Match 66.7%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPPTVMFP 15
DB 1 QPLPPTVMFP 10

RESULT 9

AAB72523
ID AAB72523 standard; Peptide; 10 AA.

XX
AC AAB72523;

XX
DT 09-MAY-2001 (first entry)

XX Colostrinin peptide #24.

XX Dermatological; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX
PD 22-FEB-2001.

XX
PF 17-AUG-2000; 2000WO-US22665.

XX
PR 17-AUG-1999; 99US-0149310.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX
DR WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -

PS Claim 6; Page 26; 48pp; English.

XX The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.

XX Sequence 10 AA;

Query Match 66.7%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPPTVMFP 15
DB 1 QPLPPTVMFP 10

RESULT 10

AAB72555
ID AAB72555 standard; Peptide; 10 AA.

XX
AC AAB72555;

XX
DT 09-MAY-2001 (first entry)

XX Colostrinin peptide #24.

XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.

XX Unidentified.

XX WO200112651-A2.

XX
PD 22-FEB-2001.

CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casain homologue precursor, and corresponds to
 CC casain amino acids 164-173. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the
 CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.
 XX
 SQ Sequence 10 AA;

Query Match 66.7%; Score 10; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QLPPTVMFP 15
 DB 1 QLPPTVMFP 10
 |||||

RESULT 13
 AA014601
 ID AA014601 standard; peptide; 10 AA.
 AC AA014601;
 XX
 XX 27-MAY-2002 (first entry)
 DT
 DE Neural cell regulatory colostrinin peptide 24.
 XX
 XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrinum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 10 /note="Optional C-terminal amide"
 FT
 XX WO200213851-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22777.
 PF
 XX 17-AUG-2000; 2000WO-US22777.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I, Stanton JG, Hughes TK;
 PI
 XX WPI; 2002-269152/31.
 DR
 XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog
 XX
 PS Claim 7; Page 21; 37pp; English.
 XX The invention comprises a method for promoting cell differentiation (e.g.

CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrinum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.
 XX
 SQ Sequence 10 AA;

Query Match 66.7%; Score 10; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QLPPTVMFP 15
 DB 1 QLPPTVMFP 10
 |||||

RESULT 14
 AA071192
 ID AA071192 standard; peptide; 11 AA.
 XX
 AC AA071192;
 XX
 XX 06-NOV-2001 (first entry)
 DT
 XX
 DE Colostrinin peptide 8.
 XX
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral.
 XX
 OS Unidentified.
 XX
 XX WO200155199-A1.
 PN
 XX 02-AUG-2001.
 PD
 XX 26-JAN-2001; 2001WO-GB00329.
 PF
 XX 26-JAN-2000; 2000GB-0001825.
 PR
 XX (REGE-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-488775/53.
 DR
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX
 PS Claim 1; Page 15; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification

CC and in persons dependent on stimulants. Colostrinin peptides are used to
CC prepare antibodies and to treat emotional disturbances, e.g. emotional
CC disturbances of psychiatric patients in a state of depression. These
CC colostrinin peptides improves the development of immune system in a new
CC born child and to correct the immunological deficiencies in a child.
CC The present sequence is colostrinin peptide 8 related to the invention.
CC Colostrinin peptide 8 corresponds to position 165-175 of beta-caesin.
XX
SQ Sequence 11 AA;

Query Match 60.0%; Score 9; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPTVMFP 15
Db 1 PLPPTVMFP 9
|||||

RESULT 15
AAE07202
ID AAE07202 standard; peptide; 12 AA.
XX
AC AAE07202;
XX
DT 06-NOV-2001 (first entry)
DE
DE Modified colostrinin cyclic peptide #8.
XX
KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
KW central nervous system disorder; neurodegenerative disorder; weight loss;
KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
KW acquired immunological deficiency; neurological disorder; dementia;
KW antiviral; cyclic.
XX
OS Synthetic.
XX
XX
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal acetyl; this residue forms a cyclic
FT linkage with Gln found at the C-terminal end"
XX
XX
XX WO200155199-A1.
XX
XX 02-AUG-2001.
XX
XX 26-JAN-2001; 2001WO-GB00329.
XX
XX 26-JAN-2000; 2000GB-0001825.
XX
XX (REG-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA;
PI
XX
XX WPI; 2001-488775/53.
XX
XX Peptide useful as an inter alia in the treatment of e.g. disorders of
XX the immune system and the central nervous system comprises ten
XX amino-terminal amino acid sequence derived from peptides present in
XX colostrinin -
XX
XX Example 2; Page 9; 40pp; English.
XX
XX The invention relates to colostrinin peptide fragments which are useful,
XX inter alia, in the treatment of chronic disorders of the immune system
XX and the central nervous system. Colostrinin peptides are used as a
XX medicament in the treatment of neurological disorders e.g., dementia,
XX neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
XX disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
XX neurosis, in acquired immunological deficiencies, chronic bacterial and
XX viral infections and diseases characterised by the presence of beta-
XX amyloid plaques and as a dietary supplement for babies, small children,

CC adults and senile persons, who have been subjected to chemotherapy or
CC have suffered from cachexia or weight loss due to the chronic disease.
CC Colostrinin peptides are also used as food additives and as an auxiliary
CC withdrawal treatment for drug addicts, after a period of detoxification
CC and in persons dependent on stimulants. Colostrinin peptides are used to
CC prepare antibodies and to treat emotional disturbances, e.g. emotional
CC disturbances of psychiatric patients in a state of depression. These
CC colostrinin peptides improves the development of immune system in a new
CC born child and to correct the immunological deficiencies in a child.
CC The present sequence is modified colostrinin cyclic peptide #8 related to
CC the invention.
XX
SQ Sequence 12 AA;

Query Match 60.0%; Score 9; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPTVMFP 15
Db 2 PLPPTVMFP 10
|||||

RESULT 16
AAB59333
ID AAB59333 standard; Peptide; 11 AA.
XX
AC AAB59333;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment C-8.
XX
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
XX
XX WO2000075173-A2.
XX
PD 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-GB02128.
XX
XX 02-JUN-1999; 99GB-0012852.
XX
XX (REG-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA;
XX
XX WPI; 2001-071058/08.
XX
XX Peptides having an N-terminal amino acid sequence isolated from
XX colostrinin for treating e.g. disorders of the central nervous system
XX and immune system, viral and bacterial infections, and diseases
XX characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
XX
XX The present invention provides the sequences of a number of peptides
XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX fragment of colostrum. These peptides can be used in the treatment of
XX central nervous system disorders such as senile dementia, Parkinson's
XX disease, Alzheimer's disease, psychosis and neurosis, immune system
XX disorders such as bacterial and viral infections, to improve the
XX development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques.
XX
SQ Sequence 11 AA;

Query Match 40.0%; Score 6; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPPT 11
 Db | | | | |
 1 QPLPPT 6

RESULT 17
 ABG95549
 ID ABG95549 standard; Peptide; 11 AA.
 XX AC
 AC ABG95549;
 XX
 DT 15-JAN-2003 (first entry)
 XX
 DE Human novel secreted protein gene 86 polypeptide #1.
 XX
 KW Human; secreted protein; autoimmune disease; chemotaxis;
 KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
 KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
 KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
 KW nervous system disorders; Alzheimer's disease; infection;
 KW ocular disorder; corneal infection; wound healing; tissue regeneration;
 KW epithelial cell proliferation; organ transplantation; food additive;
 KW preservative; nutritional.
 XX
 OS Homo sapiens.
 XX
 PN US6420526-B1.
 XX
 PD 16-JUL-2002.
 XX
 PF 08-SEP-1998; 98US-0149476.
 XX
 PR 07-MAR-1997; 97US-038621P.
 PR 07-MAR-1997; 97US-040161P.
 PR 07-MAR-1997; 97US-040182P.
 PR 07-MAR-1997; 97US-040163P.
 PR 07-MAR-1997; 97US-040333P.
 PR 07-MAR-1997; 97US-040334P.
 PR 07-MAR-1997; 97US-040336P.
 PR 07-MAR-1997; 97US-040626P.
 PR 11-APR-1997; 97US-043311P.
 PR 11-APR-1997; 97US-043312P.
 PR 11-APR-1997; 97US-043313P.
 PR 11-APR-1997; 97US-043314P.
 PR 11-APR-1997; 97US-043315P.
 PR 11-APR-1997; 97US-043568P.
 PR 11-APR-1997; 97US-043569P.
 PR 11-APR-1997; 97US-043576P.
 PR 11-APR-1997; 97US-043578P.
 PR 11-APR-1997; 97US-043580P.
 PR 11-APR-1997; 97US-043659P.
 PR 11-APR-1997; 97US-043670P.
 PR 11-APR-1997; 97US-043671P.
 PR 11-APR-1997; 97US-043672P.
 PR 11-APR-1997; 97US-043674P.
 PR 23-MAY-1997; 97US-043674P.
 PR 23-MAY-1997; 97US-047500P.
 PR 23-MAY-1997; 97US-047501P.
 PR 23-MAY-1997; 97US-047502P.
 PR 23-MAY-1997; 97US-047503P.
 PR 23-MAY-1997; 97US-047581P.
 PR 23-MAY-1997; 97US-047582P.
 PR 23-MAY-1997; 97US-047583P.
 PR 23-MAY-1997; 97US-047584P.
 PR 23-MAY-1997; 97US-047585P.
 PR 23-MAY-1997; 97US-047586P.
 PR 23-MAY-1997; 97US-047587P.
 PR 23-MAY-1997; 97US-047588P.
 PR 23-MAY-1997; 97US-047589P.
 PR 23-MAY-1997; 97US-047590P.
 PR 23-MAY-1997; 97US-047592P.
 PR 23-MAY-1997; 97US-047593P.

PR 23-MAY-1997; 97US-047594P.
 PR 23-MAY-1997; 97US-047595P.
 PR 23-MAY-1997; 97US-047596P.
 PR 23-MAY-1997; 97US-047597P.
 PR 23-MAY-1997; 97US-047598P.
 PR 23-MAY-1997; 97US-047599P.
 PR 23-MAY-1997; 97US-047600P.
 PR 23-MAY-1997; 97US-047601P.
 PR 23-MAY-1997; 97US-047612P.
 PR 23-MAY-1997; 97US-047613P.
 PR 23-MAY-1997; 97US-047614P.
 PR 23-MAY-1997; 97US-047615P.
 PR 23-MAY-1997; 97US-047617P.
 PR 23-MAY-1997; 97US-047618P.
 PR 23-MAY-1997; 97US-047632P.
 PR 23-MAY-1997; 97US-047633P.
 PR 06-JUN-1997; 97US-048964P.
 PR 06-JUN-1997; 97US-048974P.
 PR 13-JUN-1997; 97US-049610P.
 PR 08-JUL-1997; 97US-051926P.
 PR 16-JUL-1997; 97US-052874P.
 PR 18-AUG-1997; 97US-055724P.
 PR 22-AUG-1997; 97US-056630P.
 PR 22-AUG-1997; 97US-056631P.
 PR 22-AUG-1997; 97US-056632P.
 PR 22-AUG-1997; 97US-056636P.
 PR 22-AUG-1997; 97US-056637P.
 PR 22-AUG-1997; 97US-056662P.
 PR 22-AUG-1997; 97US-056664P.
 PR 22-AUG-1997; 97US-056845P.
 PR 22-AUG-1997; 97US-056862P.
 PR 22-AUG-1997; 97US-056864P.
 PR 22-AUG-1997; 97US-056872P.
 PR 22-AUG-1997; 97US-056874P.
 PR 22-AUG-1997; 97US-056875P.
 PR 22-AUG-1997; 97US-056876P.
 PR 22-AUG-1997; 97US-056877P.
 PR 22-AUG-1997; 97US-056878P.
 PR 22-AUG-1997; 97US-056879P.
 PR 22-AUG-1997; 97US-056880P.
 PR 22-AUG-1997; 97US-056881P.
 PR 22-AUG-1997; 97US-056882P.
 PR 22-AUG-1997; 97US-056884P.
 PR 22-AUG-1997; 97US-056886P.
 PR 22-AUG-1997; 97US-056887P.
 PR 22-AUG-1997; 97US-056888P.
 PR 22-AUG-1997; 97US-056889P.
 PR 22-AUG-1997; 97US-056892P.
 PR 22-AUG-1997; 97US-056893P.
 PR 22-AUG-1997; 97US-056894P.
 PR 22-AUG-1997; 97US-056903P.
 PR 22-AUG-1997; 97US-056908P.
 PR 22-AUG-1997; 97US-056909P.
 PR 22-AUG-1997; 97US-056910P.
 PR 22-AUG-1997; 97US-056911P.
 PR 22-AUG-1997; 97US-057761P.
 PR 05-SEP-1997; 97US-057650P.
 PR 05-SEP-1997; 97US-057659P.
 PR 12-SEP-1997; 97US-058785P.
 PR 02-OCT-1997; 97US-061060P.
 PR 06-MAR-1998; 98WO-US04493.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;
 PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
 PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
 XX
 DR WPI; 2002-634796/68.
 XX
 PT New isolated human secreted protein for diagnosing, preventing,
 treating or ameliorating medical conditions and used as a food additive

PT or preservative -
 PS Disclosure; Column 78; 129pp; English.
 XX
 CC The invention relates to an isolated protein that is one of 186 human
 CC secreted proteins, given in the specification, encoded by one of
 CC 309 cDNA sequences also given in the specification. The protein is used
 CC in a pharmaceutical composition used to prevent, treat or ameliorate a
 CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
 CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional
 CC components. The present sequence represents one of the novel human
 CC secreted proteins of the invention.
 XX
 SQ Sequence 11 AA;
 Query Match 40.0%; Score 6; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HOPPOP 7
 Db 1 HOPPOP 6
 RESULT 18
 AAW39006
 ID AAW39006 standard; peptide; 15 AA.
 AC AAW39006;
 XX
 XX 27-MAR-1998 (first entry)
 DT
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:405.
 XX
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 XX Synthetic.
 OS
 XX WO9730074-A1.
 PN
 XX
 XX 21-AUG-1997.
 PD
 XX
 XX 14-FEB-1997; 97WO-US02298.
 PF
 XX
 XX 16-FEB-1996; 96US-0602999.
 PR
 XX (CYTO-) CYTOGEN CORP.
 PA (UYN-) UNIV NORTH CAROLINA.
 PA
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 DR
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 PS Claim 22; Page 93; 131pp; English.

XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 SQ Sequence 15 AA;
 Query Match 40.0%; Score 6; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PPQPLP 9
 Db 8 PPQPLP 13
 RESULT 19
 ABG72660
 ID ABG72660 standard; Peptide; 15 AA.
 XX
 AC ABG72660;
 XX
 XX 26-FEB-2003 (first entry)
 DT
 DE Human K-ras 10.67 proto-oncogene protein, N-terminus.
 XX
 KW Human; K-ras 10.67; proto-oncogene; tumour; haemopathy;
 KW development disorder; human immunodeficiency virus infection; HIV;
 KW immunological disease; inflammation.
 XX
 OS Homo sapiens.
 XX
 XX CN1352063-A.
 PN
 XX 05-JUN-2002.
 PD
 XX 02-NOV-2000; 2000CN-0127155.
 PF
 XX 02-NOV-2000; 2000CN-0127155.
 PR
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA
 XX Mao Y, Xie Y;
 PI
 XX WPI; 2002-658691/71.
 DR
 XX New human K-ras proto-oncogene protein 10.67 polypeptide for treating
 PT malignant tumors, hemopathy, development disorder, human
 PT immunodeficiency virus infection, immunological diseases and various
 PT inflammations -
 XX
 PS Example 5; Page 19 (disclosure); 33pp; Chinese.
 XX
 XX The present invention discloses a new kind of polypeptide,
 CC human K-ras proto-oncogene protein 10.67, polynucleotides encoding the
 CC polypeptide and a DNA recombination process to produce the polypeptide.
 CC The present invention also discloses applying the polypeptide in
 CC treating various diseases, such as malignant tumours, haemopathy,

CC development disorder, human immunodeficiency virus (HIV) infection,
 CC immunological diseases and various inflammations. The present invention
 CC also discloses the antagonist resisting the polypeptide and its
 CC treatment effect. The present invention also discloses application of
 CC the polynucleotides encoding human K-ras proto-oncogene protein 10.67.
 CC The present sequence represents human K-ras proto-oncogene protein
 CC 10.67, N-terminus, used in an ELISA (enzyme-linked immunosorbent assay)
 CC experiment.

SQ Sequence 15 AA;
 Query Match 40.0%; Score 6; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQLPP 10
 Db 10 PQLPP 15
 |||||

RESULT 20
 AA25442
 ID AA25442 standard; peptide; 16 AA.

XX AC AA25442;
 XX DT 27-MAR-1998 (first entry)

DE Grb2 N-terminal SH3 domain binding peptide SEQ ID NO:227.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX OS Synthetic.
 OS Unidentified.

XX WO9730074-A1.

XX 21-AUG-1997.

PF 14-FEB-1997; 97WO-US02298.

PR 16-FEB-1996; 96US-0602999.

PA (CYTO-) CYTOGEN CORP.

PA (UYNC-) UNIV NORTH CAROLINA.

XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;

XX WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

PS Claim 20; Page 101; 131pp; English.

XX The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune

CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

SQ Sequence 16 AA;

Query Match 40.0%; Score 6; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTVM 13
 Db 9 LPPTVM 14
 |||||

RESULT 21
 AAY41630
 ID AAY41630 standard; peptide; 7 AA.

XX AC AAY41630;

XX DT 02-DEC-1999 (first entry)

XX Mammalian ion channel proline rich motif containing peptide #24.

XX SH3 domain; binding motif; potassium channel; protein tyrosine kinase;
 KW proline rich.

XX Mus sp.

XX US5955259-A.

XX 21-SEP-1999.

PF 19-DEC-1996; 96US-0769745.

PR 19-DEC-1996; 96US-0769745.

XX (UYER-) UNIV BRANDEIS.

XX Holmes TC, Levitan IB;

XX WPI; 1999-560490/47.

XX Identification of compounds that modulate potassium ion channel binding
 PT with protein tyrosine kinase SH3 domains -

XX Disclosure; Column 8; 18pp; English.

XX A method has been developed for determining if a compound modulates the
 CC binding of a potassium ion channel to the SH3 domain of a protein
 CC tyrosine kinase by contacting the channel with a polypeptide comprising
 CC the SH3 domain and the compound to be assessed and measuring channel-SH3
 CC binding. The method is useful for assessing the ability of a compound to
 CC modulate the formation of channel-SH3 domain complexes to improve the
 CC understanding of mechanisms of potassium channel blockage and assess the
 CC ability of potential therapeutics to inhibit blockage. AAY41607 to
 CC AAY41644 represent mammalian ion channel peptides with proline-rich
 CC motifs.

SQ Sequence 7 AA;

Query Match 33.3%; Score 5; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
 Db 1 QPLPP 5
 |||||

RESULT 22

```
AAB17247
ID AAB17247 standard; Peptide; 7 AA.
XX AC
XX AAB17247;
XX
XX 31-OCT-2000 (first entry)
XX DT
XX DE
XX DE SH3 antagonist peptide sequence SEQ ID NO:303.
XX
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
XX KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
XX KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
XX KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
XX KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
XX KW vascular endothelial growth factor; matrix metalloproteinase;
XX KW asthma; thrombosis; pharmaceutical.
XX
XX Synthetic.
XX OS
XX WO200024782-A2.
XX FN
XX PD
XX PD 04-MAY-2000.
XX
XX 25-OCT-1999; 99WO-US25044.
XX PF
XX PF 23-OCT-1998; 98US-0103371.
XX PR
XX PR 22-OCT-1999; 99US-0428082.
XX
XX (AMGE-) AMGEN INC.
XX PA
XX
XX Feige U, Liu C, Cheetham J, Boone TC;
XX PI
XX WPI; 2000-350702/30.
XX DR
XX
XX Novel composition of matter comprising an Fc domain and
XX PT pharmacologically active peptides, useful for treating cancer and
XX PT autoimmune diseases -
XX
XX Claim 39; Page 302; 608pp; English.
XX PS
XX
XX The present invention describes composition of matter (I) comprising an
XX CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
XX CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
XX CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
XX CC where P1, P2, P3, and P4 = are each independently sequences of
XX CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
XX CC independently linkers; and a, b, c, d, e, and f = are each independently
XX CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
XX CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
XX CC activities. DNAs, vectors and host cells from the present invention can
XX CC be used for producing pharmaceutical compositions. The compositions are
XX CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
XX CC The use of an Fc domain (rather than a Fab domain) can provide a longer
XX CC half-life or incorporate functions such as Fc receptor binding, protein
XX CC A binding, complement fixation, and possibly placental transfer. AAB69443
XX CC to AAB69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
XX CC sequences used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
XX SQ
XX
XX Query Match 33.3%; Score 5; DB 21; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 PLPPT 11
XX DB 2 PLPPT 6
XX
XX RESULT 23
XX AAB72269
XX ID AAB72269 standard; peptide; 7 AA.
XX
XX AAB72269;
XX AC
XX 14-MAY-2001 (first entry)
XX DT
XX DE
XX DE Colostrinin derived cytokine inducing peptide SEQ ID 24.
XX
XX Colostrinin; immune response; cytokine; blood cell proliferation;
XX KW central nervous system disorder; neurological disorder; mental disorder;
XX KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
XX KW neurosis; infection.
XX
XX Synthetic.
XX OS
XX WO200111937-A2.
XX FN
XX PD
XX PD 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22818.
XX PF
XX PF 17-AUG-1999; 99US-0149311.
XX PR
XX PR (TEXA ) UNIV TEXAS SYSTEM.
XX PA (REGE-) REGEN THERAPEUTICS PLC.
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX PI
XX WPI; 2001-202804/20.
XX DR
XX
XX Inducing a cytokine and modulating an immune response, useful for
XX PT treating central nervous system diseases and bacterial and viral
XX PT infections, comprises administering colostrinin as an immunological
XX PT regulator -
XX
XX Claim 1; Page 34; 50pp; English.
XX PS
XX
XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
XX CC a proline rich polypeptide aggregate contained in colostrum. The
XX CC peptides have immune response modulatory activity, and are capable of
XX CC inducing cytokines. Colostrinin and its derived peptides are useful for
XX CC inducing cytokine production, for modulating an immunological response
XX CC and for inducing blood cell proliferation. The peptides are useful in the
XX CC treatment of disorders of the central nervous system, neurological
XX CC disorders, mental disorders, dementia, neurodegenerative diseases,
XX CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic
XX CC disorders of the immune system, bacterial and viral infections and
XX CC acquired immunological deficiencies.
XX
XX Sequence 7 AA;
XX SQ
XX
XX Query Match 33.3%; Score 5; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MHQPP 5
XX DB 3 MHQPP 7
XX
XX RESULT 24
XX AAB72522
XX ID AAB72522 standard; Peptide; 7 AA.
XX
XX AAB72522;
XX AC
XX 09-MAY-2001 (first entry)
XX DT
XX DE Colostrinin peptide #23.
XX
XX Dermatological; oxidative stress regulator; colostrinin.
XX KW
XX OS Unidentified.
XX
```

PN WO200112650-A2.
 XX 22-FEB-2001.
 XX 17-AUG-2000; 2000WO-US22665.
 XX 17-AUG-1999; 99US-0149310.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Stanton GJ, Hughes TK, Boldogh I;
 XX WPI; 2001-218342/22.
 XX Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX
 XX Claim 6; Page 26; 48pp; English.
 XX The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidizing species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 33.3%; Score 5; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPP 5
 |||||
 Db 3 MHQPP 7

RESULT 25
 AAB72554
 ID AAB72554 standard; Peptide; 7 AA.
 XX AAB72554;
 XX 09-MAY-2001 (first entry)
 XX Colostrinin peptide #23.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX Unidentified.
 OS
 XX WO200112651-A2.
 XX 22-FEB-2001.
 XX 17-AUG-2000; 2000WO-US22774.
 XX 17-AUG-1999; 99US-0149633.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Boldogh I;
 XX WPI; 2001-226545/23.
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX
 XX Claim 6; Page 21; 35pp; English.

XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 33.3%; Score 5; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPP 5
 |||||
 Db 3 MHQPP 7

RESULT 26
 AAB59332
 ID AAB59332 standard; Peptide; 7 AA.
 XX AAB59332;
 XX 21-MAR-2001 (first entry)
 XX Ewe colostrinin peptide fragment C-7.
 XX
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX Ovis sp.
 XX WO200075173-A2.
 XX 14-DEC-2000.
 XX 02-JUN-2000; 2000WO-GB02128.
 XX 02-JUN-1999; 99GB-0012852.
 XX (REGE-) REGEN THERAPEUTICS PLC.
 XX Georgiades JA;
 XX WPI; 2001-071058/08.
 XX Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 XX characterized by amyloid plaques -
 XX Claim 7; Page 27; 63pp; English.
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 33.3%; Score 5; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPP 5
 |||||
 Db 3 MHQPP 7

RESULT 27
AAE20251
ID AAE20251 standard; peptide; 7 AA.
XX AC AAE20251;
XX AC AAE20251;
XX DT 18-JUN-2002 (first entry)
XX DE Colostrinin constituent peptide #23.
XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
XX KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX KW transplantation; implantation; dermatological; vulnery.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT Modified-site 7 /note= "Optionally C-terminal amide"
XX PN WO200213850-A1.
XX PD 21-FEB-2002.
XX PF 17-AUG-2000; 2000WO-US22776.
XX PR 17-AUG-2000; 2000WO-US22776.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Stanton GJ, Hughes TK, Boldogh I;
XX DR WPI; 2002-269151/31.
XX PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX PS Claim 6; Page 26; 51pp; English.
XX CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/
CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide.
XX SQ Sequence 7 AA;
Query Match 33.3%; Score 5; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHQPP 5
Db 3 MHQPP 7
RESULT 28
AAM51058

ID AAM51058 standard; Peptide; 7 AA.
XX AC AAM51058;
XX DT 30-MAY-2002 (first entry)
XX DE Colostrinin constituent peptide (casein amino acids 157-163).
XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;
XX KW blood cell regulator; cytokine inducer; beta-casein; human.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Modified-site 7 /note= "optional C-terminal amidation"
XX PN WO200213849-A1.
XX PD 21-FEB-2002.
XX PF 17-AUG-2000; 2000WO-US22775.
XX PR 17-AUG-2000; 2000WO-US22775.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PA (REGE-) REGEN THERAPEUTICS PLC.
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX DR WPI; 2002-269150/31.
XX PT Modulation of blood cell proliferation in a patient involves use of
PT blood cell regulator selected from colostrinin, its constituent peptide
PT and/or analogue -
XX PS Claim 1; Page 34; 54pp; English.
XX CC The present sequence is that of a colostrinin constituent peptide
CC that is used as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. It is classified
CC as having a beta-casein homologue precursor, and corresponds to
CC casin amino acids 157-163. Methods are claimed for: inducing a
CC cytokine in a cell by contact with an immunological regulator,
CC where the cell is present in a cell culture; a tissue, an organ
CC or an organism, and the cell is mammalian, including human;
CC modulating an immune response in a cell by contact with the
CC immunological regulator under conditions effective to induce a
CC cytokine; modulating an immune response in a patient by administering
CC an immunological regulator under conditions effective to induce a
CC cytokine, where the immunological regulator is administered topically
CC or as part of a dietary supplement, and where the immune response is
CC specific or non specific, an interferon response or an antibody
CC response; modulating blood cell proliferation by contacting blood
CC cells with a blood cell regulator, where the blood cells are present
CC in a cell culture or an organism, are mammalian or human, and where
CC the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patent. A
CC claimed cytokine-inducing composition comprises a pharmaceutical
CC carrier and an active agent such as the present peptide.
XX SQ Sequence 7 AA;
Query Match 33.3%; Score 5; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHQPP 5
Db 3 MHQPP 7
RESULT 29
AAM51058

AAO14600
 ID AAO14600 standard; peptide; 7 AA.
 AC AAO14600;
 XX
 DT 27-MAY-2002 (first entry)
 XX
 DE Neural cell regulatory colostrinin peptide 23.
 XX
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 7 /note= "Optional C-terminal amide"
 FT
 XX WO200213851-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX
 XX 17-AUG-2000; 2000WO-US22777.
 XX
 PR 17-AUG-2000; 2000WO-US22777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;
 XX
 XX WPI; 2002-269152/31.
 XX
 PT Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 FT analog -
 XX
 XX Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.
 XX
 SQ Sequence 7 AA;
 Query Match 33.3%; Score 5; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHOPP 5
 |||||
 Db 3 MHOPP 7
 RESULT 30
 ABB73240
 ID ABB73240 standard; Peptide; 7 AA.
 AC ABB73240;
 XX
 XX 05-APR-2002 (first entry)
 DT
 XX
 DE Src homology3 (SH3) antagonist peptide SEQ ID NO:303.
 XX
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;

TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 sleep disorder; neurological degenerative disease; anaemia;
 thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 Fanconi's syndrome.
 KW
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX
 PN WO200183525-A2.
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14310.
 PF
 XX
 XX 03-MAY-2000; 2000US-0563286.
 PR
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 PI
 XX WPI; 2002-130313/17.
 DR
 XX
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -
 XX
 XX Claim 39; Page 55; 176pp; English.
 XX
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 33.3%; Score 5; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PLPPT 11
 |||||
 Db 2 PLPPT 6
 RESULT 31
 AAM00293
 ID AAM00293 standard; Peptide; 8 AA.
 XX
 XX AAM00293;
 XX

PT
XX
PS
XX
XX
Example 2; Page 29; 41pp; English.
CC The invention relates to isolating, from a naive polypeptide (I)
CC repertoire (antibody or T-cell receptor polypeptides), which has not been
CC preselected with a specific target ligand, a polypeptide of interest (II)
CC capable of interacting with the specific target ligand. The method
CC involves direct screening of (I) with the target ligand in order to
CC identify (II). The polypeptides selected by the method may be used in any
CC process which involves ligand-polypeptide binding including in vivo
CC therapeutic and prophylactic applications, in vitro and in vivo
CC diagnostic applications, in vitro assay and reagent applications. Enzyme
CC variants generated and selected by the method may be assayed for
CC activity, either in vitro or in vivo using standard techniques. Antibody
CC polypeptides selected by the method are used diagnostically in Western
CC analysis and in situ protein detection. The selected antibodies are
CC useful for preventing, suppressing or treating inflammatory states,
CC allergic hypersensitivity, cancer, bacterial or viral infection and
CC autoimmune disorders e.g., type I diabetes, multiple sclerosis,
CC rheumatoid arthritis, systemic lupus erythematosus, Crohn's disease and
CC myasthenia gravis. The selected polypeptides may be used extracorporeally
CC or in vitro selectively to kill, deplete or effectively remove a target
CC cell population from a heterogeneous collection of cells. Sequences
CC AAB84968-979 represent complementary determining regions (CDRs) of scFv
CC heavy and light chains binding to target antigens M and D.
XX
SQ Sequence 9 AA;
Query Match 33.3%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 QPLPP 10
Db 3 QPLPP 7
RESULT 34
ABR28252
ID ABR28252 standard; Peptide; 9 AA.
XX
AC ABR28252;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 187P3F2 HLA peptide #1087.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
FN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response

PT in cancer patients -
XX
PS Claim 13; Page 413; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
SQ Sequence 9 AA;
Query Match 33.3%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QPPQP 7
Db 1 QPPQP 5
RESULT 35
ABR28257
ID ABR28257 standard; Peptide; 9 AA.
XX
AC ABR28257;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 187P3F2 HLA peptide #1092.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
FN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
PS Claim 13; Page 413; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.

SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7
 DB 4 QPPQP 8
 |||||
 |||||

RESULT 36
 ABR28346
 ID ABR28346 standard; Peptide; 10 AA.
 AC ABR28346;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 187P3F2 HLA peptide #1181.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.

PS Claim 13; Page 414; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.

SQ Sequence 10 AA;

Query Match 33.3%; Score 5; DB 24; Length 10;

Best Local Similarity 100.0%; Pred. No. 59;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7
 DB 4 QPPQP 8
 |||||
 |||||

RESULT 37
 ABR28347
 ID ABR28347 standard; Peptide; 10 AA.
 XX
 AC ABR28347;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 187P3F2 HLA peptide #1182.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 CC proteins and polynucleotides, useful for therapeutic, prognostic and
 CC diagnostic reagents for eliciting cellular or humoral immune response
 CC in cancer patients

PS Claim 13; Page 414; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.

SQ Sequence 10 AA;

Query Match 33.3%; Score 5; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7
 DB 1 QPPQP 5
 |||||
 |||||

RESULT 38
 AAM00291

ID AAM00291 standard; Peptide; 12 AA.
XX AAM00291;
AC
XX
DT 01-OCT-2001 (first entry)
DT
DE Human protein fragment SEQ ID NO: 835.
DE
XX Human; single nucleotide polymorphism; SNP; paternity test;
XX forensic test; aberrant protein expression.
KW
KW
XX Homo sapiens.
OS
XX WO200151670-A2.
PN
XX 19-JUL-2001.
PD
XX 05-JAN-2001; 2001WO-US00322.
PF
XX 07-JAN-2000; 2000US-0174962.
PR
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach MD;
FI
XX WPI; 2001-451871/48.
DR
XX N-PSDB; AAH89404.
DR
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -
PT
XX Disclosure; Page 344; 475pp; English.
PS
XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberosus
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a peptide encoded by a
CC polymorphism-containing oligonucleotide fragment of the invention.
XX
SQ Sequence 12 AA;
Query Match 33.3%; Score 5; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 QPLPP 10
Db 5 QPLPP 9
RESULT 39
AAR93368
ID AAR93368 standard; peptide; 13 AA.
XX AAR93368;
AC
XX 24-APR-1996 (first entry)
DT
XX PI3K protein tyrosine kinase derived peptide #3.
DE
XX SH3 ligand; SH3 binding agent; biased phage library;
KW recognition sequence; src SH3 domain; Paget's disease; restenosis;
KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;
KW p67; complex; chronic myelogenous leukaemia; cancer.
XX
OS Synthetic.

XX WO9524419-A1.
PN
XX 14-SEP-1995.
PD
XX 13-MAR-1995; 95WO-US03208.
PF
XX 06-JAN-1995; 95US-0369832.
PR
XX 11-MAR-1994; 94US-0209835.
PR
XX (ARIA-) ARIAD PHARM INC.
PA
XX Botfield MC, Brugge JS, Rickles RJ, Zoller MJ;
XX WPI; 1995-328231/42.
PI
XX Identification of peptide(s) binding specifically to SH3 domains -
PT for use in inhibiting interactions mediated by SH3 domains in
PT treatment of e.g. osteoporosis and cancer
PT
XX Disclosure; Fig 2; 74pp; English.
PS
XX The sequences given in AAR93343-68 represent peptides which are SH3
CC ligands/SH3 binding agents. They represent a biased phage library
CC which comprises six random amino acids flanking the hexapeptide
CC RSLRPL- which was identified as a recognition sequence for the src
CC SH3 domain. These sequences were identified using the method of the
CC invention. The method comprises contacting the SH3 domain with a
CC mixture of peptides under conditions permitting a ligand to bind to
CC an SH3 domain to form a complex. Any unbound peptides are removed
CC and the complexed peptide ligands are dissociated from the complexes.
CC The selected peptides are enriched by re-contacting them with the
CC SH3 domain and then candidates which bind to the SH3 domain are
CC detected. The isolated SH3 binding peptides may be used in the
CC diagnosis, prevention and treatment of conditions or diseases resulting
CC from cellular processes mediated by an SH3-based interaction. Such
CC diseases include Paget's disease. Other conditions treatable with these
CC peptides include restenosis, rheumatoid arthritis, gout and other
CC problems in which an SH3 of neutrophil oxidase p47 and p67 complex is
CC implicated, etc.
XX
SQ Sequence 13 AA;
Query Match 33.3%; Score 5; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PLPPT 11
Db 5 PLPPT 9
RESULT 40
AAW11112
ID AAW11112 standard; peptide; 13 AA.
XX AAW11112;
AC
XX 25-JUN-1997 (first entry)
DT
XX Src SH3 domain-binding peptide used in signal transduction modulation.
DE
XX Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
KW protein tyrosine kinase; signal transduction; RNA processing;
KW trafficking; translation.
XX
OS Synthetic.
XX WO9603649-A1.
PN
XX 08-FEB-1996.
PD
XX 24-JUL-1995; 95WO-US09382.
PF

XX 07-JUN-1995; 95US-0483555.
 PR 22-JUL-1994; 94US-0278865.
 XX (UYN-)- UNIV NORTH CAROLINA.
 PA
 XX Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;
 PI WPI; 1996-117151/12.
 DR
 XX Peptide with binding affinity for Src homology region 3 (SH3)
 PT domains of proteins - useful for e.g. modulating signal transduction
 PT pathways at the cellular level, esp. protein tyrosine
 PT kinase-mediated
 XX
 PS Claim 38; Page 87; 116pp; English.
 XX
 CC AAW11098-W11124 are peptides that bind to the Src SH3 domain. The SH3
 CC binding peptides are useful in modulating signal transduction pathways
 CC at the cellular level (especially protein tyrosine kinase-mediated),
 CC modulating oncogenic protein activity, or providing compounds for the
 CC development of drugs with the ability to modulate broad classes, as
 CC well as specific classes, of proteins involved in signal transduction
 CC and also for regulating the processing, trafficking or translation of
 CC RNA. Conjugates of the peptides with detectable labels or imaging agents
 CC are useful for imaging cells, tissues and organs in which Src or
 CC Src-related proteins are expressed.
 XX
 SQ Sequence 13 AA;
 Query Match 33.3%; Score 5; DB 17; Length 13;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PLPPT 11
 Db |||||
 5 PLPPT 9
 RESULT 41
 AAB44382
 ID AAB44382 standard; Protein; 13 AA.
 XX
 AC AAB44382;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Human secreted protein encoded by gene 49 clone HPWAV82.
 XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 XX WO200058358-A1.
 PN
 XX 05-OCT-2000.
 PD
 XX 23-MAR-2000; 2000WO-US07725.
 PF
 XX 26-MAR-1999; 99US-0126602.
 PR
 PR 14-JAN-2000; 2000US-0176063.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX
 DR WPI; 2000-594640/56.
 DR N-PSDB; AAC79045.
 XX

PT Forty nine nucleic acid molecules encoding human secreted proteins,
 PT useful in the prevention, treatment and diagnosis of cancer, immune
 PT disorders, cardiovascular disorders and neurological diseases -
 XX
 XX Claim 11; Page 356; 367pp; English.
 PS
 XX Sequences AAB44335-B44382 represent the amino acid sequences of 49
 CC human secreted proteins encoded by the genes AAC69084-C69119. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 XX
 SQ Sequence 13 AA;
 Query Match 33.3%; Score 5; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PPQPL 8
 Db |||||
 6 PPQPL 10
 RESULT 42
 AAE21396
 ID AAE21396 standard; peptide; 13 AA.
 XX
 AC AAE21396;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Escherichia coli 3-isopropylmalate dehydrogenase (IPMDH) peptide #1.
 XX
 KW Protein thermostability; 3-isopropylmalate dehydrogenase; IPMDH;
 KW isocitrate dehydrogenase; ICDH; enzyme.
 XX
 OS Escherichia coli.
 XX
 PN EP1182253-A2.
 XX
 PD 27-FEB-2002.
 XX
 PF 03-JUL-2001; 2001EP-0115642.
 XX
 PR 04-JUL-2000; 2000JP-0201920.
 PR 31-MAY-2001; 2001JP-0164332.
 XX
 XX (AJIN) AJINOMOTO CO INC.
 PA
 XX Yamagishi A;
 PI
 XX WPI; 2002-294076/34.
 DR
 XX Improving protein thermostability of protein by estimating amino acid
 PT sequence of ancestral protein (AP), and replacing amino acids of
 PT desired protein, which differ from those of AP with the same amino
 PT acids of AP -
 XX
 XX Example 4; Fig 9; 73pp; English.
 PS
 XX The invention relates to a method for improving thermostability of
 CC proteins. The method involves comparing amino acid sequences derived
 CC

CC from two or more species which evolutionarily correspond to each other
CC in phylogenetic tree; estimating amino acid sequence of ancestral
CC protein and replacing amino acids of desired protein, which differ
CC from those of ancestral protein with the same amino acids of ancestral
CC protein. The method is used for improving thermostability of proteins
CC preferably 3-isopropylmalate dehydrogenase (IPMDH) and isocitrate
CC dehydrogenase (ICDH). The invention also relates to a protein having
CC an improved thermostability and a nucleic acid encoding such protein.
CC The present sequence is Escherichia coli IPMDH peptide.
XX
SQ Sequence 13 AA;

Query Match 33.3%; Score 5; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 1 QPLPP 5
|||||

RESULT 43
ABP81159
ID ABP81159 standard; peptide; 13 AA.
XX AC ABP81159;
XX 27-FEB-2003 (first entry)
DT Human TPO peptide with MCH class II binding activity #112.
DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
XX
XX Homo sapiens.
XX WO200268469-A2.
XX 06-SEP-2002.
XX 22-FEB-2002; 2002WO-EP01931.
XX PT Modified thrombopoietin molecule for use in pharmaceutical
XX compositions, has same activity of human thrombopoietin, but is
XX non-immunogenic or less immunogenic than other non-modified molecules
XX with same activity -
XX (MERE) MERCK PATENT GMBH.
XX Carr FJ, Carter G;
XX WPI; 2003-103168/09.
XX PT Modified thrombopoietin molecule for use in pharmaceutical
XX compositions, has same activity of human thrombopoietin, but is
XX non-immunogenic or less immunogenic than other non-modified molecules
XX with same activity -
XX Disclosure; Page 12; 36pp; English.
XX
CC The invention relates to a novel modified molecule having the biological
CC activity of human thrombopoietin (TPO) and being substantially
CC non-immunogenic or less immunogenic than any non-modified molecule having
CC the same biological activity when used in vivo. The invention also
CC discloses T-cell epitope peptides created from non-modified TPO, and
CC having potential MHC class II binding activity. The protein of the
CC invention has immunosuppressive and antiallergic activity. A peptide of
CC the invention is useful in the manufacture of TPO having substantially no
CC or less immunogenicity than any non-modified molecule with the same
CC biological activity when used in vivo. The protein is useful in
CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
CC allergies and autoimmune disease treatment. The sequences shown in
CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
XX invention.
XX
SQ Sequence 13 AA;

Query Match 33.3%; Score 5; DB 24; Length 13;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 5 PLPPT 9
|||||

RESULT 45
ABP81160
ID ABP81160 standard; peptide; 13 AA.
XX AC ABP81160;
XX 27-FEB-2003 (first entry)
DT Human TPO peptide with MCH class II binding activity #113.
DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
XX
XX Homo sapiens.
XX WO200268469-A2.
XX 06-SEP-2002.
XX 22-FEB-2002; 2002WO-EP01931.
XX PT Modified thrombopoietin molecule for use in pharmaceutical
XX compositions, has same activity of human thrombopoietin, but is
XX non-immunogenic or less immunogenic than other non-modified molecules
XX with same activity -
XX (MERE) MERCK PATENT GMBH.
XX Carr FJ, Carter G;
XX WPI; 2003-103168/09.
XX PT Modified thrombopoietin molecule for use in pharmaceutical
XX compositions, has same activity of human thrombopoietin, but is
XX non-immunogenic or less immunogenic than other non-modified molecules
XX with same activity -
XX Disclosure; Page 12; 36pp; English.
XX
CC The invention relates to a novel modified molecule having the biological
CC activity of human thrombopoietin (TPO) and being substantially
CC non-immunogenic or less immunogenic than any non-modified molecule having
CC the same biological activity when used in vivo. The invention also
CC discloses T-cell epitope peptides created from non-modified TPO, and
CC having potential MHC class II binding activity. The protein of the
CC invention has immunosuppressive and antiallergic activity. A peptide of
CC the invention is useful in the manufacture of TPO having substantially no
CC or less immunogenicity than any non-modified molecule with the same
CC biological activity when used in vivo. The protein is useful in
CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
CC allergies and autoimmune disease treatment. The sequences shown in
CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
XX invention.
XX
SQ Sequence 13 AA;

Query Match 33.3%; Score 5; DB 24; Length 13;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 5 PLPPT 9
|||||

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ABP81161
ID ABP81161 standard; peptide; 13 AA.
XX
AC ABP81161;
XX
DT 27-FEB-2003 (first entry)
XX
DE Human TPO peptide with MCH class II binding activity #114.
XX
KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
XX
OS Homo sapiens.
XX
PN WO200268469-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-EP01931.
XX
PR 26-FEB-2001; 2001EP-0104702.
XX
PA (MERE.) MERCK PATENT GMBH.
XX
PI Carr FJ, Carter G;
XX
DR WPI; 2003-103168/09.
XX
PT Modified thrombopoietin molecule for use in pharmaceutical
PT compositions, has same activity of human thrombopoietin, but is
PT non-immunogenic or less immunogenic than other non-modified molecules
PT with same activity -
XX
PS Disclosure; Page 12; 36pp; English.
XX
CC The invention relates to a novel modified molecule having the biological
CC activity of human thrombopoietin (TPO) and being substantially
CC non-immunogenic or less immunogenic than any non-modified molecule having
CC the same biological activity when used in vivo. The invention also
CC discloses T-cell epitope peptides created from non-modified TPO, and
CC having potential MHC class II binding activity. The protein of the
CC invention has immunosuppressive and antiallergic activity. A peptide of
CC the invention is useful in the manufacture of TPO having substantially no
CC or less immunogenicity than any non-modified molecule with the same
CC biological activity when used in vivo. The protein is useful in
CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
CC allergies and autoimmune disease treatment. The sequences shown in
CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
CC invention.
XX
SQ Sequence 13 AA;
Query Match 33.3%; Score 5; DB 24; Length 13;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PLPPT 11
DB 4 PLPPT 8
RESULT 46
ABP81162
ID ABP81162 standard; peptide; 13 AA.
XX
AC ABP81162;
XX
DT 27-FEB-2003 (first entry)
XX
DE Human TPO peptide with MCH class II binding activity #115.
XX
KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
XX
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XX
OS Homo sapiens.
XX
PN WO200268469-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-EP01931.
XX
PR 26-FEB-2001; 2001EP-0104702.
XX
PA (MERE.) MERCK PATENT GMBH.
XX
PI Carr FJ, Carter G;
XX
DR WPI; 2003-103168/09.
XX
PT Modified thrombopoietin molecule for use in pharmaceutical
PT compositions, has same activity of human thrombopoietin, but is
PT non-immunogenic or less immunogenic than other non-modified molecules
PT with same activity -
XX
PS Disclosure; Page 12; 36pp; English.
XX
CC The invention relates to a novel modified molecule having the biological
CC activity of human thrombopoietin (TPO) and being substantially
CC non-immunogenic or less immunogenic than any non-modified molecule having
CC the same biological activity when used in vivo. The invention also
CC discloses T-cell epitope peptides created from non-modified TPO, and
CC having potential MHC class II binding activity. The protein of the
CC invention has immunosuppressive and antiallergic activity. A peptide of
CC the invention is useful in the manufacture of TPO having substantially no
CC or less immunogenicity than any non-modified molecule with the same
CC biological activity when used in vivo. The protein is useful in
CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
CC allergies and autoimmune disease treatment. The sequences shown in
CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
CC invention.
XX
SQ Sequence 13 AA;
Query Match 33.3%; Score 5; DB 24; Length 13;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PLPPT 11
DB 2 PLPPT 6
RESULT 47
ABP81163
ID ABP81163 standard; peptide; 13 AA.
XX
AC ABP81163;
XX
DT 27-FEB-2003 (first entry)
XX
DE Human TPO peptide with MCH class II binding activity #116.
XX
KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
XX
OS Homo sapiens.
XX
PN WO200268469-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-EP01931.
XX
PR 26-FEB-2001; 2001EP-0104702.
XX
```

PA (WERE) MERCK PATENT GMBH.
 XX Carr FJ, Carter G;
 XX WPI; 2003-103168/09.
 DR
 XX Modified thrombopoietin molecule for use in pharmaceutical
 PT compositions, has same activity of human thrombopoietin, but is
 PT non-immunogenic or less immunogenic than other non-modified molecules
 PT with same activity -
 XX
 XX Disclosure; Page 12; 36pp; English.
 PS
 XX The invention relates to a novel modified molecule having the biological
 CC activity of human thrombopoietin (TPO) and being substantially
 CC non-immunogenic or less immunogenic than any non-modified molecule having
 CC the same biological activity when used in vivo. The invention also
 CC discloses T-cell epitope peptides created from non-modified TPO, and
 CC having potential MHC class II binding activity. The protein of the
 CC invention has immunosuppressive and anti-allergic activity. A peptide of
 CC the invention is useful in the manufacture of TPO having substantially no
 CC or less immunogenicity than any non-modified molecule with the same
 CC biological activity when used in vivo. The protein is useful in
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
 CC allergies and autoimmune disease treatment. The sequences shown in
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
 CC invention.
 XX
 XX Sequence 13 AA;
 SQ

Query Match 33.3%; Score 5; DB 24; Length 13;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
 DB 1 PLPPT 5

RESULT 48
 AA03679
 ID AAY03679 standard; peptide; 14 AA.
 XX
 XX AC AAY03679;
 XX
 XX DT 07-JUN-1999 (first entry)
 XX
 XX DE Amino acid sequence of the malaria (M) string CTL epitope BCG.
 DE
 XX CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope;
 KW cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour;
 KW malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer;
 KW melanoma; HIV; breast; colon; vaccination.
 XX
 XX OS Mycobacterium tuberculosis.
 OS
 XX WO9856919-A2.
 XX
 XX PD 17-DEC-1998.
 XX
 XX PF 09-JUN-1998; 98WO-GB01681.
 XX
 XX PR 09-JUN-1997; 97GB-0011957.
 XX
 XX PA (ISIS-) ISIS INNOVATION LTD.
 XX
 XX PI Blanchard T, Gilbert SC, Hanke T, Hill AVS, McMichael AJ;
 PI Plebanski M, Schneider J, Smith GL;
 XX WPI; 1999-070325/06.
 DR N-PSDB; AAX29219.
 XX
 XX Generating CD8-positive T cell response to target antigen using

PT recombinant poxvirus - for treating or preventing malaria and HIV
 PT infection, also epitope strings from Plasmodium and HIV
 XX
 XX Claim 38; Page 19; 85pp; English.
 PS
 XX The invention relates to methods and reagents for generating a
 CC protective CD8+ T-cell immune response against at least one target
 CC antigen. The kits of the invention comprises (i) as priming composition,
 CC a source of one or more CD8+ T-cell [cytotoxic T lymphocytes-(CTL)]
 CC epitopes of the target antigen, plus a carrier, and (ii) as boosting the
 CC composition a source of CTL epitopes, with at least one CTL epitope the
 CC same as used in (i), with this source being a non-replicating or
 CC replication-impaired recombinant poxvirus vector (PVV) plus a carrier. If
 CC the source of CTL epitopes in (i) is a viral vector, then the vector in
 CC (ii) is from a different virus. The kits are used to generate an immune
 CC response (prophylactic or therapeutic) against pathogens or tumours,
 CC specifically against malaria parasites such as P. falciparum, or HIV, and
 CC also many other bacterial, viral or parasitic pathogens. The kits are
 CC also used for protective response against melanoma and cancer of breast
 CC or colon, and generally wherever a strong CD8+ response is protective.
 CC The boosting composition may be used alone to boost a naturally primed
 CC response against malaria. The specified PVV provide an excellent booster
 CC effect, better than that from wild-type poxvirus, resulting in complete
 CC rather than partial protection against sporozoite challenge. Also PVV are
 CC safer to use than wild-type virus. Sequences AAY03661-680 represent CTL
 CC peptide epitopes of the malaria (M) string.
 XX
 XX Sequence 14 AA;
 SQ

Query Match 33.3%; Score 5; DB 20; Length 14;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
 DB 5 QPLPP 9

RESULT 49
 AAM00448
 ID AAM00448 standard; Peptide; 14 AA.
 XX
 XX AC AAM00448;
 XX
 XX DT 01-OCT-2001 (first entry)
 XX
 XX DE Human protein fragment SEQ ID NO: 996.
 DE
 XX Human; single nucleotide polymorphism; SNP; paternity test;
 KW forensic test; aberrant protein expression.
 KW
 XX Homo sapiens.
 OS
 XX WO200151670-A2.
 PN
 XX 19-JUL-2001.
 PD
 XX 05-JAN-2001; 2001WO-US00322.
 PF
 XX 07-JAN-2000; 2000US-0174962.
 PR
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shimkets RA, Leach MD;
 PI
 XX WPI; 2001-451871/48.
 DR N-PSDB; AAH89565.
 DR
 XX Isolated human polynucleotides containing single nucleotide
 PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
 PT infection and diabetes -
 XX
 XX Disclosure; Page 389; 475pp; English.
 PS

XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a peptide encoded by a
CC polymorphism-containing oligonucleotide fragment of the invention.

XX Sequence 14 AA;
CC
CC Query Match 33.3%; Score 5; DB 22; Length 14;
CC Best Local Similarity 100.0%; Pred. No. 79;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
DB 5 QPLPP 9
|||||

RESULT 50
AAB46171
ID AAB46171 standard; peptide; 14 AA.
AC AAB46171;
XX
XX 04-APR-2001 (first entry)
XX
XX Bacille Calmette-Guérin universal T epitope.
XX
XX Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200072880-A2.
XX
XX 07-DEC-2000.
XX
XX 26-MAY-2000; 2000WO-US14810.
XX
XX 28-MAY-1999; 99US-0322289.
XX
XX (NEUR-) NEURALAB LTD.
XX
XX Schenk DB, Bard F, Vasquez NU, Yednock T;
XX WPI; 2001-032104/04.
XX
XX Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX
XX Disclosure; Page 28; 143pp; English.

XX This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have neurotropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.

XX Sequence 14 AA;
CC
CC Query Match 33.3%; Score 5; DB 22; Length 14;
CC Best Local Similarity 100.0%; Pred. No. 79;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
DB 5 QPLPP 9
|||||

RESULT 51
AAB49070
ID AAB49070 standard; peptide; 14 AA.
XX
XX AAB49070;
XX
XX 27-MAR-2001 (first entry)
XX
XX BCG T-cell epitope, SEQ ID NO:6.
XX
XX Amyloid disease; amyloid fibril deposition; amyloid plaque;
KW immunogenic; antibody; vaccine; Alzheimer's disease;
KW type 2 diabetes; reactive system amyloidosis;
KW systemic senile amyloidosis; familial amyloid cardiomyopathy;
KW transmissible spongiform encephalopathy; Creutzfeldt-Jakob disease; Kuru;
KW haemodialysis-associated beta-2-microglobulin deposition;
KW carrier protein; universal T-cell epitope.
XX
XX Mycobacterium bovis.
XX
XX WO200072876-A2.
XX
XX 07-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US15239.
XX
XX 01-JUN-1999; 99US-0137010.
XX
XX (NEUR-) NEURALAB LTD.
XX
XX Schenk DB;
XX WPI; 2001-070921/08.
XX
XX Pharmaceutical composition comprising immunogen against amyloid
PT component such as fibril peptide or protein, or antibody against
PT amyloid component useful for treating amyloid diseases or amyloidoses -
XX
XX Disclosure; Page 43; 140pp; English.

XX The invention relates to a novel pharmaceutical composition for
CC preventing or treating a disease characterised by amyloid fibril
CC deposits (amyloid plaques) in a patient. The pharmaceutical composition
CC comprises an agent that will induce an immune response against an amyloid
CC component, or an antibody or antibody fragment that binds to an amyloid
CC component. The invention also relates to a method for determining
CC the prognosis of a patient undergoing treatment for an amyloid disorder
CC which involves measuring a patient serum amount of immunoreactivity
CC against a selected amyloid component. A patient serum immunoreactivity
CC of at least four times a base line serum immunoreactivity control level
CC indicates a prognosis of improved status with respect to the disorder.
CC The pharmaceutical compositions of the invention are useful for treating
CC a wide variety of disorders characterised by amyloid fibril deposition in
CC a patient. Such disorders include Alzheimer's disease characterised by
CC amyloid beta peptide fibril deposits; type 2 diabetes characterised by
CC amyloid islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic
CC amyloidosis associated with systemic inflammatory diseases (e.g.,
CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA
CC fibrils derived from serum amyloid A protein (ApoSAA); systemic senile
CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR
CC fibrils derived from transthyretin (TTR); transmissible spongiform

CC encephalopathies (e.g. Creutzfeld-Jakob disease, Kuru) characterised by
CC prion protein deposits; and beta-2-microglobulin deposits which form as
CC a result of long term haemodialysis treatment. The present sequence
CC represents a universal T-cell epitope which may be used as a
CC carrier for an epitope derived from an amyloid plaque component in a
CC composition of the invention.

XX
XX
SQ Sequence 14 AA;

Query Match 33.3%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 5 QPLPP 9

RESULT 52
AAW38958
ID AAW38958 standard; peptide; 15 AA.
XX
AC AAW38958;
XX
DT 27-MAR-1998 (first entry)
XX
DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:355.
XX
KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
OS Synthetic.
XX
PN WO9730074-A1.
XX
PD 21-AUG-1997.
XX
PF 14-FEB-1997; 97WO-US02298.
XX
PR 16-FEB-1996; 96US-0602999.
XX
PA (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI Sparks AB, Thorn JM;
XX
DR WPI; 1997-424972/39.
XX
PT Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinase(s) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
PS Claim 22; Page 91; 131pp; English.
XX
CC The present sequence represents a peptide which resembles a Src homology
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
CC binding peptides can be used in the method to identify inhibitors of
CC their binding to their respective SH3 domains, which could be used to
CC modulate the pharmacological activity of proteins or polypeptide
CC containing the SH3 domain. The peptides can also be used to activate
CC Src or Src-related protein tyrosine kinases, to stimulate the immune
CC response by increasing the production of certain lymphokines, e.g.
CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC conjugated molecule to certain cellular compartments containing Src or

CC Src related proteins.
XX
SQ Sequence 15 AA;

Query Match 33.3%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 9 PLPPT 13

RESULT 53
AAW39036
ID AAW39036 standard; peptide; 15 AA.
XX
AC AAW39036;
XX
DT 27-MAR-1998 (first entry)
XX
DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:437.
XX
KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
OS Synthetic.
XX
PN WO9730074-A1.
XX
PD 21-AUG-1997.
XX
PF 14-FEB-1997; 97WO-US02298.
XX
PR 16-FEB-1996; 96US-0602999.
XX
PA (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI Sparks AB, Thorn JM;
XX
DR WPI; 1997-424972/39.
XX
PT Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinase(s) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
PS Claim 22; Page 94; 131pp; English.
XX
CC The present sequence represents a peptide which resembles a Src homology
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
CC binding peptides can be used in the method to identify inhibitors of
CC their binding to their respective SH3 domains, which could be used to
CC modulate the pharmacological activity of proteins or polypeptide
CC containing the SH3 domain. The peptides can also be used to activate
CC Src or Src-related protein tyrosine kinases, to stimulate the immune
CC response by increasing the production of certain lymphokines, e.g.
CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC conjugated molecule to certain cellular compartments containing Src or
CC Src related proteins.

XX
SQ Sequence 15 AA;

Query Match 33.3%; Score 5; DB 18; Length 15;

Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
DB 2 QPLPP 6

RESULT 54
AAW38976
ID AAW38976 standard; peptide; 15 AA.
XX AC AAW38976;
XX
XX
XX 27-MAR-1998 (first entry)
XX
XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:373.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
FN
XX 21-AUG-1997.
PD
XX 14-FEB-1997; 97WO-US02298.
PF
XX 16-FEB-1996; 96US-0602999.
PR
XX (CYTO-) CYTOGEN CORP.
XX (UYN-) UNIV NORTH CAROLINA.
XX
XX Der CU, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
FI Sparks AB, Thorn JM;
PI
XX WPI; 1997-424972/39.
DR
XX
XX Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinases) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 92; 131pp; English.

The present sequence represents a peptide which resembles a Src homology region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
(a) peptides which bind the SH3 domain of Cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk; (h) peptides which bind the SH3 domain of Grb2. The purified binding peptides can be used in the method to identify inhibitors of their binding to their respective SH3 domains, which could be used to modulate the pharmacological activity of proteins or polypeptide containing the SH3 domain. The peptides can also be used to activate Src or Src-related protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. tumour necrosis factor-alpha and interleukin-1, or to deliver a conjugated molecule to certain cellular compartments containing Src or Src related proteins.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7
DB 1
DB 1

RESULT 55
AAG78855
ID AAG78855 standard; Peptide; 15 AA.
XX AC AAG78855;
XX
XX 12-DEC-2001 (first entry)
XX
XX Growth hormone family protein 11 peptide fragment.
XX
XX Growth hormone; cytostatic; virucidal; immunomodulator; antiinflammatory;
KW haemostatic; gene therapy; malignant tumour; haemopathy; HIV infection;
KW immunological disease; inflammation.
XX
XX Unidentified.
OS
XX WO200172832-A1.
FN
XX 04-OCT-2001.
PD
XX 26-MAR-2001; 2001WO-CN00489.
PF
XX 27-MAR-2000; 2000CN-0115180.
PR
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
PI
XX WPI; 2001-602854/68.
DR
XX New polypeptide for the diagnosis and treatment of malignant neoplasm,
PT hemopathy, HIV infection, immunological diseases and inflammations,
PT comprises protein 11 of the growth hormone family -
XX
XX Example 5; Page 19; 35pp; Chinese.

The present invention relates to protein 11 of the growth hormone family (see AAI65179 and AAG78854). The growth hormone protein and its coding sequence are useful in the diagnosis and treatment of malignant tumours, haemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is an N-terminal peptide fragment of the growth hormone protein which was used in an example from the present invention.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
DB 8 PLPPT 12

RESULT 56
ABR38292
ID ABR38292 standard; Peptide; 15 AA.
XX AC ABR38292;
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 187P3F2 HLA peptide #1423.
DE
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX

PN WO200283921-A2.
 XX 24-OCT-2002.
 XX 10-APR-2002; 2002WO-US11654.
 XX 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 XX Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.
 DR Claim 13; Page 616; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX Sequence 15 AA;
 SQ Query Match 33.3%; Score 5; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QPPQP 7
 Db 8 QPPQP 12
 RESULT 57
 ABR38293
 ID ABR38293 standard; Peptide; 15 AA.
 XX ABR38293;
 AC ABR38293;
 XX 19-MAY-2003 (first entry)
 DT Human cancer-related protein 187P3F2 HLA peptide #1424.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 XX human leukocyte antigen.
 KW Homo sapiens.
 XX WO200283921-A2.
 PN 24-OCT-2002.
 XX 10-APR-2002; 2002WO-US11654.
 XX 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 XX Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.
 DR Claim 13; Page 616; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX Sequence 15 AA;
 SQ Query Match 33.3%; Score 5; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QPPQP 7
 Db 8 QPPQP 12
 RESULT 57
 ABR38293
 ID ABR38293 standard; Peptide; 15 AA.
 XX ABR38293;
 AC ABR38293;
 XX 19-MAY-2003 (first entry)
 DT Human cancer-related protein 187P3F2 HLA peptide #1424.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 XX human leukocyte antigen.
 KW Homo sapiens.
 XX WO200283921-A2.
 PN 24-OCT-2002.
 XX 10-APR-2002; 2002WO-US11654.
 XX 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 XX Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.
 DR Claim 13; Page 616; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX Sequence 15 AA;
 SQ Query Match 33.3%; Score 5; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QPPQP 7
 Db 8 QPPQP 12
 RESULT 57
 ABR38293
 ID ABR38293 standard; Peptide; 15 AA.
 XX ABR38293;
 AC ABR38293;
 XX 19-MAY-2003 (first entry)
 DT Human cancer-related protein 187P3F2 HLA peptide #1425.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 XX WO200283921-A2.
 PN 24-OCT-2002.
 XX 10-APR-2002; 2002WO-US11654.
 XX 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 XX Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.
 DR Claim 13; Page 616; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX Sequence 15 AA;
 SQ Query Match 33.3%; Score 5; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QPPQP 7
 Db 7 QPPQP 11
 RESULT 58
 ABR38294
 ID ABR38294 standard; Peptide; 15 AA.
 XX ABR38294;
 AC ABR38294;
 XX 19-MAY-2003 (first entry)
 DT Human cancer-related protein 187P3F2 HLA peptide #1425.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 XX WO200283921-A2.
 PN 24-OCT-2002.
 XX 10-APR-2002; 2002WO-US11654.
 XX 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 XX Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.
 DR Claim 13; Page 616; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX Sequence 15 AA;
 SQ Query Match 33.3%; Score 5; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QPPQP 7
 Db 7 QPPQP 11

PA (AGEN-) AGENSYS INC.
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.
 DR New composition comprising a substance that modulates the structure of
 XX proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX Claim 13; Page 616; 1021pp; English.
 PS The present invention relates to novel human cancer-related genes and
 XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX Sequence 15 AA;
 SQ Query Match 33.3%; Score 5; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QPPQP 7
 Db 7 QPPQP 11
 RESULT 58
 ABR38294
 ID ABR38294 standard; Peptide; 15 AA.
 XX ABR38294;
 AC ABR38294;
 XX 19-MAY-2003 (first entry)
 DT Human cancer-related protein 187P3F2 HLA peptide #1425.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 XX WO200283921-A2.
 PN 24-OCT-2002.
 XX 10-APR-2002; 2002WO-US11654.
 XX 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 XX Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.
 DR New composition comprising a substance that modulates the structure of
 XX proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -

Best,Local Similarity 100.0%; Pred.No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPPQP 7
Db 11 QPPQP 15

RESULT 61
ABR38391
ID ABR38391 standard; Peptide; 15 AA.
XX AC ABR38391;
XX XX
DT 19-MAY-2003 (first entry)
XX XX
DE Human cancer-related protein 187P3F2 HLA peptide #1522.
XX XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX XX
OS Homo sapiens.
XX XX
PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients
XX XX
PS Claim 13; Page 618; 1021pp; English.
XX XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX SQ Sequence 15 AA;
Query Match 33.3%; Score 5; DB 24; Length 15;
Best Local Similarity 100.0%; Pred.No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPPQP 7
Db 5 QPPQP 9

RESULT 62
ABR38392
ID ABR38392 standard; Peptide; 15 AA.
XX AC ABR38392;
XX XX
DT 19-MAY-2003 (first entry)
XX XX
DE Human cancer-related protein 187P3F2 HLA peptide #1545.
XX XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.

ID ABR38392 standard; Peptide; 15 AA.
XX AC ABR38392;
XX XX
DT 19-MAY-2003 (first entry)
XX XX
DE Human cancer-related protein 187P3F2 HLA peptide #1523.
XX XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX XX
OS Homo sapiens.
XX XX
PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients
XX XX
PS Claim 13; Page 618; 1021pp; English.
XX XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX SQ Sequence 15 AA;
Query Match 33.3%; Score 5; DB 24; Length 15;
Best Local Similarity 100.0%; Pred.No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPPQP 7
Db 3 QPPQP 7

RESULT 63
ABR38414
ID ABR38414 standard; Peptide; 15 AA.
XX AC ABR38414;
XX XX
DT 19-MAY-2003 (first entry)
XX XX
DE Human cancer-related protein 187P3F2 HLA peptide #1545.
XX XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.

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XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX PR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients
XX PS Claim 13; Page 619; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 15 AA;
XX Query Match 33.3%; Score 5; DB 24; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 84;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 QPPQP 7
XX DB 10 QPPQP 14
XX
RESULT 64
ABR38502
XX ID ABR38502 standard; Peptide; 15 AA.
XX AC ABR38502;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 187P3P2 HLA peptide #1633.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR
XX

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PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX PR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients
XX PS Claim 13; Page 620; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 15 AA;
XX Query Match 33.3%; Score 5; DB 24; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 84;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 QPPQP 7
XX DB 10 QPPQP 14
XX
RESULT 65
AAW25427
XX ID AAW25427 standard; peptide; 16 AA.
XX AC AAW25427;
XX DT 27-MAR-1998 (first entry)
XX DE Yes SH3 domain binding peptide SEQ ID NO:213.
XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX OS Synthetic.
XX OS Unidentified.
XX PN WO9730074-A1.
XX PD 21-AUG-1997.
XX PF 14-FEB-1997; 97WO-US02298.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX PI Sparks AB, Thorn JW;
XX PR WPI; 1997-424972/39.

```

XX PT Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX PS Claim 19; Page 100; 13lpp; English.
 XX CC The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX SQ Sequence 16 AA;

Query Match 33.3%; Score 5; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
 Db 5 PLPPT 9

RESULT 66
 AAW25376
 ID AAW25376 standard; peptide; 16 AA.
 XX AC AAW25376;
 XX DT 27-MAR-1998 (first entry)
 XX DE Src SH3 domain binding peptide SEQ ID NO:158.
 XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX OS Synthetic.
 OS Unidentified.
 XX PN WO9730074-A1.
 XX PD 21-AUG-1997.
 XX PF 14-FEB-1997; 97WO-US02298.
 XX PR 16-FEB-1996; 96US-0602999.
 XX PA (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX PI Der CU, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX DR WPI; 1997-424972/39.
 XX PT Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

XX Claim 16; Page 99; 13lpp; English.
 XX CC The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX SQ Sequence 16 AA;

Query Match 33.3%; Score 5; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
 Db 5 PLPPT 9

RESULT 67
 AAW25380
 ID AAW25380 standard; peptide; 16 AA.
 XX AC AAW25380;
 XX DT 27-MAR-1998 (first entry)

Src SH3 domain binding peptide SEQ ID NO:147.

Cortactin; SH3 domain; binding peptide; Src homology region 3;
 tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX OS Synthetic.
 OS Unidentified.
 XX PN WO9730074-A1.

XX PD 21-AUG-1997.

XX PF 14-FEB-1997; 97WO-US02298.

XX PR 16-FEB-1996; 96US-0602999.

XX PA (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX DR WPI; 1997-424972/39.

XX PT Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

XX Claim 16; Page 99; 13lpp; English.

XX CC The present sequence represents a Src homology region 3 (SH3) binding

CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53b2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

XX
 SQ Sequence 16 AA;

Query Match 33.3%; Score 5; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
 |||||
 Db 5 PLPPT 9

RESULT 68
 ABP82678
 ID ABP82678 standard; Peptide; 16 AA.
 XX
 AC ABP82678;
 DT 04-MAR-2003 (first entry)
 XX
 DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1351.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

XX Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US50107.

XX 19-DEC-2000; 2000US-257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -

XX Claim 1; Fig 2; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, host
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 16 AA;

Query Match 33.3%; Score 5; DB 24; Length 16;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
 |||||
 Db 10 PLPPT 14

RESULT 69
 AAB39277
 ID AAB39277 standard; Protein; 17 AA.

XX AAB39277;

XX 02-FEB-2001 (first entry)

XX DE Gene 31 human secreted protein homologous amino acid sequence #157.

XX Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
 KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;
 KW ophthalmological; autoimmune disease; rheumatoid arthritis; angio genesis;
 KW hyperproliferative disorder; cardiovascular disorder; infection;
 KW cerebrovascular disorder; nervous system disorder; ocular disorder;
 KW wound healing; chemotaxis.

XX Homo sapiens.

XX WO2000056754-A1.

XX 28-SEP-2000.

XX 16-MAR-2000; 2000WO-US06792.

XX 19-MAR-1999; 99US-0125362.

XX 10-DEC-1999; 99US-0169980.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen GA, Ruben SM, Komatsoulis G;

XX WPI; 2000-579483/54.

PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
XX Disclosure; Page 52; 434pp; English.

XX The polynucleotide sequences given in AAC74223-C74279 encode the human
CC secreted proteins represented in AAB39179-B39226. Sequences
CC AAB39227-B39308 are alternative proteins encoded by the genes, and also
CC protein sequences with which they share homology. The proteins have
CC activities based on the tissues and cells in which they are expressed.
CC Examples of activities include: immunosuppressive; antiarthritic;
CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
CC cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
CC fungicide; and ophthalmological. The human secreted proteins,
CC polynucleotides, antagonists and agonists of the invention may be useful
CC in the treatment, prevention, and/or diagnosis of various diseases,
CC disorders and conditions such as autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
CC also be used to aid wound healing and epithelial cell proliferation, to
CC regenerate tissues, maintain organs before transplantation, in
CC chemotaxis and as a food additive or preservative e.g. to increase
CC storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used
CC during the isolation and characterisation of the genes of the invention.

XX Sequence 17 AA;

Query Match 33.3%; Score 5; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
DB 1 QPLPP 5

RESULT 70
ABG57154
ID ABG57154 standard; Peptide; 18 AA.

XX ABG57154;
XX
XX 25-FEB-2003 (first entry)
XX Human liver peptide, SEQ ID No 35802.
XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX hypercholesterolaemia; coronary heart disease.

OS Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for
PT analysing gene expression in human adult liver -
XX
XX Claim 27; SEQ ID No 35802; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult
CC liver. (I) may be used for predicting, measuring and displaying gene
CC expression in samples derived from human adult liver. The genes
CC identified may be involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
CC is associated with coronary heart disease. ABG47348-ABG53930 represent
CC human liver single exon encoded peptides of the invention.
CC Note: The sequence information for this patent does not appear in the
CC printed specification but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQLPL 9
DB 9 PQLPL 13

RESULT 71
ABB41714
ID ABB41714 standard; Peptide; 18 AA.

XX ABB41714;
XX
XX 04-FEB-2002 (first entry)
XX Peptide #9220 encoded by human foetal liver single exon probe.
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX Homo sapiens.
XX WO200157277-A2.

PN 09-AUG-2001.

PP 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for
PT analysing gene expression in human fetal liver -

XX Claim 27; SEQ ID No 34349; 639pp + sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal

STANDARD
ECONOMICS
CATERPILLAR
ECONOMICS

XX
DE
Peptide #9548 encoded by probe for measuring placental gene expression.

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XX KW Probe: microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX DR WPI; 2001-488897/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human placenta -
XX XX
XX PS Claim 27; SEQ ID No 35780; 654pp; English.
XX XX
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AA13315-AA15746). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders.
XX XX
XX SQ Sequence 18 AA;
XX
Query Match 33.3%; Score 5; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PQLP 9
Db 9 PQLP 13

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RESULT 75

AAE03955
ID AAE03955 standard; peptide; 18 AA.

XX AC AAE03955;

XX DT 09-AUG-2001 (first entry)

XX DE Human gene 10 encoded secreted protein fragment, SEQ ID NO:126.
XX KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnery;
KW cell culture; chemotaxis; food additive; gene therapy;
KW binding partner identification.

XX OS Homo sapiens.

PN WO200077022-A1.
XX PD 21-DEC-2000.
XX PF 01-JUN-2000; 2000WO-US15136.
XX PR 11-JUN-1999; 99US-0138629.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Rosen CA, Ruben SM, Komatsoulis GA;
XX XX
XX DR WPI; 2001-367020/38.
XX XX
XX PT Nucleic acids encoding 50 human secreted polypeptides, useful for
XX PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's
XX PT disease, botulism, cancers and Scimitar syndrome -
XX XX
XX PS Disclosure; Page 566-567; 614pp; English.

XX CC AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
CC protein genes and AAE03898-AAE03947 represent the proteins they encode.
CC AAE03948-AAE03996 represent human secreted protein fragments or variants.
CC The genes and their secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 50 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumours, foetal and developmental
CC abnormalities, haematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein fragment referred to in the disclosure of the invention.

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 11 QPLPP 15

Search completed: November 25, 2003, 19:27:24
Job time : 39.2849 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 24.0698 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-34

Perfect score: 15

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Searched: 673684 seqs, 184443283 residues

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Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	US-10-281-652-34	Sequence 34, Appl
2	10	66.7	10	US-10-281-652-25	Sequence 25, Appl
3	8	53.3	10	US-10-185-815-89	Sequence 89, Appl
4	6	40.0	11	US-09-809-391-689	Sequence 689, Appl
5	6	40.0	11	US-09-882-171-689	Sequence 689, Appl
6	6	40.0	15	US-10-161-791-405	Sequence 405, Appl
7	6	40.0	16	US-10-161-791-227	Sequence 227, Appl
8	5	33.3	7	US-10-286-457-359	Sequence 359, Appl
9	5	33.3	7	US-10-281-652-24	Sequence 24, Appl
10	5	33.3	9	US-10-062-109A-382	Sequence 382, Appl
11	5	33.3	9	US-10-062-109A-458	Sequence 458, Appl
12	5	33.3	9	US-10-062-109A-563	Sequence 563, Appl
13	5	33.3	9	US-10-005-480A-382	Sequence 382, Appl
14	5	33.3	9	US-10-005-480A-458	Sequence 458, Appl
15	5	33.3	9	US-10-005-480A-563	Sequence 563, Appl

16	5	33.3	10	US-09-794-346-1	Sequence 1, Appl
17	5	33.3	12	US-10-148-936-1	Sequence 1, Appl
18	5	33.3	13	US-09-938-315-93	Sequence 93, Appl
19	5	33.3	13	US-09-897-107-89	Sequence 69, Appl
20	5	33.3	13	US-10-161-791-90	Sequence 90, Appl
21	5	33.3	13	US-10-161-791-93	Sequence 93, Appl
22	5	33.3	14	US-10-079-167-38	Sequence 38, Appl
23	5	33.3	14	US-10-367-405-18	Sequence 18, Appl
24	5	33.3	15	US-10-302-896-30	Sequence 30, Appl
25	5	33.3	15	US-10-161-791-355	Sequence 355, Appl
26	5	33.3	15	US-10-161-791-373	Sequence 373, Appl
27	5	33.3	15	US-10-161-791-437	Sequence 437, Appl
28	5	33.3	16	US-10-161-791-213	Sequence 213, Appl
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30	5	33.3	17	US-10-029-386-31396	Sequence 31396, A
31	5	33.3	18	US-09-864-761-45132	Sequence 45132, A
32	5	33.3	18	US-10-302-896-31	Sequence 31, Appl
33	5	33.3	19	US-09-964-201A-17	Sequence 17, Appl
34	5	33.3	20	US-09-308-511-11	Sequence 11, Appl
35	5	33.3	20	US-10-161-791-147	Sequence 147, Appl
36	4	26.7	6	US-09-500-700-104	Sequence 104, Appl
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43	4	26.7	7	US-10-161-791-9	Sequence 9, Appl
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46	4	26.7	8	US-09-745-078A-30	Sequence 30, Appl
47	4	26.7	8	US-10-052-578-82	Sequence 82, Appl
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49	4	26.7	8	US-10-374-624-30	Sequence 30, Appl
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52	4	26.7	9	US-08-344-824-322	Sequence 322, Appl
53	4	26.7	9	US-08-344-824-323	Sequence 323, Appl
54	4	26.7	9	US-08-854-825-43	Sequence 43, Appl
55	4	26.7	9	US-09-834-765-48	Sequence 48, Appl
56	4	26.7	9	US-09-834-765-130	Sequence 130, Appl
57	4	26.7	9	US-09-834-765-356	Sequence 356, Appl
58	4	26.7	9	US-09-834-765-462	Sequence 462, Appl
59	4	26.7	9	US-09-834-765-546	Sequence 546, Appl
60	4	26.7	9	US-09-938-315-11	Sequence 11, Appl
61	4	26.7	9	US-09-780-053-165	Sequence 165, Appl
62	4	26.7	9	US-09-780-053-456	Sequence 456, Appl
63	4	26.7	9	US-09-780-053-517	Sequence 517, Appl
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65	4	26.7	9	US-09-945-917-34	Sequence 34, Appl
66	4	26.7	9	US-03-745-078A-29	Sequence 29, Appl
67	4	26.7	9	US-09-972-656-26	Sequence 26, Appl
68	4	26.7	9	US-09-932-165-3	Sequence 3, Appl
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72	4	26.7	9	US-10-161-791-11	Sequence 11, Appl
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79	4	26.7	10	US-09-780-053-505	Sequence 505, Appl
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81	4	26.7	10	US-09-780-053-588	Sequence 588, Appl
82	4	26.7	10	US-09-780-053-675	Sequence 675, Appl
83	4	26.7	10	US-09-908-322-53	Sequence 53, Appl
84	4	26.7	10	US-09-745-078A-28	Sequence 28, Appl
85	4	26.7	10	US-09-783-931-53	Sequence 53, Appl
86	4	26.7	10	US-09-572-404B-22	Sequence 22, Appl
87	4	26.7	10	US-09-572-404B-636	Sequence 636, Appl
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 92 4 26.7 10 12 US-09-932-165-516
 93 4 26.7 10 12 US-09-932-165-701
 94 4 26.7 10 12 US-09-932-165-920
 95 4 26.7 10 12 US-09-932-165-1297
 96 4 26.7 10 12 US-10-316-253-210
 97 4 26.7 10 12 US-10-374-624-28
 98 4 26.7 10 12 US-10-192-381-60
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ALIGNMENTS

RESULT 1
 US-10-281-652-34
 ; Sequence 34, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/10/281,652
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/09/641,803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 34
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-10-281-652-34

Query Match 100.0%; Score 15; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
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 DB 1 MHQPPQPLPPTVMFP 15

RESULT 2
 US-10-281-652-25
 ; Sequence 25, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/10/281,652
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/09/641,803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-10-281-652-25

Query Match 66.7%; Score 10; DB 15; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPPTVMFP 15
 DB 1 QPLPPTVMFP 10

RESULT 3
 US-10-185-815-89
 ; Sequence 89, Application US/10185815
 ; Publication No. US20030096354A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elan Corporation, plc
 ; APPLICANT: O'Mahony, Daniel
 ; APPLICANT: Lambkin, Imelda
 ; APPLICANT: Higgins, Lisa
 ; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
 ; FILE REFERENCE: E1067-20093
 ; CURRENT APPLICATION NUMBER: US/10/185,815
 ; CURRENT FILING DATE: 2002-10-09
 ; PRIOR APPLICATION NUMBER: 60/302,591
 ; PRIOR FILING DATE: 2001-07-02
 ; NUMBER OF SEQ ID NOS: 99
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 89
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
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 US-10-185-815-89

Query Match 53.3%; Score 8; DB 15; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPPQPL 8
 DB 3 MHQPPQPL 10

RESULT 4
 US-09-809-391-689
 ; Sequence 689, Application US/09809391
 ; Publication No. US20030049618A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: P2002P2
 ; CURRENT APPLICATION NUMBER: US/09/809,391
 ; CURRENT FILING DATE: 2001-03-16
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 761
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 689
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 Best Local Similarity 100.0%; Pred. No. 12;

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Qy      2  HQPPQP 7
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Db      1  HQPPQP 6

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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
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; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
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;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,631
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR APPLICATION NUMBER: 60/047,614
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;; PRIOR APPLICATION NUMBER: 60/056,908
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/048,964
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/057,650
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: 60/056,884
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/057,669
;; PRIOR FILING DATE: 1997-09-05

Query Match 40.0%; Score 6; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOPPOP 7
Db 1 HOPPOP 6

RESULT 6
US-10-161-791-405
; Sequence 405, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 405:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-405

Query Match 40.0%; Score 6; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQPLP 9
Db 8 PPQPLP 13

RESULT 7
US-10-161-791-227
; Sequence 227, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME

```
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/161,791
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/602,999
/ FILING DATE: 16-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Misrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-202
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8964
/ INFORMATION FOR SEQ ID NO: 227:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
US-10-161-791-227

Query Match 40.0%; Score 6; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTVM 13
Db 9 LPPTVM 14

RESULT 8
US-10-286-457-359
; Sequence 359, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 359
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-359

Query Match 33.3%; Score 5; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11

/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/161,791
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/602,999
/ FILING DATE: 16-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Misrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-202
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8964
/ INFORMATION FOR SEQ ID NO: 227:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
US-10-161-791-227

Query Match 40.0%; Score 6; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTVM 13
Db 9 LPPTVM 14

RESULT 8
US-10-286-457-359
; Sequence 359, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 359
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-359

Query Match 33.3%; Score 5; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11

Db 2 PLPPT 6

RESULT 9
US-10-281-652-24
; Sequence 24, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-24

Query Match 33.3%; Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPP 5
Db 3 MHQPP 7

RESULT 10
US-10-062-109A-382
; Sequence 382, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-382

Query Match 33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 8 LPPTV 12
 |||||
 Db 1 LPPTV 5

RESULT 11

US-10-062-109A-458
 ; Sequence 458, Application US/10062109A
 ; Publication No. US20030165505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Eid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; TITLE OF INVENTION: Cancer
 ; FILE REFERENCE: 51158-20062.01
 ; CURRENT APPLICATION NUMBER: US/10/062,109A
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 10/005,480
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 458
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-062-109A-458

Query Match 33.3%; Score 5; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTV 12
 |||||
 Db 1 LPPTV 5

RESULT 12

US-10-062-109A-563
 ; Sequence 563, Application US/10062109A
 ; Publication No. US20030165505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Eid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; TITLE OF INVENTION: Cancer
 ; FILE REFERENCE: 51158-20062.01
 ; CURRENT APPLICATION NUMBER: US/10/062,109A
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 10/005,480
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 563
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-062-109A-563

Query Match 33.3%; Score 5; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTV 12
 |||||
 Db 1 LPPTV 5

RESULT 13

US-10-005-480A-382
 ; Sequence 382, Application US/10005480A
 ; Publication No. US20030191073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Eid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; TITLE OF INVENTION: Cancer
 ; FILE REFERENCE: 51158-20062.00
 ; CURRENT APPLICATION NUMBER: US/10/005,480A
 ; CURRENT FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 382
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-005-480A-382

Query Match 33.3%; Score 5; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTV 12
 |||||
 Db 1 LPPTV 5

RESULT 14

US-10-005-480A-458
 ; Sequence 458, Application US/10005480A
 ; Publication No. US20030191073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Eid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; TITLE OF INVENTION: Cancer
 ; FILE REFERENCE: 51158-20062.00
 ; CURRENT APPLICATION NUMBER: US/10/005,480A
 ; CURRENT FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 458
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-005-480A-458

Query Match 33.3%; Score 5; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTV 12
 |||||

Db 1 LPPTV 5

RESULT 15

US-10-005-480A-563

Sequence 563, Application US/10005480A

Publication No. US20030191073A1

GENERAL INFORMATION:

APPLICANT: Agensys

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Karen Jane Meyrick

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

TITLE OF INVENTION: Cancer

FILE REFERENCE: 51158-20062.00

CURRENT APPLICATION NUMBER: US/10/005,480A

CURRENT FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 765

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 563

LENGTH: 9

TYPE: PRT

ORGANISM: Homo Sapien

US-10-005-480A-563

Query Match 33.3%; Score 5; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTV 12

Db 1 LPPTV 5

RESULT 16

US-09-794-346-1

Sequence 1, Application US/09794346

Patent No. US20010031857A1

GENERAL INFORMATION:

APPLICANT: Aventis Pharma Deutschland GmbH

FILE REFERENCE: 02481.1728

CURRENT APPLICATION NUMBER: US/09/794,346

CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: EP 00104114.4

PRIOR FILING DATE: 2000-02-29

PRIOR APPLICATION NUMBER: PCT/EP 01/01661

PRIOR FILING DATE: 2001-02-15

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

LENGTH: 10

TYPE: PRT

ORGANISM: artificial sequence

NAME/KEY: misc feature

OTHER INFORMATION: Description of Artificial Sequence: Memnoniella echinata, FH 227

US-09-794-346-1

Query Match 33.3%; Score 5; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 98; 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10

Db 6 QPLPP 10

RESULT 17

US-10-148-936-1

Sequence 1, Application US/10148936

Publication No. US20030113819A1

GENERAL INFORMATION:

APPLICANT: Horton, Jeffrey

APPLICANT: Smith, John

APPLICANT: Teear, Michelle

APPLICANT: Kendall, Jonathan

APPLICANT: Michael, Nigel

TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells

FILE REFERENCE: PA9963

CURRENT APPLICATION NUMBER: US/10/148,936

CURRENT FILING DATE: 2000-12-04

PRIOR APPLICATION NUMBER: PCT/GB00/04593

PRIOR FILING DATE: 2000-12-04

PRIOR APPLICATION NUMBER: GB 9928674.2

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 12

TYPE: PRT

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: synthetic oligomer

US-10-148-936-1

Query Match 33.3%; Score 5; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11

Db 4 PLPPT 8

RESULT 18

US-09-938-315-93

Sequence 93, Application US/09938315

Patent No. US20020091085A1

GENERAL INFORMATION:

APPLICANT: KAY, BRIAN K.

SPARKS, ANDREW B.

THORN, JUDITH M.

QUILLIAM, LAWRENCE A.

DER, CHANNING J.

TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF

ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,315

FILING DATE: 23-Aug-2001

CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Villacorta, Gilberto M.

REGISTRATION NUMBER: 34,038

REFERENCE/DOCKET NUMBER: 4980-007-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

```

;
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 13 amino acids
;   TYPE: amino acid
;   TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-09-938-315-93

Query Match      33.3%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 P L P P T 11
Db      5 P L P P T 9

RESULT 19
US-09-897-107-69
; Sequence 69, Application US/09897107
; Patent No. US20020137094A1
; GENERAL INFORMATION:
; APPLICANT: YAMAGISHI, Akihiko
; TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAVING
; FILE REFERENCE: 2103830S0
; CURRENT APPLICATION NUMBER: US/09/897,107
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: JP2000-201920
; PRIOR FILING DATE: 2000-07-04
; PRIOR APPLICATION NUMBER: JP2001-164332
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 13
; TYPE: PPT
; ORGANISM: Escherichia coli
US-09-897-107-69

Query Match      33.3%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 Q P L P P 10
Db      1 Q P L P P 5

RESULT 20
US-10-161-791-90
; Sequence 90, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

```

```

;
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 13 amino acids
;   TYPE: amino acid
;   TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-90

Query Match      33.3%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 P L P P T 11
Db      8 P L P P T 12

RESULT 21
US-10-161-791-93
; Sequence 93, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-93

Query Match 33.3%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 5 PLPPT 9

RESULT 22
US-10-079-167-38
; Sequence 38, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-079-167-38

Query Match 33.3%; Score 5; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 5 QPLPP 9

RESULT 23
US-10-367-405-18
; Sequence 18, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch

; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT APPLICATION NUMBER: US/10/367,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-367-405-18

Query Match 33.3%; Score 5; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POPLP 9
Db 10 POPLP 14

RESULT 24
US-10-302-896-30
; Sequence 30, Application US/10302896
; Publication No. US20030180307A1
; GENERAL INFORMATION:
; APPLICANT: GUISSO-MACLOUP, NICOLE
; APPLICANT: BOURSAX-ETUDE, CAROLINE
; TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS
; TITLE OF INVENTION: OF PERTACTIN IN BORDETELLA PERTUSSIS, BORDETELLA PARAPERTUSSIS,
; TITLE OF INVENTION: AND BORDETELLA BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 02356.0081
; CURRENT APPLICATION NUMBER: US/10/302,896
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/06457
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/206,969
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bordetella sp.
US-10-302-896-30

Query Match 33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7
Db 2 QPPQP 6

RESULT 25
US-10-161-791-355

```

; Sequence 355, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 355:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-355

Query Match 33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
DB 9 PLPPT 13

RESULT 26
US-10-161-791-373
; Sequence 373, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-373

Query Match 33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 OPPQP 7
DB 10 OPPQP 14

RESULT 27
US-10-161-791-437
; Sequence 437, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:

```

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 437:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-437

Query Match 33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 2 QPLPP 6

RESULT 28
US-10-161-791-213
Sequence 213, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKS, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-213

Query Match 33.3%; Score 5; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 5 PLPPT 9

RESULT 29
US-10-225-567A-1351
Sequence 1351, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patent In version 3.1
SEQ ID NO 1351
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-1351

Query Match 33.3%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 10 PLPPT 14

RESULT 30
US-10-029-386-31396
Sequence 31396, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31396
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO ALL18558.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
US-10-029-386-31396

US-09-864-761-45132

Query Match 33.3%; Score 5; DB 12; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
 |||||
 Db 8 QPLPP 12

RESULT 31
 US-09-864-761-45132
 ; Sequence 45132, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aecmca-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 45132
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC015670.4
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.76
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.63
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.81
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.84

US-09-864-761-45132

Query Match 33.3%; Score 5; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLPP 9
 |||||
 Db 9 QPLPP 13

RESULT 32
 US-10-302-896-31
 ; Sequence 31, Application US/10302896
 ; Publication No. US20030180307A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GUISSO-MACLOUF, NICOLE
 ; APPLICANT: BOURSAX-UEDE, CAROLINE
 ; TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS
 ; TITLE OF INVENTION: OF PERTACTIN IN BORDETTELLA PERTUSSIS, BORDETTELLA PARAPERTUSSIS,
 ; TITLE OF INVENTION: AND BORDETTELLA BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
 ; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
 ; FILE REFERENCE: 02356.0081
 ; CURRENT APPLICATION NUMBER: US/10/302,896
 ; CURRENT FILING DATE: 2002-11-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06457
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: 60/206,969
 ; PRIOR FILING DATE: 2000-05-25
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Bordetella sp.
 ; US-10-302-896-31

Query Match 33.3%; Score 5; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7
 |||||
 Db 2 QPPQP 6

RESULT 33
 US-09-964-201A-17
 ; Sequence 17, Application US/09964201A
 ; Publication No. US20030091575A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kenten, John H
 ; APPLICANT: Tramontano, Alfonso
 ; APPLICANT: Pilon, Aprile L
 ; APPLICANT: Lohnas, Gerald L
 ; APPLICANT: Roberts, Steven F
 ; TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
 ; FILE REFERENCE: U.S. Patent Application No. US20030091575A1 09\026,276
 ; CURRENT APPLICATION NUMBER: US/09/964,201A
 ; CURRENT FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 17
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium tuberculosis
 ; US-09-964-201A-17

Query Match 33.3%; Score 5; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10

Db |||||
6 QPLPP 10

RESULT 34

US-09-308-511-11
; Sequence 11, Application US/09308511
; Patent No. US20020103145A1
; GENERAL INFORMATION:
; APPLICANT: BOT and BONA
; TITLE OF INVENTION: IMMUNIZATION OF INFANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue &
; Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,511
; FILING DATE: 19-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29889-165/29528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2558
; TELEFAX: 212-765-2519
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacteria
; FEATURE:
; NAME/KEY:
; LOCATION: 350...369
; OTHER INFORMATION: Heat Shock Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-308-511-11

Query Match 33.3%; Score 5; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10

Db |||||
6 QPLPP 10

RESULT 35

US-10-161-791-147
; Sequence 147, Application US/10161791
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-147

Query Match 33.3%; Score 5; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11

Db |||||
7 PLPPT 11

RESULT 36

US-09-500-700-104
; Sequence 104, Application US/09500700
; Publication No. US20030059767A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR

; FILE REFERENCE: SCRIPI160-4
; CURRENT APPLICATION NUMBER: US/09/500,700
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 08/863,813
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: US 08/676,318
; PRIOR FILING DATE: 1996-12-30
; PRIOR APPLICATION NUMBER: PCI/US95/00829
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/312,604
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: US 08/183,119

Query Match 33.3%; Score 5; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10

Db |||||
6 QPLPP 10

; PRIOR FILING DATE: 1994-01-18
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified sequence of finger 2 of zif268
US-09-500-700-104

Query Match 26.7%; Score 4; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PQL 8
|||
Db 1 PQL 4

RESULT 37
US-10-092-219-11
; Sequence 11, Application US/10092219
; Publication No. US20020115114A1
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; TITLE OF INVENTION: No. US20020115114A1 Lipid Kinase
; FILE REFERENCE: 1064HG/50947
; CURRENT APPLICATION NUMBER: US/10/092,219
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 03/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-219-11

Query Match 26.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
|||
Db 2 PLPP 5

RESULT 38
US-09-019-679-4
; Sequence 4, Application US/09019679
; Patent No. US20020012943A1
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M
; APPLICANT: Thorp, H. Holden
; TITLE OF INVENTION: Electrochemical Probes for Detection of Molecular
; TITLE OF INVENTION: Interactions and Drug Discovery
; FILE REFERENCE: 97082-B
; CURRENT APPLICATION NUMBER: US/09/019,679
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: 60/036,919
; EARLIER FILING DATE: 1997-02-06
; EARLIER APPLICATION NUMBER: 60/059,049
; EARLIER FILING DATE: 1997-09-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 7

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Src SH3
; OTHER INFORMATION: Binding motif
US-09-019-679-4

Query Match 26.7%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
|||
Db 2 PLPP 5

RESULT 39
US-09-879-957-45
; Sequence 45, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-879-957-45

Query Match 26.7%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
|||

Db 2 PLPP 5

RESULT 40

US-09-938-315-9

Sequence 9, Application US/09938315

Patent No. US20020091085A1

GENERAL INFORMATION:

APPLICANT: KAY, BRIAN K.

SPARKS, ANDREW B.

THORN, JUDITH M.

QUILLIAM, LAWRENCE A.

DER, CHANNING J.

TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patencin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,315

FILING DATE: 23-Aug-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Villacorta, Gilberto M.

REGISTRATION NUMBER: 34,038

REFERENCE/DOCKET NUMBER: 4980-007-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-938-315-9

Query Match 26.7%; Score 4; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10

Db 2 PLPP 5

RESULT 41

US-10-052-578-286

Sequence 286, Application US/10052578

Publication No. US20030134787A1

GENERAL INFORMATION:

APPLICANT: Sloan-Kettering Institute for Cancer Research

APPLICANT: Rothman, James E.

APPLICANT: Mayhew, Mark

APPLICANT: Hoe, Mee H.

APPLICANT: Houghton, Alan

APPLICANT: Hartl, Ulrich

APPLICANT: Querfelli, Ouathek

APPLICANT: Moroi, Yoichi

TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES

FILE REFERENCE: 11746/46003

CURRENT APPLICATION NUMBER: US/10/053,520

CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: 08/961,707

PRIOR FILING DATE: 1997-10-31

NUMBER OF SEQ ID NOS: 321

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 286

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: peptide in ml3 coliphage

US-10-053-520-286

Query Match 26.7%; Score 4; DB 12; Length 7;

Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10

Db 4 PLPP 7

RESULT 43

US-10-161-791-9

Sequence 9, Application US/10161791

Publication No. US20030186863A1

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.

APPLICANT: QUILLIAM, Lawrence A.

APPLICANT: DER, Channing J.

APPLICANT: FOWLKES, Dana M.

FILE REFERENCE: 11746/46003

CURRENT APPLICATION NUMBER: US/10/052,578

CURRENT FILING DATE: 2002-01-17

PRIOR APPLICATION NUMBER: 08/961,707

PRIOR FILING DATE: 1997-10-31

NUMBER OF SEQ ID NOS: 321

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 286

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: peptide in ml3 coliphage

US-10-052-578-286

Query Match 26.7%; Score 4; DB 12; Length 7;

Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10

Db 4 PLPP 7

RESULT 42

US-10-053-520-286

Sequence 286, Application US/10053520

Publication No. US20030166530A1

GENERAL INFORMATION:

APPLICANT: Sloan-Kettering Institute for Cancer Research

APPLICANT: Rothman, James E.

APPLICANT: Mayhew, Mark

APPLICANT: Hoe, Mee H.

APPLICANT: Houghton, Alan

APPLICANT: Hartl, Ulrich

APPLICANT: Querfelli, Ouathek

APPLICANT: Moroi, Yoichi

TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES

FILE REFERENCE: 11746/46004

CURRENT APPLICATION NUMBER: US/10/053,520

CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: 08/961,707

PRIOR FILING DATE: 1997-10-31

NUMBER OF SEQ ID NOS: 321

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 286

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: peptide in ml3 coliphage

US-10-053-520-286

Query Match 26.7%; Score 4; DB 12; Length 7;

Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10

Db 4 PLPP 7

RESULT 43

US-10-161-791-9

Sequence 9, Application US/10161791

Publication No. US20030186863A1

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.

APPLICANT: QUILLIAM, Lawrence A.

APPLICANT: DER, Channing J.

APPLICANT: FOWLKES, Dana M.

```
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-9

Query Match 26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 2 PLPP 5

RESULT 44
US-10-053-498B-286
; Sequence 286, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-498B-286

Query Match 26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 4 PLPP 7

RESULT 45
US-09-894-018-76
; Sequence 76, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-09-894-018-76

Query Match 26.7%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PQPL 8
Db 5 PQPL 8

RESULT 46
US-09-745-078A-30
; Sequence 30, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/09/745,078A
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
```

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-09-745-078A-30

Query Match          26.7%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPTV 12
Db 5 PPTV 8

RESULT 47
US-10-052-578-82
; Sequence 82, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-052-578-82

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 4 PLPP 7

RESULT 48
US-10-053-520-82
; Sequence 82, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31

; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-053-520-82

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPTV 12
Db 5 PPTV 8

RESULT 49
US-10-374-624-30
; Sequence 30, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-30

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPTV 12
Db 5 PPTV 8

RESULT 50
US-10-053-498B-82
; Sequence 82, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
```

; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-498B-82

Query Match 26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
|
|
|
|
Db 4 PLPP 7

RESULT 51
US-08-344-824-102
; Sequence 102, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-102

Query Match 26.7%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQP 7
|
|
|
|
Db 2 PPQP 5

RESULT 52
US-08-344-824-322
; Sequence 322, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 322:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-322

Query Match 26.7%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQP 7
|
|
|
|
Db 5 PPQP 8

RESULT 53
US-08-344-824-323
; Sequence 323, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 323:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-323

Query Match 26.7%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQP 7
Db 1 PPQP 4

RESULT 54
US-08-854-825-43
; Sequence 43, Application US/08854825
; Publication No. US20020115061A1
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; APPLICANT: Cerny, Andreas
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,825
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silvert, Donald J.
; REGISTRATION NUMBER: 37552
; REFERENCE/DOCKET NUMBER: 61230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-854-825-43

Query Match 26.7%; Score 4; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 1 PLPP 4

RESULT 55
US-09-834-765-48
; Sequence 48, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-48

Query Match 26.7%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQPL 8
Db 4 PQPL 7

RESULT 56
US-09-834-765-130
; Sequence 130, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-834-765-130

  Query Match          26.7%; Score 4; DB 9; Length 9;
  Best Local Similarity 100.0%; Pred. No. 6e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQPL 8
Db 6 PQPL 9

RESULT 57
US-09-834-765-356
; Sequence 356, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 356
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-356

  Query Match          26.7%; Score 4; DB 9; Length 9;
  Best Local Similarity 100.0%; Pred. No. 6e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQPL 8
Db 2 PQPL 5

RESULT 58
US-09-834-765-462
; Sequence 462, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-462

  Query Match          26.7%; Score 4; DB 9; Length 9;
  Best Local Similarity 100.0%; Pred. No. 6e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQPL 8
Db 6 PQPL 9

RESULT 59
US-09-834-765-546
; Sequence 546, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 546
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-546

  Query Match          26.7%; Score 4; DB 9; Length 9;
  Best Local Similarity 100.0%; Pred. No. 6e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQPL 8
Db 6 PQPL 9

RESULT 60
US-09-938-315-11
; Sequence 11, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SIX SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
```

```
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Villacorta, Gilberto M.
/ REGISTRATION NUMBER: 34, 038
/ REFERENCE/DOCKET NUMBER: 4980-007-0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 413-3000
/ TELEFAX: (703) 413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-938-315-11

Query Match          26.7%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      2 PLPP 5

RESULT 61
US-09-780-053-165
/ Sequence 165, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Challita-Eid
/ APPLICANT: Mary Faris
/ APPLICANT: Elana Levin
/ APPLICANT: Steve Chappell Mitchell
/ APPLICANT: Ava Jakobovits
/ TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.5USU1
/ CURRENT APPLICATION NUMBER: US/09/780,053
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/181,261
/ PRIOR FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 716
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 165
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-780-053-165

Query Match          26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPTV 12
Db      6 PPTV 9

RESULT 62
US-09-780-053-456
/ Sequence 456, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Challita-Eid
/ APPLICANT: Mary Faris
/ APPLICANT: Elana Levin

/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Steve Chappell Mitchell
/ APPLICANT: Ava Jakobovits
/ TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.5USU1
/ CURRENT APPLICATION NUMBER: US/09/780,053
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/181,261
/ PRIOR FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 716
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 456
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-780-053-456

Query Match          26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPTV 12
Db      5 PPTV 8

RESULT 63
US-09-780-053-517
/ Sequence 517, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Challita-Eid
/ APPLICANT: Mary Faris
/ APPLICANT: Elana Levin
/ APPLICANT: Steve Chappell Mitchell
/ APPLICANT: Ava Jakobovits
/ TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.5USU1
/ CURRENT APPLICATION NUMBER: US/09/780,053
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/181,261
/ PRIOR FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 716
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 517
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-780-053-517

Query Match          26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPTV 12
Db      5 PPTV 8

RESULT 64
US-09-780-053-620
/ Sequence 620, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Challita-Eid
/ APPLICANT: Mary Faris
/ APPLICANT: Elana Levin
/ APPLICANT: Steve Chappell Mitchell
```


; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83PG4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: HIGHLY EXPRESSED IN PROSTATE CANCER
; CURRENT APPLICATION NUMBER: 129-5USU1
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 620
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-620

Query Match 26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 PPTV 12
Db 5 PPTV 8

RESULT 65
US-09-945-917-34
; Sequence 34, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-34

Query Match 26.7%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 PLPP 10
Db 4 PLPP 7

RESULT 66
US-09-745-078A-29
; Sequence 29, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/09/745,078A
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-09-745-078A-29

Query Match 26.7%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 PPTV 12
Db 5 PPTV 8

RESULT 67
US-09-972-656-26
; Sequence 26, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-26

Query Match 26.7%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 8 LPPT 11
Db 6 LPPT 9

RESULT 68
US-09-932-165-3
; Sequence 3, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-3

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TVMF 14
Db 6 TVMF 9

RESULT 69
US-09-932-165-648
; Sequence 648, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-ED, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELIANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatP2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-648

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TVMF 14
Db 6 TVMF 9

RESULT 70
US-09-845-917A-34
; Sequence 34, Application US/09845917A
; Publication No. US20030167538A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-34

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 4 PLPP 7

RESULT 71
US-10-374-624-29
; Sequence 29, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-29

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPTV 12
Db 5 PPTV 8

RESULT 72
US-10-161-791-11
; Sequence 11, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-11

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 2 PLPP 5

RESULT 73
US-10-042-202-49
; Sequence 49, Application US/10042202
; Publication No. US20020136733A1
; GENERAL INFORMATION:
; APPLICANT: Adrian Vivian Sinton HILL, Michael AIDOO,
; Catherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena
; PIEBANSKI, Hilton Carter WHITTLE,
; TITLE OF INVENTION: MALARIA PEPTIDES
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESS: WENDEROTH, LIND & PONACK, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800,
; CITY: Washington
; STATE: D.C.,
; COUNTRY: U.S.A.
; ZIP: 20006-1021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordpad for Windows 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/042,202
; FILING DATE: 11-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,175
; FILING DATE: 28-JAN-1997
; APPLICATION NUMBER: WO PCT/GB95/26982
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: GB 9406492.0
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: 2002_0026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-721-8200

TELEFAX: (202)-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-042-202-49

Query Match 26.7%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 3 PLPP 6

RESULT 74
US-10-158-596A-102
; Sequence 102, Application US/10158596A
; Publication No. US20030068900A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela
; APPLICANT: Flynn, Christine
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLE NUCLEATION, SHAPE AND CRYSTAL
; FILE REFERENCE: 119927-1052
; CURRENT APPLICATION NUMBER: US/10/158,596A
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/296,013
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide retrieved from phage biopanning
US-10-158-596A-102

Query Match 26.7%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQP 7
Db 2 PPQP 5

RESULT 75
US-10-254-446A-102
; Sequence 102, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopar
US-10-254-446A-102

Query Match      26.7%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPQP 7
      ||||
Db      2 PPQP 5
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Search completed: November 25, 2003, 20:37:09
Job time : 24.0698 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 12,1221 Seconds
(without alignments)
52,356 Million cell updates/sec

Title: US-09-641-801-34
Perfect score: 15
Sequence: 1 MHQPPQLPPTWMP 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*
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5: /cgn2_6/prodata/1/iaa/PCFUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	100.0	15	4	US-09-641-803-34
2	10	66.7	10	4	US-09-641-803-25
3	6	40.0	11	4	US-09-149-476-689
4	6	40.0	15	3	US-08-602-999A-405
5	6	40.0	15	4	US-09-500-124-405
6	6	40.0	16	3	US-08-602-999A-227
7	6	40.0	16	4	US-09-500-124-227
8	5	33.3	7	2	US-08-769-745-26
9	5	33.3	7	4	US-09-641-803-24
10	5	33.3	11	1	US-08-336-343A-24
11	5	33.3	11	3	US-08-652-877-34
12	5	33.3	11	3	US-08-476-515A-34
13	5	33.3	13	3	US-08-602-999A-90
14	5	33.3	13	3	US-08-602-999A-93
15	5	33.3	13	4	US-08-278-865-93
16	5	33.3	13	4	US-09-500-124-90
17	5	33.3	13	4	US-09-500-124-93
18	5	33.3	15	3	US-08-602-999A-355
19	5	33.3	15	3	US-08-602-999A-373
20	5	33.3	15	3	US-08-602-999A-437
21	5	33.3	15	4	US-09-500-124-355
22	5	33.3	15	4	US-09-500-124-373
23	5	33.3	16	3	US-09-500-124-437
24	5	33.3	16	3	US-08-602-999A-213
25	5	33.3	16	4	US-09-500-124-213
26	5	33.3	19	4	US-09-026-276-17
27	5	33.3	20	2	US-08-363-276B-11

28	5	33.3	20	3	US-08-602-999A-147	Sequence 147, App
29	5	33.3	20	3	US-08-755-034-11	Sequence 11, Appl
30	5	33.3	20	4	US-09-500-124-147	Sequence 147, App
31	5	33.3	20	5	PCT-US95-16718-11	Sequence 11, Appl
32	5	33.3	20	5	PCT-US96-08995-11	Sequence 11, Appl
33	4	26.7	6	4	US-09-355-160D-11	Sequence 11, Appl
34	4	26.7	7	1	US-08-127-499A-7	Sequence 7, Appl
35	4	26.7	7	1	US-08-230-047-40	Sequence 40, Appl
36	4	26.7	7	1	US-08-482-847-7	Sequence 7, Appl
37	4	26.7	7	2	US-08-340-283-38	Sequence 38, Appl
38	4	26.7	7	2	US-08-769-745-7	Sequence 7, Appl
39	4	26.7	7	3	US-08-602-999A-9	Sequence 9, Appl
40	4	26.7	7	4	US-08-278-865-9	Sequence 9, Appl
41	4	26.7	7	4	US-08-630-915A-45	Sequence 45, Appl
42	4	26.7	7	4	US-09-500-124-9	Sequence 9, Appl
43	4	26.7	7	5	PCT-US94-01840-11	Sequence 11, Appl
44	4	26.7	8	1	US-09-641-640-8	Sequence 8, Appl
45	4	26.7	8	2	US-08-612-857-8	Sequence 8, Appl
46	4	26.7	8	3	US-08-747-221B-43	Sequence 43, Appl
47	4	26.7	8	3	US-09-005-051-43	Sequence 43, Appl
48	4	26.7	8	5	PCT-US91-05177-19	Sequence 19, Appl
49	4	26.7	9	1	US-08-214-650-43	Sequence 43, Appl
50	4	26.7	9	1	US-08-615-181-110	Sequence 110, App
51	4	26.7	9	1	US-08-146-028-441	Sequence 441, App
52	4	26.7	9	2	US-08-146-028-442	Sequence 442, App
53	4	26.7	9	2	US-08-146-028-443	Sequence 443, App
54	4	26.7	9	2	US-08-146-028-445	Sequence 445, App
55	4	26.7	9	2	US-08-146-028-446	Sequence 446, App
56	4	26.7	9	2	US-08-318-856A-49	Sequence 49, Appl
57	4	26.7	9	3	US-08-723-425A-441	Sequence 441, App
58	4	26.7	9	3	US-08-723-425A-442	Sequence 442, App
59	4	26.7	9	3	US-08-723-425A-443	Sequence 443, App
60	4	26.7	9	3	US-08-723-425A-445	Sequence 445, App
61	4	26.7	9	3	US-08-723-425A-446	Sequence 446, App
62	4	26.7	9	3	US-08-602-999A-11	Sequence 11, Appl
63	4	26.7	9	3	US-09-112-206-441	Sequence 441, App
64	4	26.7	9	3	US-09-112-206-442	Sequence 442, App
65	4	26.7	9	3	US-09-112-206-443	Sequence 443, App
66	4	26.7	9	3	US-09-112-206-445	Sequence 445, App
67	4	26.7	9	4	US-09-112-206-446	Sequence 446, App
68	4	26.7	9	4	US-08-278-865-11	Sequence 11, Appl
69	4	26.7	9	4	US-09-500-124-11	Sequence 11, Appl
70	4	26.7	10	1	US-08-230-047-12	Sequence 12, Appl
71	4	26.7	10	1	US-08-212-190A-8	Sequence 8, Appl
72	4	26.7	10	2	US-08-146-028-444	Sequence 444, App
73	4	26.7	10	2	US-08-769-745-5	Sequence 5, Appl
74	4	26.7	10	2	US-08-769-745-6	Sequence 6, Appl
75	4	26.7	10	2	US-08-900-321-8	Sequence 8, Appl
76	4	26.7	10	3	US-08-336-553A-12	Sequence 12, Appl
77	4	26.7	10	3	US-08-336-553A-43	Sequence 43, Appl
78	4	26.7	10	3	US-08-336-553A-65	Sequence 65, Appl
79	4	26.7	10	3	US-08-723-425A-444	Sequence 444, App
80	4	26.7	10	3	US-09-112-206-444	Sequence 444, App
81	4	26.7	10	3	US-08-981-392-53	Sequence 53, Appl
82	4	26.7	10	4	US-08-439-157-12	Sequence 12, Appl
83	4	26.7	10	4	US-08-439-157-43	Sequence 43, Appl
84	4	26.7	10	4	US-08-439-157-65	Sequence 65, Appl
85	4	26.7	10	4	US-09-437-895-12	Sequence 12, Appl
86	4	26.7	10	4	US-09-437-895-43	Sequence 43, Appl
87	4	26.7	10	4	US-09-437-895-65	Sequence 65, Appl
88	4	26.7	10	5	PCT-US95-03610-8	Sequence 8, Appl
89	4	26.7	11	1	US-07-794-288D-24	Sequence 24, Appl
90	4	26.7	11	1	US-08-336-343A-25	Sequence 25, Appl
91	4	26.7	11	1	US-08-323-531-22	Sequence 22, Appl
92	4	26.7	11	1	US-08-198-094-22	Sequence 22, Appl
93	4	26.7	11	3	US-08-602-999A-260	Sequence 260, App
94	4	26.7	11	3	US-08-602-999A-265	Sequence 265, App
95	4	26.7	11	3	US-08-652-877-22	Sequence 22, Appl
96	4	26.7	11	3	US-08-652-877-32	Sequence 32, Appl
97	4	26.7	11	3	US-08-652-877-35	Sequence 35, Appl
98	4	26.7	11	3	US-08-652-877-36	Sequence 36, Appl
99	4	26.7	11	3	US-08-107-794A-22	Sequence 22, Appl
100	4	26.7	11	3	US-08-476-515A-22	Sequence 22, Appl

ALIGNMENTS

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RESULT 1
US-09-641-803-34
; Sequence 34, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-34

Query Match          100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPPQLPPTVMFP 15
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Db 1 MHQPPQLPPTVMFP 15

RESULT 2
US-09-641-803-25
; Sequence 25, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-25

Query Match          66.7%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPPTVMFP 15
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Db 1 QPLPPTVMFP 10

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RESULT 3
US-09-149-476-689
; Sequence 689, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580

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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 40.0%; Score 6; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOPPOP 7
|||
DB 1 HOPPOP 6

RESULT 4

US-08-602-999A-405
; Sequence 405, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 405:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLESCULE TYPE: peptide
US-08-602-999A-405

Query Match 40.0%; Score 6; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQPLP 9
Db 8 PPQPLP 13

RESULT 5
US-09-500-124-405
Sequence 405, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 405:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLESCULE TYPE: peptide
US-09-500-124-405

Query Match 40.0%; Score 6; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQPLP 9
Db 8 PPQPLP 13

RESULT 6
US-08-602-999A-227
Sequence 227, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-227

Query Match 40.0%; Score 6; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTVM 13
Db 9 LPPTVM 14

RESULT 7

US-09-500-124-227
Sequence 227, Application US/09500124
Patent No. 6432920

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-227

Query Match 40.0%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTVM 13
Db 9 LPPTVM 14

RESULT 8

US-08-769-745-26
Sequence 26, Application US/08769745
Patent No. 595259
GENERAL INFORMATION:
APPLICANT: Holmes, Todd C.
APPLICANT: Levitan, Irwin B.
APPLICANT: Brandeis University
TITLE OF INVENTION: Mechanism for the Regulation of Ion
TITLE OF INVENTION: Channel Activity
FILE REFERENCE: BRU96-02
CURRENT FILING DATE: 1996-12-19
CURRENT APPLICATION NUMBER: US/08/769,745
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 7
TYPE: PRT
ORGANISM: Mouse
US-08-769-745-26

Query Match 33.3%; Score 5; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 1 QPLPP 5

RESULT 9

US-09-641-803-24
Sequence 24, Application US/09641803
Patent No. 6500798
GENERAL INFORMATION:
APPLICANT: STANTON, G. John
APPLICANT: HUGHES, Thomas K.
APPLICANT: BOLDOGH, Istvan
TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
FILE REFERENCE: 265.00220101
CURRENT APPLICATION NUMBER: US/09/641,803
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/149,310
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-09-641-803-24

Query Match 33.3%; Score 5; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPP 5
Db 3 MHQPP 7

RESULT 10

US-08-336-343A-24

Sequence 24, Application US/08336343A
Patent No. 5677144
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Alves, Frauke
TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,343A
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-336-343A-24

Query Match 33.3%; Score 5; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
DB 7 PLPPT 11

RESULT 11
US-08-652-877-34
Sequence 34, Application US/08652877
Patent No. 6187548
GENERAL INFORMATION:
APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalms, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh

OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355E-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-652-877-34

Query Match 33.3%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
DB 7 PLPPT 11

RESULT 12
US-08-476-515A-34
Sequence 34, Application US/08476515A
Patent No. 6239270
GENERAL INFORMATION:
APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalms, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Martin Savitzky
STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.,
STREET: 3C43,
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Compaq PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 7.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA: WO PCT/SE94/00483
APPLICATION NUMBER: 23,699
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 23,699
REFERENCE/DOCKET NUMBER: A1355D
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-476-515A-34

Query Match 33.3%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
|||||
Db 7 PLPPT 11

RESULT 13
US-08-602-999A-90
Sequence 90, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602.999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-93
Query Match 33.3%; Score 5; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-90

Query Match 33.3%; Score 5; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
|||||
Db 8 PLPPT 12

RESULT 14
US-08-602-999A-93
Sequence 93, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602.999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-93

Query Match 33.3%; Score 5; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
|||||

Db 5 PLPPT 9

RESULT 15

US-08-278-865-93
 ; Sequence 93, Application US/08278865
 ; Patent No. 6303574
 ; GENERAL INFORMATION:
 ; APPLICANT: KAY, BRIAN K.
 ; APPLICANT: SPARKS, ANDREW B.
 ; APPLICANT: THORN, JUDITH M.
 ; APPLICANT: QUILLIAM, LAWRENCE A.
 ; APPLICANT: DER, CHANNING J.
 ; TITLE OF INVENTION: SFC SH3 BINDING PEPTIDES AND METHODS OF
 ; TITLE OF INVENTION: ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/278,865
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Villacorta, Gilberto M.
 ; REGISTRATION NUMBER: 34,038
 ; REFERENCE/DOCKET NUMBER: 4980-007-0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 413-3000
 ; TELEFAX: (703) 413-2220
 ; TELEX: 248855 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 93:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-278-865-93

Query Match 33.3%; Score 5; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPPT 11

Db 5 PLPPT 9

RESULT 16

US-09-500-124-90
 ; Sequence 90, Application US/09500124
 ; Patent No. 6432920
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; TITLE OF INVENTION: ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/500,124
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/602,999
 ; FILING DATE: 16-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-3741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 90:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-09-500-124-90

Query Match 33.3%; Score 5; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPPT 11

Db 8 PLPPT 12

RESULT 17

US-09-500-124-93
 ; Sequence 93, Application US/09500124
 ; Patent No. 6432920
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; TITLE OF INVENTION: ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/500,124

```
;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/602,999
; APPLICATION DATE: 16-FEB-1996
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-93

Query Match      33.3%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PLPPT 11
Db      5 PLPPT 9

RESULT 18
US-08-602-999A-355
; Sequence 355, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 355:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
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```
;
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-355

Query Match      33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PLPPT 11
Db      9 PLPPT 13

RESULT 19
US-08-602-999A-373
; Sequence 373, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-373

Query Match      33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 QPPQP 7
Db      10 QPPQP 14

RESULT 20
US-08-602-999A-437
; Sequence 437, Application US/08602999A
; Patent No. 6184205
```

;/ GENERAL INFORMATION:
;/ APPLICANT: SPARKS, Andrew B.
;/ APPLICANT: KAY, Brian K.
;/ APPLICANT: THORN, Judith M.
;/ APPLICANT: QUILLIAM, Lawrence A.
;/ APPLICANT: DER, Channing J.
;/ APPLICANT: FOWLKES, Dana M.
;/ APPLICANT: RIDER, James E.
;/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;/ TITLE OF INVENTION: ISOLATING AND USING SAME
;/ NUMBER OF SEQUENCES: 467
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Pennie & Edmonds
;/ STREET: 1155 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10036-2711
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/602,999A
;/ FILING DATE: 16-FEB-1996
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Misrock, S. Leslie
;/ REGISTRATION NUMBER: 18,872
;/ REFERENCE/DOCKET NUMBER: 1101-202
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212) 790-9090
;/ TELEFAX: (212) 869-9741/8864
;/ TELEX: 66141 PENNIE
;/ INFORMATION FOR SEQ ID NO: 437:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 15 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: peptide
;/ US-08-602-999A-437

Query Match 33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 2 QPLPP 6

RESULT 21
US-09-500-124-355
; Sequence 355, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

;/ ZIP: 10036-2711
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/500,124
;/ FILING DATE:
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/602,999
;/ FILING DATE: 16-FEB-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Misrock, S. Leslie
;/ REGISTRATION NUMBER: 18,872
;/ REFERENCE/DOCKET NUMBER: 1101-202
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212) 790-9090
;/ TELEFAX: (212) 869-9741/8864
;/ TELEX: 66141 PENNIE
;/ INFORMATION FOR SEQ ID NO: 355:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 15 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: peptide
;/ US-09-500-124-355

Query Match 33.3%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 9 PLPPT 13

RESULT 22
US-09-500-124-373
; Sequence 373, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 355:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-355

NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 373:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-373

Query Match 33.3%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7
Db 10 QPPQP 14

RESULT 23
US-09-500-124-437
Sequence 437, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 437:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-437

Query Match 33.3%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 2 QPLPP 6

RESULT 24
US-08-602-999A-213
Sequence 213, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-213

Query Match 33.3%; Score 5; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 5 PLPPT 9

RESULT 25
US-09-500-124-213
Sequence 213, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-213

Query Match 33.3%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPPT 11
Db 5 PLPPT 9

RESULT 26
US-09-026-276-17
Sequence 17, Application US/09026276
Patent No. 6319503
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Tramontano, Alfonso
APPLICANT: Pilon, Aprile L
APPLICANT: Lohnas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 6319503 09/026,276
CURRENT APPLICATION NUMBER: US/09/026,276
CURRENT FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 17
LENGTH: 19
TYPE: PPT
ORGANISM: Mycobacterium tuberculosis
US-09-026-276-17

Query Match 33.3%; Score 5; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 QPLPP 10
Db 6 QPLPP 10

RESULT 27
US-08-363-276B-11
Sequence 11, Application US/08363276B
Patent No. 5969109
GENERAL INFORMATION:
APPLICANT: BONA ET AL.
TITLE OF INVENTION: CHIMERIC ANTIBODIES
TITLE OF INVENTION: COMPRISING ANTIGEN BINDING SITES AND B AND T CELL EPITOPES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue &
ADDRESSEE: Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,276B
FILING DATE: 22-DECEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/486,546
FILING DATE: 28-FEBRUARY-1990 (ABANDONED)
APPLICATION NUMBER: USSN 07/687,376
FILING DATE: 18-APRIL-1991 (ABANDONED)
APPLICATION NUMBER: USSN 08/327,636
FILING DATE: 24-OCTOBER-1994 (ABANDONED)
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29889-165/29528
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacteria
FEATURE:
NAME/KEY:
LOCATION: 350...369
OTHER INFORMATION: Heat Shock Protein
US-08-363-276B-11

Query Match 33.3%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 QPLPP 10
Db 6 QPLPP 10


```
RESULT 28
US-08-602-999A-147
; Sequence 147, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-147

Query Match 33.3%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 7 PLPPT 11

RESULT 29
US-08-755-034-11
; Sequence 11, Application US/08755034
; Patent No. 6204250
; GENERAL INFORMATION:
; APPLICANT: BOT and BONA
; TITLE OF INVENTION: IMMUNIZATION OF INFANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue &
; ADDRESSEE: Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
```

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ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,034
; FILING DATE: 22-NOVEMBER-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29889-165/29528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2558
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacteria
; FEATURE:
; NAME/KEY:
; LOCATION: 350...369
; OTHER INFORMATION: Heat Shock Protein
; US-08-755-034-11

Query Match 33.3%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 6 QPLPP 10

RESULT 30
US-09-500-124-147
; Sequence 147, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-147

Query Match 33.3%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PLPPT 11
Db 7 PLPPT 11
RESULT 31
PCT-US95-16718-11
Sequence 11, Application PC/TUS9516718
GENERAL INFORMATION:
APPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF THE
APPLICANT: CITY UNIVERSITY OF NEW YORK
TITLE OF INVENTION: CHIMERIC ANTIBODIES
TITLE OF INVENTION: COMPRISING ANTIGEN BINDING SITES AND B AND T CELL EPITOPES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue &
ADDRESSEE: Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16718
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29889-165/29528
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacteria
FEATURE:
NAME/KEY:
LOCATION: 350...369
OTHER INFORMATION: Heat Shock Protein
PCT-US95-16718-11

Query Match 33.3%; Score 5; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPLPP 10
Db 6 QPLPP 10

RESULT 32
PCT-US96-08995-11
Sequence 11, Application PC/TUS9608995
GENERAL INFORMATION:
APPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF THE CITY
APPLICANT: UNIVERSITY OF NEW YORK
TITLE OF INVENTION: REGYLATED MODIFIED PROTEINS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,421
FILING DATE: 7-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29889-165/29528
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacteria
FEATURE:
NAME/KEY:
LOCATION: 350...369
OTHER INFORMATION: Heat Shock Protein
PCT-US96-08995-11

Query Match 33.3%; Score 5; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      6 QPLPP 10
Db      6 QPLPP 10

RESULT 33
US-09-355-160D-11
; Sequence 11, Application US/09355160D
; Patent No. 6436671
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; TITLE OF INVENTION: No. 6436671el Lipid Kinase
; FILE REFERENCE: 2332-1-004
; CURRENT APPLICATION NUMBER: US/09/355,160D
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-355-160D-11

Query Match      26.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      2 PLPP 5

RESULT 34
US-08-127-499A-7
; Sequence 7, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
```

```
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-127-499A-7

Query Match      26.7%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPQP 7
Db      1 PPQP 4

RESULT 35
US-08-230-047-40
; Sequence 40, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-40

Query Match      26.7%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      3 PLPP 6

RESULT 36
US-08-482-847-7
; Sequence 7, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
```

;; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/482,847
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/127,499
;; FILING DATE: 28-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 51916/104/INBI
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; US-08-482-847-7

Query Match 26.7%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQP 7
Db 1 PPQP 4

RESULT 37
US-08-340-283-38
; Sequence 38, Application US/08340283
; Patent No. 5861318
; GENERAL INFORMATION:
; APPLICANT: Elhammer, Ake P.
; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
; TITLE OF INVENTION: N-ACETYL GALACTOSAMINYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 205
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law
; ADDRESSEE: (1920-32-1)
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,283
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:

;; NAME: Wootton, Thomas A.
;; REGISTRATION NUMBER: 35,004
;; REFERENCE/DOCKET NUMBER: 4828
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (616) 385-7914
;; TELEFAX: (616) 385-6897
;; TELEX: 224401
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; US-08-340-283-38

Query Match 26.7%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 4 PLPP 7

RESULT 38
US-08-769-745-7
; Sequence 7, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
; US-08-769-745-7

Query Match 26.7%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 2 PLPP 5

RESULT 39
US-08-602-999A-9
; Sequence 9, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467

;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Pennie & Edmonds
;/ STREET: 1155 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10036-2711
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/602,999A
;/ FILING DATE: 16-FEB-1996
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Misrock, S. Leslie
;/ REGISTRATION NUMBER: 18,872
;/ REFERENCE/DOCKET NUMBER: 1101-202
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212) 790-9090
;/ TELEFAX: (212) 869-9741/8864
;/ TELEX: 66141 PENNIE
;/ INFORMATION FOR SEQ ID NO: 9:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 7 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: peptide
;/ US-08-602-999A-9

Query Match 26.7%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 2 PLPP 5

RESULT 40
US-08-278-865-9
;/ Sequence 9, Application US/08278865
;/ Patent No. 6303574
;/ GENERAL INFORMATION:
;/ APPLICANT: KAY, BRIAN K.
;/ APPLICANT: SPARKS, ANDREW B.
;/ APPLICANT: THORN, JUDITH M.
;/ APPLICANT: QUILLIAM, LAWRENCE A.
;/ APPLICANT: DER, CHANNING J.
;/ TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
;/ TITLE OF INVENTION: ISOLATING AND USING SAME
;/ NUMBER OF SEQUENCES: 106
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;/ STREET: 1755 S. Jefferson Davis Highway, Suite 400
;/ CITY: Arlington
;/ STATE: Virginia
;/ COUNTRY: U.S.A.
;/ ZIP: 22202
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/278,865
;/ FILING DATE:
;/ CLASSIFICATION: 514
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Villacorta, Gilberto M.

;/ REGISTRATION NUMBER: 34,038
;/ REFERENCE/DOCKET NUMBER: 4980-007-0
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (703) 413-3000
;/ TELEFAX: (703) 413-2220
;/ TELEX: 248855 OPAT UR
;/ INFORMATION FOR SEQ ID NO: 9:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 7 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: peptide
;/ US-08-278-865-9

Query Match 26.7%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 2 PLPP 5

RESULT 41
US-08-630-915A-45
;/ Sequence 45, Application US/08630915A
;/ Patent No. 6309820
;/ GENERAL INFORMATION:
;/ APPLICANT: SPARKS, Andrew B.
;/ APPLICANT: HOFFMAN, No. 6309820h
;/ APPLICANT: KAY, Brian K.
;/ APPLICANT: FOWLKES, Dana M.
;/ APPLICANT: MCCONNELL, Stephen J.
;/ TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
;/ TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
;/ NUMBER OF SEQUENCES: 227
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Pennie & Edmonds LLP
;/ STREET: 1155 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: USA
;/ ZIP: 10036-2711
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/630,915A
;/ FILING DATE: 03-APR-1996
;/ CLASSIFICATION: 536
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Misrock, S. Leslie
;/ REGISTRATION NUMBER: 18,872
;/ REFERENCE/DOCKET NUMBER: 1101-174
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212) 790-9090
;/ TELEFAX: (212) 869-8864/9741
;/ TELEX: 66141 PENNIE
;/ INFORMATION FOR SEQ ID NO: 45:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 7 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS:
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: peptide
;/ US-08-630-915A-45

Query Match 26.7%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
 Db 2 PLPP 5

RESULT 42

US-09-500-124-9
 ; Sequence 9, Application US/09500124
 ; Patent No. 6432920
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/500,124
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/602,999
 ; FILING DATE: 16-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-09-500-124-9

Query Match 26.7%; Score 4; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
 Db 2 PLPP 5

RESULT 43

PCT-US94-01840-11
 ; Sequence 11, Application PC/TUS9401840
 ; GENERAL INFORMATION:
 ; APPLICANT: Christopher E. Rudd
 ; APPLICANT: Prasad Kanteti
 ; APPLICANT: Lewis Cantley
 ; TITLE OF INVENTION: CD4 MEDIATED MODULATION OF

; TITLE OF INVENTION: LIPID KINASES
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/01840
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/023,915
 ; FILING DATE: February 26, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Janis K. Fraser
 ; REGISTRATION NUMBER: 34,819
 ; REFERENCE/DOCKET NUMBER: 00530/063001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: Linear
 ; PCT-US94-01840-11

Query Match 26.7%; Score 4; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
 Db 3 PLPP 6

RESULT 44

US-09-641-640-8
 ; Sequence 8, Application US/09641640
 ; Patent No. RE37952
 ; GENERAL INFORMATION:
 ; APPLICANT: SCHWEIGHOFFER, Fabien
 ; TOCQUE, Bruno
 ; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Rd. 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/641,640
 ; FILING DATE: 15-Aug-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/612,857

```

; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Smith Ph.D., Julie K.
;   REGISTRATION NUMBER: 38,619
;   REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (610)454-3839
;   TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..8
;   OTHER INFORMATION: /note= "3BP1 peptide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-641-640-8

Query Match          26.7%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      3 PLPP 6

RESULT 45
US-08-612-857-8
; Sequence 8, Application US/08612857
; Patent No. 5831048
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; APPLICANT: TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/612,857
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93-10971
; FILING DATE: 15-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:

```

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..8
;   OTHER INFORMATION: /note= "3BP1 peptide"
US-08-612-857-8

Query Match          26.7%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      3 PLPP 6

RESULT 46
US-08-747-221B-43
; Sequence 43, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-747-221B-43

Query Match          26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPTV 12
Db      2 PPTV 5

```

RESULT 47
US-09-005-051-43
; Sequence 43, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-005-051-43
Query Match 26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PPTV 12
Db 2 PPTV 5

RESULT 48
PCT-US91-05177-19
; Sequence 19, Application PC/TUS9105177
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathy L
; TITLE OF INVENTION: GAMMA-CARBOXYLASE AND METHODS OF USE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05177
; FILING DATE: 19910722
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/557,220
; FILING DATE: 23-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.544PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; FRAGMENT TYPE: internal
PCT-US91-05177-19
Query Match 26.7%; Score 4; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PQPL 8
Db 2 PQPL 5
RESULT 49
US-08-214-650-43
; Sequence 43, Application US/08214650
; Patent No. 5709995
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; APPLICANT: Certy, Andreas
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,650
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Silver, Donald J.
; REGISTRATION NUMBER: 37552
; REFERENCE/DOCKET NUMBER: 61230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-214-650-43

Query Match 26.7%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
|||
Db 1 PLPP 4

RESULT 50

US-08-615-181-110
; Sequence 110, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUMI, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
; TITLE OF INVENTION: CURING AIDS
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,181
FILING DATE: 04-APR-1996
CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: PCT/JP94/01756
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 261302/1993
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-796-0 PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-08-615-181-110

Query Match 26.7%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPT 11
|||
Db 1 LPPT 4

RESULT 51

US-08-146-028-441

; Sequence 441, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:

; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-146-028-441

Query Match 26.7%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
|||
Db 6 PLPP 9

RESULT 52

US-08-146-028-442
; Sequence 442, Application US/08146028
; Patent No. 5891640

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 442:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-146-028-442

Query Match 26.7%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
|||
Db 5 PLPP 8

RESULT 53

US-08-146-028-443
; Sequence 443, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES

; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR

; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED

; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,

; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

; NUMBER OF SEQUENCES: 453

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,028

; INFORMATION FOR SEQ ID NO: 443:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-146-028-443

Query Match 26.7%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
|||
Db 4 PLPP 7

RESULT 54

US-08-146-028-445
; Sequence 445, Application US/08146028
; Patent No. 5891640

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES

; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR

; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED

; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,

; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

; NUMBER OF SEQUENCES: 453

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,028

; INFORMATION FOR SEQ ID NO: 445:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-146-028-445

Query Match 26.7%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
|||
Db 2 PLPP 5

RESULT 55

US-08-146-028-446
; Sequence 446, Application US/08146028
; Patent No. 5891640

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES

; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR

; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED

; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,

; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

; NUMBER OF SEQUENCES: 453

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,028

; INFORMATION FOR SEQ ID NO: 446:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-146-028-446

Query Match 26.7%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
|||
Db 1 PLPP 4

RESULT 56

US-08-318-856A-49
; Sequence 49, Application US/08318856A
; Patent No. 5972351

; GENERAL INFORMATION:

; APPLICANT: Adrian V.S. Hill, et al.

; TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-

; TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-BRYTHROCYTIC STAGE

; TITLE OF INVENTION: ANTIGENS (AS AMENDED)

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

; STREET: 2033 K Street, N.W., Suite 800

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect 5.1+

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/318,856A

; FILING DATE: October 3, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 92 08 068.8

; FILING DATE: April 3, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 92 17 704.7

; FILING DATE: August 20, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB93/00711

; FILING DATE: April 5, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee Cheng

```
;
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 263-PP1R1577US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-856A-49

Query Match          26.7%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 5 PLPP 8

RESULT 57
US-08-723-425A-441
; Sequence 441, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 441:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-441

Query Match          26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 6 PLPP 9

RESULT 58
US-08-723-425A-442
; Sequence 442, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 442:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-442

Query Match          26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 5 PLPP 8

RESULT 59
US-08-723-425A-443
; Sequence 443, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 443:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-443

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 4 PLPP 7

RESULT 60
US-08-723-425A-445
; Sequence 445, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 446:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-446

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 1 PLPP 4

RESULT 62
US-08-602-999A-11
; Sequence 11, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
```

; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James F.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-11

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
|||
Db 2 PLPP 5

RESULT 63
US-09-112-206-441
; Sequence 441, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,206
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 441:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-112-206-441
Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
|||
Db 6 PLPP 9

RESULT 64
US-09-112-206-442
; Sequence 442, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,206
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 442:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-112-206-442

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
|||
Db 5 PLPP 8

RESULT 65
US-09-112-206-443
; Sequence 443, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/112.206
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/146,028
;; FILING DATE:
;; INFORMATION FOR SEQ ID NO: 443:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-112-206-443

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 4 PLPP 7

RESULT 66
US-09-112-206-445
;; Sequence 445, Application US/09112206
;; Patent No. 6210903
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
;; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
;; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
;; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
;; NUMBER OF SEQUENCES: 453
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/112.206
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/146,028
;; FILING DATE:
;; INFORMATION FOR SEQ ID NO: 445:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-112-206-445

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 2 PLPP 5

RESULT 67
US-09-112-206-446
;; Sequence 446, Application US/09112206
;; Patent No. 6210903
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
;; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR

;; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
;; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
;; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
;; NUMBER OF SEQUENCES: 453
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/112.206
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/146,028
;; FILING DATE:
;; INFORMATION FOR SEQ ID NO: 446:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-112-206-446

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 1 PLPP 4

RESULT 68
US-08-278-865-11
;; Sequence 11, Application US/08278865
;; Patent No. 6303574
;; GENERAL INFORMATION:
;; APPLICANT: KAY, BRIAN K.
;; APPLICANT: SPARKS, ANDREW B.
;; APPLICANT: THORN, JUDITH M.
;; APPLICANT: QUILLIAM, LAWRENCE A.
;; APPLICANT: DER, CHANNING J.
;; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 106
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 S. Jefferson Davis Highway, Suite 400
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/278,865
;; FILING DATE:
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Villacorta, Gilberto M.
;; REGISTRATION NUMBER: 34,038
;; REFERENCE/DOCKET NUMBER: 4980-007-0
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 413-3000
;; TELEFAX: (703) 413-2220
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-278-865-11

Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 2 PLPP 5

RESULT 69

US-09-500-124-11
; Sequence 11, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-11

Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 2 PLPP 5

RESULT 70

US-08-230-047-12
; Sequence 12, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-12

Query Match 26.7%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 7 PLPP 10

RESULT 71

US-08-212-190A-8
; Sequence 8, Application US/08212190A
; Patent No. 5652223
; GENERAL INFORMATION:
; APPLICANT: KOHN, Elise C.
; APPLICANT: LIOTTA, Lance A.
; APPLICANT: KIM, Young Sook
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICANT: Brandeis University
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/POCKET NUMBER: 15280-204US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-212-190A-8

```

```

Query Match      26.7%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      7 PLPP 10
      ||||
Db      7 PLPP 10

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RESULT 72

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US-08-146-028-444
; Sequence 444, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:

```

```

; APPLICANT: Holmes, Todd C.
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINILATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:

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; APPLICATION FOR SEQ ID NO: 444:
; INFORMATION FOR SEQ ID NO: 444:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-146-028-444

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Query Match      26.7%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      7 PLPP 10
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Db      3 PLPP 6

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RESULT 73

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US-08-769-745-5
; Sequence 5, Application US/08769745
; Patent No. 5955259

```

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; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Rat
; US-08-769-745-5

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Query Match      26.7%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      7 PLPP 10
      ||||
Db      4 PLPP 7

```

RESULT 74

```

US-08-769-745-6
; Sequence 6, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:

```

```

; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02

```

```

; CURRENT APPLICATION NUMBER: US/08/769,745

```

```

; CURRENT FILING DATE: 1996-12-19

```

```

; NUMBER OF SEQ ID NOS: 41

```

```

; SOFTWARE: FastSeq for Windows Version 3.0

```

```

; SEQ ID NO 6

```

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; LENGTH: 10

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; TYPE: PRT

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; ORGANISM: Homo sapien

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```

; US-08-769-745-6

```

```

Query Match      26.7%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 PLPP 10
      ||||
Db      4 PLPP 7

```

RESULT 75

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US-08-900-321-8
; Sequence 8, Application US/08900321
; Patent No. 5981712
; GENERAL INFORMATION:

```

```

; APPLICANT: Kohn, Elise C.

```

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; APPLICANT: Liotta, Lance A.

```

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; APPLICANT: Kim, Young S.

```

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; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and

```

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; TITLE OF INVENTION: Uses Thereof

```

```

; NUMBER OF SEQUENCES: 10

```

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; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Townsend and Townsend and Crew LLP

```

```

; STREET: Two Embarcadero Center, Eighth Floor

```

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; CITY: San Francisco

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; STATE: California

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; COUNTRY: USA

```


ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,321
FILING DATE: 25-JUL-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,190
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-204100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-900-321-8

Query Match 26.7%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10

Db 7 PLPP 10

Search completed: November 25, 2003, 20:30:09
Job time : 12.1221 secs